

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 16:01:16 : Search time 81 seconds  
(without alignments)  
21,555 Million cell updates/sec

Title: US-09-787-443-20  
Perfect score: 11  
Sequence: 1 AKKKEQKQNA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 274822

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	21	AA198548 NCAM Igl binding p
2	11	100.0	11	23	ABG69348 Human neural cell
3	5	45.5	13	23	AAE27474 Human keratinocyte
4	5	45.5	13	23	AAE27475 Human keratinocyte
5	5	45.5	13	23	ABG79751 Human keratinocyte
6	5	45.5	13	23	ABG79752 Human keratinocyte
7	5	45.5	13	23	AAU93293 Granulocyte colony
8	4	36.4	8	20	AAW78346 perception sensiti
9	4	36.4	8	20	AAW78347

10	4	36.4	8	21	AAV20444
11	4	36.4	8	22	AA1A774
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17	4	36.4	8	22	AAE38104
18	4	36.4	8	22	AAE38104
19	4	36.4	8	22	AAE38104
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09/787443













PF 05-FEB-2002; 2002WO-EP01175.  
 XX  
 PR 06-FEB-2001; 2001EP-0102574.  
 PR 19-FEB-2001; 2001EP-0103954.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 XX Carr FJ, Carter G, Jones T, Williams S;  
 XX  
 DR WPI: 2002-657523/70.  
 XX  
 XX New modified molecule having the biological activity of keratinocyte  
 PT growth factor (KGF) and being non-immunogenic, for reducing propensity  
 PT of the polypeptide to elicit an immune response upon administration to  
 PT a human subject .  
 XX  
 XX Claim 6: Page 12; 40pp: English.  
 PS  
 CC The invention relates to modified molecules having the biological  
 CC activity of keratinocyte growth factor (KGF) and being non-immunogenic or  
 CC less immunogenic than any non-modified molecule having the same  
 CC biological activity when used in vivo. The modified peptides can then  
 CC elicit an immune response upon administration to a human subject. The  
 CC invention also relates to identifying potential T-cell epitopes within  
 CC the amino acid sequence of the protein and determining binding of the  
 CC peptides to major histocompatibility complex (MHC) molecules using in  
 CC vitro or in silico techniques or biological assays, and designing new  
 CC sequence variants with one or more amino acids within the identified  
 CC potential T-cell epitopes modified to reduce or eliminate the activity of  
 CC the T-cell epitope. This sequence represents a human KGF T-cell epitope  
 CC with MHC Class II binding potential.  
 XX  
 SQ Sequence 13 AA:  
 Query Match: 45.5%; Score 5; EB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KKEQK 7  
 Db 9 KKEQK 13  
 RESULT 6  
 ARG79752  
 ID ARG79752 standard; Peptide: 13 AA.  
 XX  
 AC ARG79752:  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Human keratinocyte growth factor (KGF) T-cell epitope #46.  
 XX  
 KW Human: keratinocyte growth factor; KGF; Major histocompatibility complex;  
 KW MHC; immunomodulatory; T-cell epitope.  
 XX  
 QS Homo sapiens.  
 XX  
 PN WO200262842-A1.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 05-FEB-2002; 2002WO-EP01175.  
 XX  
 PR 06-FEB-2001; 2001EP-0102574.  
 PR 19-FEB-2001; 2001EP-0103954.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 XX Carr FJ, Carter G, Jones T, Williams S;  
 XX  
 DR WPI: 2002-657523/70.  
 XX

PT New modified molecule having the biological activity of keratinocyte  
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 PT a human subject .  
 XX  
 XX Claim 6: Page 12; 40pp: English.  
 PS  
 CC The invention relates to modified molecules having the biological  
 CC activity of keratinocyte growth factor (KGF) and being non-immunogenic or  
 CC less immunogenic than any non-modified molecule having the same  
 CC biological activity when used in vivo. The modified peptides can then  
 CC elicit an immune response upon administration to a human subject. The  
 CC invention also relates to identifying potential T-cell epitopes within  
 CC the amino acid sequence of the protein and determining binding of the  
 CC peptides to major histocompatibility complex (MHC) molecules using in  
 CC vitro or in silico techniques or biological assays, and designing new  
 CC sequence variants with one or more amino acids within the identified  
 CC potential T-cell epitopes modified to reduce or eliminate the activity of  
 CC the T-cell epitope. This sequence represents a human KGF T-cell epitope  
 CC with MHC Class II binding potential.  
 XX  
 SQ Sequence 13 AA:  
 Query Match: 45.5%; Score 5; EB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KKEQK 7  
 Db 9 KKEQK 13  
 RESULT 7  
 ARG79752  
 ID ARG79752 standard; Peptide: 13 AA.  
 XX  
 AC ARG79752:  
 XX  
 DT 02-FEB-2002 (first entry)  
 XX  
 DE Human: keratinocyte growth factor; KGF; Major histocompatibility complex;  
 KW Human: keratinocyte growth factor; KGF; Major histocompatibility complex;  
 KW MHC; immunomodulatory; T-cell epitope.  
 XX  
 QS Homo sapiens.  
 XX  
 PN WO200262842-A1.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 05-FEB-2002; 2002WO-EP01175.  
 XX  
 PR 06-FEB-2001; 2001EP-0102574.  
 PR 19-FEB-2001; 2001EP-0103954.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 XX Carr FJ, Carter G, Jones T, Williams S;  
 XX  
 DR WPI: 2002-657523/70.  
 XX

CC colony stimulating factor receptor (G-CSFR). The compounds contain  
 CC specific sequences of the generic peptides appearing as AAG79402 AAG79406  
 CC and the generic sequences XV\_1XV\_2XV\_4XV\_5XV\_6XV\_7XV\_8 (where  
 CC XV\_1 = E, C, Q, V or Y; XV\_2 = E, A, L, M, S, W or Q; XV\_3 = K, R or D;  
 CC XV\_4 = L, A or Q; XV\_5 = R, A, M, A, E, V, L, G, D, Q or S; XV\_6 = E or  
 CC V; XV\_7 = A or G; and XV\_8 = R, H, G or D) and XVI\_1XVI\_2XVI\_3XVI\_4XVI\_5  
 CC XVI\_6XVI\_7XVI\_8XVI\_9 (where XVI\_1 = A, E or G; XVI\_2 = E, H or D;  
 CC XVI\_3 = R or G; XVI\_4 = K, V, M, N, Q, R, B, L, S or E; XVI\_5 = A, S or  
 CC P; XVI\_6 = E, D, T, Q, K or A; XVI\_7 = R, W, K, L, S, A or G; XVI\_8 = R  
 CC or E; and XVI\_9 = W, G or R). The compounds are used for treating  
 CC conditions associated with depressed neutrophil count, e.g. chemotherapy  
 CC induced neutropenia, AIDS-induced neutropenia or chemotherapy-induced  
 CC pneumonia-induced pneumonia. The compounds are useful as *in vitro* and  
 CC tools for understanding the biological role of granulocyte colony  
 CC stimulating factor (G-CSF) a haematopoietic growth factor and  
 CC cytokine that stimulates neutrophil proliferation and differentiation,  
 CC including evaluation of many factors thought to influence, and be  
 CC influenced by, production of white blood cells, in the development of  
 CC compounds that bind to G-CSFR, as reagents for detecting G-CSF receptor  
 CC or related receptor on living cells, fixed cells, in biological fluids, in  
 CC tissue homogenates or in purified natural biological materials; *in situ*  
 CC staining, fluorescence-activated cell sorting (FACS), western blotting or  
 CC enzyme-linked immunosorbent assay (ELISA); in receptor purification or  
 CC in purifying cells expressing G-CSFR on the cell surface (or inside  
 CC permeabilised cells) as a commercial research reagent for various medical  
 CC and diagnostic uses or to treat a disease that would benefit from the  
 CC ability of a compound to mimic the effects of G-CSF *in vivo*.  
 CC The compounds bind specifically to G-CSFR and allow for studies of  
 CC biological activities mediated by the receptor and for the treatment of  
 CC diseases, disorders and conditions that would benefit from activating or  
 CC inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of  
 CC the invention.

XX Sequence 13 AA:

Query Match 45.5%, Score 17 (E 23), Length 13;  
 Best Local Similarity 100.0%; Pref. No. 5;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKEQ 6  
 DQ 11111  
 DB 1 KKKEQ 5

RESULT 8  
 AAW78346  
 ID AAW78346 standard; peptide; b AA.

XX AAW78346;

AC AAW78346;

DT 27-APR-1995 (first entry)

DE Perception sensitivity inhibitory peptide BRL 3 BP.

XX Perception sensitivity inhibitory peptide; no receptor; no plate

XX hot plate test.

OS Synthetic.

GS Bos taurus.

XX JPT1021298 A.

PN 26-JAN 1999.

XX 02-JUL 1997; 97JP-0176905.

XX 02-JUL 1997; 97JP-0176905.

XX (EISA) EISA CO LTD.

PA WPI: 1999-163218/14.

XX New perception sensitivity inhibitory peptide - useful for

XX PT

PT Inhibiting pain and pain sensation. Tested on prostaglandin synthase  
 XX Example 5; Page 6; 97JP-0176905.  
 ES This peptide represents a polypeptide sensitivity inhibitory peptide of  
 CC the invention. The peptide is derived from the bovine mastocytin gene.  
 CC and corresponds to amino acids 127-137. The peptide is useful for  
 CC inhibiting pain and pain sensation, especially from a hot plate test.

XX Sequence b AA

Query Match 45.5%, Score 17 (E 23), Length 13;  
 Best Local Similarity 100.0%; Pref. No. 5;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKEQ 6  
 DQ 11111  
 DB 1 KKKEQ 5

RESULT 4

AAW78347

ID AAW78347 standard; peptide; b AA.

XX AAW78347;

AC AAW78347;

DT 27-APR-1995 (first entry)

DE Perception sensitivity inhibitory peptide BRL 3 BP.

XX Perception sensitivity inhibitory peptide; no receptor; no plate

XX hot plate test.

OS Synthetic.

GS Bos taurus.

XX JPT1021298 A.

PN 26-JAN 1999.

XX 02-JUL 1997; 97JP-0176905.

XX 02-JUL 1997; 97JP-0176905.

XX (EISA) EISA CO LTD.

PA WPI: 1999-163218/14.

XX New perception sensitivity inhibitory peptide - useful for

XX PT







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XX PA (OKLA:) OKLAHOMA MEDICAL RES FOUND.
XX P1 Harley JB, James JA, Scofield RH;
XX X1 WPI: 2001-335087/35.
XX
XX Generating systemic lupus erythematosus animal model by immunizing
XX non-human animal with non-immunoglobulin peptide having amino acid
XX sequence of self-antigen bound by autoantibody population in early
XX stage of disease
XX
XX Claim 10: Column 100; 63pp; English.
XX
XX The patent discloses a specific method of generating an animal model
XX of systemic lupus erythematosus (SLE), comprising immunising a non-
XX human animal with non-immunoglobulin peptide which comprises an
XX epitope immunoreactive with auto-antibody (AAb) from patient with
XX SLE. The epitope includes a region of self-antigen which is bound
XX by AAb population present in early stage in patient with SLE. The
XX method is used for generating an animal model of SLE. It is useful
XX for screening therapeutics effective in treating autoimmune disorders.
XX (vaccine to block the AAbs produced, by eliciting immune response),
XX and in research on the possible causes of the autoimmune diseases.
XX The method is used to interrupt the course of an autoimmune disease,
XX once autoimmunity against the autoantigen is established. The amino
XX acid sequences are used to make agents for neutralising circulating
XX antibodies or immobilised on substrates in extracorporeal devices for
XX specific removal of AAbs. The reagents identified by using the method
XX are useful in manufacturing and testing autoantigens. The method is
XX useful as models for screening of compounds which induce autoimmunity,
XX inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX in diagnosis of autoimmunity and as therapeutics for the treatment of
XX autoimmune disorders. The present sequence is a peptide from human ribo-
XX nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX of the invention.
XX
XX Sequence 8 AA:
XX
XX Query Match 36.4%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 KEQK 7
XX IIII
XX Db 3 KEQK 6
XX
XX RESULT 15
XX ID AAE08106 standard; peptide; 8 AA.
XX AC AAE08106;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Peptide #5 from human ribonucleoprotein, 60 kD Ro/SSA.
XX
XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
XX autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.
XX
XX OS Homo sapiens.
XX
XX PN US6232522-B1.
XX
XX PD 15-MAY-2001.
XX
XX PF 30-NOV-1993; 93US-0160604.
XX
XX PR 31-JAN-1990; 90US-0472947.
XX PR 31-JAN-1991; 91US-0648205.
XX PR 13-APR-1992; 92US-0867819.

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XX (KLA:) OKLAHOMA MEDICAL RES FOUND.
XX P1 Harley JB, James JA, Scofield RH;
XX X1 WPI: 2001-335087/35.
XX
XX Generating systemic lupus erythematosus animal model by immunizing
XX non-human animal with non-immunoglobulin peptide having amino acid
XX sequence of self-antigen bound by autoantibody population in early
XX stage of disease
XX
XX Claim 10: Column 100; 63pp; English.
XX
XX The patent discloses a specific method of generating an animal model
XX of systemic lupus erythematosus (SLE), comprising immunising a non-
XX human animal with non-immunoglobulin peptide which comprises an
XX epitope immunoreactive with auto-antibody (AAb) from patient with
XX SLE. The epitope includes a region of self-antigen which is bound
XX by AAb population present in early stage in patient with SLE. The
XX method is used for generating an animal model of SLE. It is useful
XX for screening therapeutics effective in treating autoimmune disorders.
XX (vaccine to block the AAbs produced, by eliciting immune response),
XX and in research on the possible causes of the autoimmune diseases.
XX The method is used to interrupt the course of an autoimmune disease,
XX once autoimmunity against the autoantigen is established. The amino
XX acid sequences are used to make agents for neutralising circulating
XX antibodies or immobilised on substrates in extracorporeal devices for
XX specific removal of AAbs. The reagents identified by using the method
XX are useful in manufacturing and testing autoantigens. The method is
XX useful as models for screening of compounds which induce autoimmunity,
XX inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX in diagnosis of autoimmunity and as therapeutics for the treatment of
XX autoimmune disorders. The present sequence is a peptide from human ribo-
XX nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX of the invention.
XX
XX Sequence 8 AA:
XX
XX Query Match 36.4%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 KEQK 7
XX IIII
XX Db 3 KEQK 6
XX
XX RESULT 16
XX ID AAE08135
XX AC AAE08135 standard; peptide; 8 AA.
XX AC AAE08135;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Peptide #54 from human ribonucleoprotein, 60 kD Ro/SSA.
XX
XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
XX autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.
XX
XX OS Homo sapiens.
XX
XX PN US6232522-B1.
XX
XX PD 15-MAY-2001.
XX
XX PF 30-NOV-1993; 93US-0160604.
XX
XX PR 31-JAN-1990; 90US-0472947.
XX PR 31-JAN-1991; 91US-0648205.
XX PR 13-APR-1992; 92US-0867819.

```

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX Harley JB, James JA, Scofield RH;  
 XX WPI: 2001-335087/35.  
 XX Generating systemic lupus erythematosus animal model by immunizing  
 PT non-human animal with non-immunoglobulin peptide having amino acid  
 PT sequence of self-antigen bound by autoantibody population in early  
 PT stage of disease  
 XX  
 XX Example 1: Column 15; 63pp; English.  
 XX The patent discloses a specific method of generating an animal model  
 CC of systemic lupus erythematosus (SLE), comprising immunising a non-  
 CC human animal with non-immunoglobulin peptide which comprises an  
 CC epitope immunoreactive with auto-antibody (AAB) from patient with  
 CC SLE. The epitope includes a region of self-antigen which is bound  
 CC by AAB population present in early stage in patient with SLE. The  
 CC method is used for generating an animal model of SLE. It is useful  
 CC for screening therapeutics effective in treating autoimmune disorders.  
 CC It is useful as a component in a diagnostic assay, as a therapeutic  
 CC (vaccine to block the AABs produced, by eliciting immune response),  
 CC and in research on the possible causes of the autoimmune diseases.  
 CC The method is used to interrupt the course of an autoimmune response.  
 CC Once autoimmunity against the autoantigen is established, the amino  
 CC acid sequences are used to make agents for neutralising circulating  
 CC antibodies or immobilised on substrates in extracorporeal devices for  
 CC specific removal of AABs. The reagents identified by using the method  
 CC are useful in manufacturing and testing autoantigens. The method is  
 CC useful as models for screening of compounds which induce autoimmunity,  
 CC inhibit induction of autoimmunity, suppress autoimmunity, it is useful  
 CC in diagnosis of autoimmunity and as therapeutics for the treatment of  
 CC autoimmune disorders. The present sequence is a peptide from human ribo-  
 CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification  
 CC of the invention.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 36.48; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 4,3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;  
 QY 7 KQRN 10  
 DB IIII  
 5 KQRN 8  
 RESULT 17  
 AAE08136  
 ID AAE08136 standard; peptide: 8 AA.  
 XX  
 AC AAE08136;  
 XX  
 DT 01-NOV-2002 (first entry)  
 XX  
 DE Peptide #35 from human ribonucleoprotein, 60 kD Ro/SSA.  
 XX  
 KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;  
 KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6232522-B1.  
 XX  
 PD 15-MAY-2001.  
 XX  
 PF 30-NOV-1993; 93US-0160604.  
 XX  
 PR 31-JAN-1990; 90US-0472947.  
 PR 31-JAN-1991; 91US-0648205.  
 PR 13-APR-1992; 92US-0867819.

XX  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX Harley JB, James JA, Scofield RH;  
 XX WPI: 2001-335087/35.  
 XX Generating systemic lupus erythematosus animal model by immunizing  
 PT non-human animal with non-immunoglobulin peptide having amino acid  
 PT sequence of self-antigen bound by autoantibody population in early  
 PT stage of disease  
 XX  
 XX Example 1: Column 15; 63pp; English.  
 XX The patent discloses a specific method of generating an animal model  
 CC of systemic lupus erythematosus (SLE), comprising immunising a non-  
 CC human animal with non-immunoglobulin peptide which comprises an  
 CC epitope immunoreactive with auto-antibody (AAB) from patient with  
 CC SLE. The epitope includes a region of self-antigen which is bound  
 CC by AAB population present in early stage in patient with SLE. The  
 CC method is used for generating an animal model of SLE. It is useful  
 CC for screening therapeutics effective in treating autoimmune disorders.  
 CC It is useful as a component in a diagnostic assay, as a therapeutic  
 CC (vaccine to block the AABs produced, by eliciting immune response),  
 CC and in research on the possible causes of the autoimmune diseases.  
 CC The method is used to interrupt the course of an autoimmune response.  
 CC Once autoimmunity against the autoantigen is established, the amino  
 CC acid sequences are used to make agents for neutralising circulating  
 CC antibodies or immobilised on substrates in extracorporeal devices for  
 CC specific removal of AABs. The reagents identified by using the method  
 CC are useful in manufacturing and testing autoantigens. The method is  
 CC useful as models for screening of compounds which induce autoimmunity,  
 CC inhibit induction of autoimmunity, suppress autoimmunity, it is useful  
 CC in diagnosis of autoimmunity and as therapeutics for the treatment of  
 CC autoimmune disorders. The present sequence is a peptide from human ribo-  
 CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification  
 CC of the invention.  
 XX  
 XX Sequence 4 AA;  
 SQ  
 Query Match 40.4%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 9,4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;  
 QY 7 KQRN 10  
 DB IIII  
 4 KQRN 7  
 RESULT 18  
 AAE08137  
 ID AAE08137 standard; peptide: 4 AA.  
 XX  
 AC AAE 4142;  
 XX  
 DT 01-NOV-2002 (first entry)  
 XX  
 DE Peptide #35 from human ribonucleoprotein, 60 kD Ro/SSA.  
 XX  
 KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;  
 KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.  
 XX  
 OS Homo sapiens  
 XX  
 PN US6232522-B1.  
 XX  
 PD 15-MAY-2001.  
 XX  
 PF 4 KQRN 1993; 93US-0160604  
 XX  
 PR 31-JAN-1990; 90US-0472947.  
 PR 31-JAN-1991; 91US-0648205.  
 PR 13-APR-1992; 92US-0867819.

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XX PA (OKLA.) OKLAHOMA MEDICAL RES FOUND.
XX PI Harley JB, James JA, Scofield RH;
XX DR WPI: 2001-335087/35.
XX PT Generating systemic lupus erythematosus animal model by immunizing
XX PT non-human animal with non-immunoglobulin peptide having amino acid
XX PT sequence of self-antigen bound by autoantibody population in early
XX PT stage of disease
XX PS Example 1; Column 15; 63pp; English.
XX CC The patent discloses a specific method of generating an animal model
XX CC of systemic lupus erythematosus (SLE), comprising immunising a non-
XX CC human animal with non-immunoglobulin peptide which comprises an
XX CC epitope immunoreactive with auto-antibody (AAb) from patient with
XX CC SLE. The epitope includes a region of self-antigen which is bound
XX CC by AAb population present in early stage in patient with SLE. The
XX CC method is used for generating an animal model of SLE. It is useful
XX CC for screening therapeutics effective in treating autoimmune disorders.
XX CC It is useful as a component in a diagnostic assay, as a therapeutic
XX CC vaccine to block the AAbs produced, by eliciting immune response),
XX CC and in research on the possible causes of the autoimmune diseases.
XX CC The method is used to interrupt the course of an autoimmune response,
XX CC once autoimmunity against the autoantigen is established. The amino
XX CC acid sequences are used to make agents for neutralising circulating
XX CC antibodies or immobilised on substrates to ex vivo removal devices for
XX CC specific removal of AAbs. The reagents identified by using the method
XX CC are useful in manufacturing and testing autoantigens. The method is
XX CC useful as models for screening of compounds which induce autoimmunity,
XX CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX CC in diagnosis of autoimmunity and as therapeutics for the treatment of
XX CC autoimmune disorders. The present sequence is a peptide from human ribo-
XX CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX CC of the invention.
XX SQ Sequence 8 AA:
      Query Match: 36.4%; Score 4; PR 22; Length 4;
      Best Local Similarity 100.0%; Prod. No. 9,36-05;
      Matches 4; Conservative 0; Mismatches 0; Gaps 0;
QY 7 QRN 10
DB 3 QRN 6
      1111
      3 QRN 6

RESULT 19
AAE08118
1D AAE08118 standard; peptide: 8 AA.
XX AC AAE08118;
XX DT 01-NOV-2001 (first entry)
XX DE Peptide #37 from human ribonucleoprotein, 60 kD Ro/SSA.
XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
XX KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.
XX OS Homo sapiens.
XX XX
XX PN US6232522-B1.
XX PD 15-MAY-2001.
XX PF 30-NOV-1993; 93US-0160604.
XX PR 31-JAN-1990; 90US-0472947.
XX PR 31-JAN-1991; 91US-0648205.
XX PR 13-APR-1992; 92US-0867819.

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XX PA (OKLA.) OKLAHOMA MEDICAL RES FOUND.
XX PI Harley JB, James JA, Scofield RH;
XX DR WPI: 2001-335087/35.
XX PT Generating systemic lupus erythematosus animal model by immunizing
XX PT non-human animal with non-immunoglobulin peptide having amino acid
XX PT sequence of self-antigen bound by autoantibody population in early
XX PT stage of disease
XX PS Example 1; Column 15; 63pp; English.
XX CC The patent discloses a specific method of generating an animal model
XX CC of systemic lupus erythematosus (SLE), comprising immunising a non-
XX CC human animal with non-immunoglobulin peptide which comprises an
XX CC epitope immunoreactive with auto-antibody (AAb) from patient with
XX CC SLE. The epitope includes a region of self-antigen which is bound
XX CC by AAb population present in early stage in patient with SLE. The
XX CC method is used for generating an animal model of SLE. It is useful
XX CC for screening therapeutics effective in treating autoimmune disorders.
XX CC It is useful as a component in a diagnostic assay, as a therapeutic
XX CC vaccine to block the AAbs produced, by eliciting immune response),
XX CC and in research on the possible causes of the autoimmune diseases.
XX CC The method is used to interrupt the course of an autoimmune response,
XX CC once autoimmunity against the autoantigen is established. The amino
XX CC acid sequences are used to make agents for neutralising circulating
XX CC antibodies or immobilised on substrates to ex vivo removal devices for
XX CC specific removal of AAbs. The reagents identified by using the method
XX CC are useful in manufacturing and testing autoantigens. The method is
XX CC useful as models for screening of compounds which induce autoimmunity,
XX CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX CC in diagnosis of autoimmunity and as therapeutics for the treatment of
XX CC autoimmune disorders. The present sequence is a peptide from human ribo-
XX CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX CC of the invention.
XX SQ Sequence 8 AA:
      Query Match: 36.4%; Score 4; PR 22; Length 4;
      Best Local Similarity 100.0%; Prod. No. 9,36-05;
      Matches 4; Conservative 0; Mismatches 0; Gaps 0;
QY 7 QRN 10
DB 3 QRN 6
      1111
      3 QRN 6

RESULT 20
AAE08119
1D AAE08119 standard; peptide: 8 AA.
XX AC AAE08119;
XX DT 01-NOV-2001 (first entry)
XX DE Peptide #38 from human ribonucleoprotein, 60 kD Ro/SSA.
XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
XX KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.
XX OS Homo sapiens.
XX XX
XX PN US6232522-B1.
XX PD 15-MAY-2001.
XX PF 30-NOV-1993; 93US-0160604.
XX PR 31-JAN-1990; 90US-0472947.
XX PR 31-JAN-1991; 91US-0648205.
XX PR 13-APR-1992; 92US-0867819.

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KW Nociceptin; hypersensitivity inhibitor; analgesic; pain relief; bovine.  
XX  
OS Bos taurus.  
XX  
PN JP2001354696-A.  
XX  
PD 25-DEC-2001.  
XX  
PF 08-JUN-2000; 2000JP-0171386.  
XX  
PR 08-JUN-2000; 2000JP-0171386.  
XX  
PA (NNSH) NIPPON SHINYAKU CO LTD.  
XX  
DR WP1; 2002-262912/31.  
XX  
PT Hypersensitivity inhibitory peptides are new -  
XX  
PS Example 13; Page 7; 8pp; Japanese.  
XX  
CC This invention describes novel nociceptin analogues which inhibit  
CC nociceptin-induced hypersensitivity and have analgesic activity. The  
CC products of the invention can be used for pain relief. This sequence  
CC represents a bovine nociceptin analogue described in the method of the  
CC invention.  
XX  
SQ Sequence 8 AA:  
Query Match 36.4%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 EQKQ 8  
DB 3 EQKQ 6  
RESULT 29  
AA013980  
ID AA013980 standard; Peptide: 8 AA.  
XX  
AC AA013980;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Cysteine-X-Cysteine chemokine receptor 4 P12 domain binding peptide.  
XX  
KW Cysteine-X-Cysteine Chemokine Receptor 4; CXCR4 binding peptide;  
KW chemoattractant cytokine; human immunodeficiency virus; HIV;  
KW HIV envelope glycoprotein; cellular CD4 receptor; env gene; gp120;  
KW gp41; CD4+ target cell; HIV-infected cell; CXCR4-binding compound;  
KW acquired immunodeficiency syndrome; AIDS; P12 binding domain;  
KW oriented linear peptide library.  
XX  
OS Synthetic.  
XX  
PN WO200170768-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US09160.  
XX  
PR 21-MAR-2000; 2000US-190945P.  
XX  
PR 21-MAR-2000; 2000US-190956P.  
XX  
PR 21-MAR-2000; 2000US-191299P.  
XX  
PR 20-MAR-2001; 2001US-081344B.  
XX  
PR 20-MAR-2001; 2001US-0813651.  
XX  
PR 20-MAR-2001; 2001US-0813653.  
XX  
PA (CONS-) CONSENSUS PHARM INC.  
XX  
PI Nestor JJ, Wilson CJ, Tan Hehir CA, Kates SA;  
XX

sk WP1; 2002-00354696-A.  
XX  
PT Identifying agents that bind to CXCR4 chemokine receptor 4 useful for  
PT treatment and prevention of acquired immunodeficiency syndrome;  
PT comprises screened compound library for members that bind to the  
PT receptor.  
XX  
PS Example 13; Page 7; 8pp; English.  
XX  
CC The invention relates to a method of identifying Cysteine-X-Cysteine  
CC chemokine receptor 4 (CXCR4) binding compounds. The method comprises  
CC testing and selecting compounds in a library for their ability to bind to  
CC CXCR4. Chemokines (chemoattractant cytokines) regulate the movement and  
CC biological activities of leukocytes in many disease states. CXCR4  
CC acts as a co-receptor for the immunodeficiency virus (HIV) as it  
CC interacts with the HIV envelope glycoproteins and the cellular CD4  
CC receptor, to facilitate HIV entry into cells. The HIV glycoproteins  
CC (encoded by the *env* gene) are translated as a precursor (gp160) which is  
CC subsequently cleaved into gp120 and gp41. gp120 binds to CXCR4 and the  
CC CD4 receptor present on the surface of susceptible CD4+ target cells,  
CC causing the virus to fuse with the cell membranes and thereby  
CC facilitating entry of the virus into the cell. The eventual expression of  
CC the env product on the surface of the HIV-infected cell enables the cell  
CC to fuse with uninfected target cells, thereby spreading the infection. The  
CC CXCR4 binding compounds of the invention inhibit the entry of HIV into  
CC the CD4+ cell and therefore are useful in the prevention of HIV infection  
CC and the treatment and prevention of acquired immunodeficiency syndrome  
CC (AIDS). The present sequence represents a peptide that binds to the CXCR4  
CC binding domain. In this sequence was isolated from an oriented linear  
CC peptide library as part of an example of the invention.  
XX  
SQ Sequence 8 AA:  
Query Match 36.4%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KKKE 5  
DB 2 KKKE 5  
HFS014 49  
AA052777  
ID AA052777 standard; Peptide: 4 AA.  
XX  
AC AA052777;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE P12 domain binding peptide.  
XX  
KW CXCR4; CX chemokine receptor 4; human HIV infected cell;  
KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
KW directed screening; identified binding domain.  
XX  
OS Synthetic.  
XX  
PN WO200171446-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US09160.  
XX  
PR 21-MAR-2000; 2000US-190945P.  
XX  
PR 21-MAR-2000; 2000US-190956P.  
XX  
PR 21-MAR-2000; 2000US-191299P.  
XX  
PR 20-MAR-2001; 2001US-081344B.  
XX  
PR 20-MAR-2001; 2001US-0813651.  
XX  
PR 20-MAR-2001; 2001US-0813653.  
XX  
PA (CONS-) CONSENSUS PHARM INC.  
XX  
PI Nestor JJ, Wilson CJ, Tan Hehir CA, Kates SA;  
XX

PI Nestor JJ, Wilson CJ, See RH, Tan Behr CA;  
 XX WPI: 2002-010610/01.  
 XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
 PT comprises binding a molecule from library to a molecule having binding  
 PT property corresponding to CCR5 and identifying bound molecule  
 XX  
 PS Example 1: Page 19; 50pp: English.  
 XX  
 CC The invention relates to a method for identifying a binding compound  
 CC for CC chemokine receptor 5 (CCR5). The method involves screening a  
 CC library of test molecules (particularly peptides) with immobilised CCR5,  
 CC and then identifying those molecules which bind. The invention also  
 CC relates to CCR5-binding molecules identified using the method of the  
 CC invention, methods for identifying consensus motifs for CCR5-binding  
 CC peptides, a transfer vector encoding tagged CCR5, a computer-aided  
 CC method for determining the relative binding affinity of a test molecule  
 CC to CCR5 and a computer aided drug screening assay that utilises the  
 CC three-dimensional structure of CCR5. Compounds identified using the  
 CC methods of the invention are useful for treating or preventing HIV  
 CC (human immunodeficiency virus) infection or AIDS (acquired  
 CC immunodeficiency syndrome) in a patient. The methods of the invention  
 CC may also be used to identify agonists or antagonists of the interaction  
 CC of CCR5 with its natural ligand, and to determine a binding motif for  
 CC CCR5. Sequences AAM52777-AAM52783 represent peptides or peptide libraries  
 CC able to bind to known protein binding domains which were used in an  
 CC in an exemplification of the invention.  
 XX  
 XX Sequence 8 AA:

Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
 IIII  
 DB 2 KKKE 5

RESULT 31  
 ABH74588  
 ID ABH74588 standard; Peptide; 8 AA.  
 XX  
 AC ABH74588;  
 XX  
 DT 18-APR-2002 (first entry)  
 XX  
 DE Transcription factor nuclear localisation signal peptide SEQ ID NO:352.  
 XX  
 KW Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; anticancer; solid tumour;  
 KW peptide; lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W0200193836-A2.  
 PN  
 XX 13-DEC-2001.  
 PD  
 XX 08-JUN-2001; 2001WO-US18657.  
 PF  
 XX 09-JUN-2000; 2000US-210525P.  
 PR  
 XX (HCU:/) BOULIKAS T.  
 PA  
 XX Boulikas T;  
 PI  
 XX WPI: 2002-164295/21.  
 DR  
 XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted

PI Liposome complexes  
 XX

Claim 14: Page 24; 30pp: English

CC The present invention describes a method for producing micelles with  
 CC entraped therapeutic agents. The method comprises: (i) combining  
 CC negatively charged agent with a cationic lipid in a ratio where a ratio  
 CC of the negatively charged agent to the cationic lipid is at least 1:1;  
 CC lipid molecules to form an electrostatic complex in which a  
 CC cationic lipid (2) is in the micelle complex of (a) with fusogenic  
 CC karyophilic peptide conjugates in a 1:0.5:1 ratio, therefore producing  
 CC micelles with entraped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent *in vivo*, comprising the administration  
 CC of the micelle. Also described is a method for specifically targeting  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic karyophilic peptides. The micelles produced can have cytotoxic  
 CC and anti-tumour activities. The peptide-lipid-polynucleotide conjugates  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed towards methods for producing peptide-lipid conjugates.  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic activity in eradicating solid tumours.  
 CC Included herein is a method for producing micelles or peptide conjugates  
 CC ABB74588. ABB74588 is a method for the encapsulation of the present  
 XX invention.  
 XX Sequence 8 AA.

Query Match 36.4%; Score 4; DB 23; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
 IIII  
 DB 2 KKKE 5

RESULT 32  
 ABH74588  
 ID ABH74588 standard; Peptide; 8 AA.  
 XX  
 AC ABH74588;  
 XX  
 DT 18-APR-2002 (first entry)  
 XX  
 DE Transcription factor nuclear localisation signal peptide SEQ ID NO:352.  
 XX  
 KW Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; anticancer; solid tumour;  
 KW peptide; lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W020193836-A2  
 PN  
 XX 13-DEC-2001  
 PD  
 XX 08-JUN-2001; 2001WO-US18657  
 PF  
 XX 09-JUN-2000; 2000US-210525P  
 PR  
 XX (HCU:/) BOULIKAS T  
 PA  
 XX Boulikas T  
 PI  
 XX WPI: 2002-164295/21  
 DR  
 XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes  
 XX  
 PS Claim 14: Page 27; 10pp: English.



XX The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 40-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (1) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelles. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and anticancer activities. The micelles produced can have cytostatic  
 CC and anticancer activities. The peptide lipopolymer-micelle complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide lipid-polymeroid  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumors  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74235 to ABB74255 are used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;

Query Match 36.43; Score 4; DB 2; Length 8;

Best Local Similarity 100.00; Prod. No. 9.4e+05; Mismatches 0; Gaps 0;

QY 2 KKKE 5  
 DB IIII  
 5 KKKE 8

RESULT 43

ABB74530  
 ID ABB74630 standard; Peptide: 8 AA.

AC ABB74630;

XX 18-APR-2002 (first entry)

XX Transcription factor nuclear localisation signal peptide SEQ ID NO:364.

XX Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; antitumor; solid tumor;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.

XX *Xenopus* sp.

OS

PN W0200193836-A2.

XX 13-DEC-2001.

PF 08-JUN-2001; 2001WO-US18657.

PR 09-JUN-2000; 2000US-210525P.

XX (BRIEF) R001IRAS T.

XX R001IRAS T.

XX WPI: 2002-164295/21.

XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes.

XX Claim 14; Page 77; 107pp; English.

XX The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining

XX neoplastic solid tumors with a cationic lipid in a ratio where 40-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (1) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelles. ABB74235 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and anticancer activities. The micelles produced can have cytostatic  
 CC and anticancer activities. The peptide lipopolymer-micelle complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide lipid-polymeroid  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumors  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74235 to ABB74255 are used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;

Query Match 36.43; Score 4; DB 2; Length 8;

Best Local Similarity 100.00; Prod. No. 9.4e+05;

Mismatches 0; Gaps 0;

QY 2 KKKE 5

DB IIII

5 KKKE 8

RESULT 43

ABB74235

XX ABB74235 standard; Peptide: 8 AA.

XX ABB74235;

XX 18-APR-2002 (first entry)

XX Synthesis of transcription factor nuclear localisation signal peptide SEQ ID NO:364.

XX Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; antitumor; solid tumor;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.

XX *Xenopus* sp.

OS

PN W0200193836-A2.

XX 13-DEC-2001.

PF 08-JUN-2001; 2001WO-US18657.

PR 09-JUN-2000; 2000US-210525P.

XX (BRIEF) R001IRAS T.

XX R001IRAS T.

XX WPI: 2002-164295/21.

XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes.

XX Claim 14; Page 77; 107pp; English.

XX The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining

XX The invention relates to extraction of an anti-apoptotic composition from  
 CC a protein isolate or a liquid mixture (e.g. soybean lexitrin) involving  
 CC mixing the protein isolate and/or liquid mixture in an aqueous solution  
 CC not containing an organic solvent and separating the aqueous solution  
 CC containing the anti-apoptotic composition from insoluble material.  
 CC The anti-apoptotic composition is useful for treating or preventing an  
 CC adverse condition associated with apoptosis, such as gastrointestinal  
 CC disorder e.g. (diarrhoea, ulcers, colitis, parasite induced damage and  
 CC gastroenteritis), deleterious dermatological conditions,  
 CC immunosuppression, or immunodeficiency, reperfusion damage resulting from  
 CC ischaemia, cardiovascular disorders, transplantation, wound healing,  
 CC tissue rejection and Alzheimer's disease, damage to the intestinal  
 CC mucosa, radiation-induced damage and gastro-intestinal perturbation  
 CC caused by viral and bacterial infection. The anti-apoptotic composition  
 CC is also useful for therapeutic, medicinal and nutritional purposes,  
 CC for preventing weight loss and nausea and to prevent hair loss.  
 CC The present sequence is the N-terminal sequence of a protein (p34  
 CC probable thiol protease precursor) isolated from soybean lexitrin and  
 CC representing a potential anti-apoptotic agent.  
 XX  
 SQ Sequence 8 AA:

Query Match 36.4% Score 41: 284 241: Domain 30  
 Best Local Similarity 100.0%: Pred. N: 1, 6, 15

Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 8 KKEQ 6  
 DQ 4 KKEQ 7  
 1111

# RESULTS

ABG71968

ID AKG71968 standard; peptide: 8 AA.

AC AKG71968:

XX 28-JAN-2003 (first entry)

DE N terminal peptide from soybean water extract (lexitin) #6.

XX Soybean; soy water extract; lexitrin; SDAF; apoptosis; plant;  
 KW soy-derived anti-apoptotic fraction; anti-inflammatory; anti-inflammatory;  
 KW dermatological; anti-apoptotic composition; gastrointestinal disorder;  
 KW diarrhoea; anti-cancer treatment side effect; HIV side effect; AIDS;  
 KW human immunodeficiency virus; acquired immunodeficiency syndrome;  
 KW surgical lavage solution; dermatological condition;  
 KW p34 probable thiol protease precursor.

XX Glycine max.

XX US6413556-B1.

XX 02-JUL-2002.

XX 07-JAN-2000: 2000US-0479431.

XX 08-JAN-1999: 99US-115102P.

XX (SKYH-) SKY HIGH LLC.

XX Bathurst IC, Foehr MW.

XX WPI: 2003-074020/07.

XX Aqueous anti-apoptotic compositions for the treatment of chemotherapy  
 PT side-effects, and other gastrointestinal disorders contain plant  
 PT protein isolates and lipids

PS Example 1: Column 13: 14pp: English.

XX The invention relates to extracting an anti-apoptotic composition from a

CC protein isolate derived from a protein isolate and/or a soy oil  
 CC mixture or raises mixing a soy oil isolate and/or a soy lipid mixture  
 CC which has not been previously treated with an aqueous solvent which contains a  
 CC organic solvent and separating the aqueous solvent from the soy lipid  
 CC mixture. The soy protein isolate is derived from soy water extract known as  
 CC lexitrin and the soy lipid isolate is known as an SDAF.  
 CC (soy-derived anti-apoptotic fraction) the anti-apoptotic composition is  
 CC useful in the treatment or prevention of an adverse condition associated  
 CC with gastroenteritis, deleterious dermatological conditions,  
 CC immunosuppression, or immunodeficiency, reperfusion damage resulting from  
 CC and tissue rejection. The soy isolate is soybean lexitrin and SDAF (soybean  
 CC derived anti-apoptotic fraction) which is caused by e.g. perturbation of  
 CC parasites and/or the inhibition of surgical lavage solution in the  
 CC protection of tissues and organs during surgery and transplantation.  
 CC procedures, the composition may also be useful for dermatological  
 CC conditions, such as weight loss and nausea and to prevent hair loss.  
 CC The present sequence is the N-terminal sequence of a protein (p34  
 CC of livestock solution) isolated from soybean lexitrin and/or treatment  
 CC of livestock solution isolated from soybean lexitrin, which can result in  
 CC considerable loss of weight loss and/or nausea. The present sequence  
 CC is an N-terminal sequence of a protein corresponding to p34 probably this  
 CC is a protease precursor.

XX Sequence 8 AA

Query Match 36.4% Score 41: 284 241: Domain 30

Best Local Similarity 100.0%: Pred. N: 1, 6, 15

Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 8 KKEQ 6  
 DQ 4 KKEQ 7  
 1111

# RESULTS

ABG71968

ID AKG71968 standard; peptide: 8 AA.

AC AKG71968:

XX 28-JAN-2003 (first entry)

DE N terminal peptide from soybean water extract (lexitin) #6.

XX Soybean; soy water extract; lexitrin; SDAF; apoptosis; plant;  
 KW soy-derived anti-apoptotic fraction; anti-inflammatory; anti-inflammatory;  
 KW dermatological; anti-apoptotic composition; gastrointestinal disorder;  
 KW diarrhoea; anti-cancer treatment side effect; HIV side effect; AIDS;  
 KW human immunodeficiency virus; acquired immunodeficiency syndrome;  
 KW surgical lavage solution; dermatological condition;  
 KW p34 probable thiol protease precursor.

XX Glycine max.

XX US6413556-B1.

XX 02-JUL-2002.

XX 07-JAN-2000: 2000US-0479431.

XX 08-JAN-1999: 99US-115102P.

XX (SKYH-) SKY HIGH LLC.

XX Bathurst IC, Foehr MW.

XX WPI: 2003-074020/07.

XX Aqueous anti-apoptotic compositions for the treatment of chemotherapy  
 PT side-effects, and other gastrointestinal disorders contain plant  
 PT protein isolates and lipids

PS Example 1: Column 13: 14pp: English.

XX The invention relates to extracting an anti-apoptotic composition from a

XX	SQ	Sequence	9 AA;
		Query Match	36.4%, Score 4; DB 16; Length 9;
		Best Local Similarity	100.0%; Pred. No. 9, 4e-05;
		Matches	4; Conservative 0; Mismatches 0; Gaps 0;
OY		4 KEUK 7	
DB		4 KEOK 7	
RESULT 47			
AAW24434			
ID		AAW24434 standard; peptide: 9 AA.	
XX	AC	AAW24434;	
XX	AC		
DT		30-sep-1997 (first entry)	
XX			
DE		K4, a nucleic acid (NA) binding peptide used in NA delivery to cells.	
XX			
NK		Nucleic acid transporter; gene therapy; binding complex; lysis agent	
KW		JIS-1; K8; alpha helix; endosome; lysosomal membrane targeting;	
XX			
OS		Synthetic.	
XX			
PN		WP9640958-A1.	
XX			
PD		19 DEC-1996.	
XX			
Pf		23-APR-1996; 96WO-US05679.	
XX			
PR		07-JUN-1995; 95US-0484777.	
XX			
PA		(BAYJ ) BAYLOR COLLEGE MEDICINE.	
XX			
Pi		Smith LC, Sparrow JT, Woo SL;	
XX		WPI; 1997-052345/05.	
XX			
Pt		Nucleic acid transporter useful in gene therapy - contains binding	
Pt		complex associated with surface and nuclear ligands and lysis agent	
XX			
PS		Disclosure: Page 49; 125pp; English.	
XX			
CC		AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both	
CC		condensing and stabilising a NA. The peptides can be conjugated to a	
CC		lytic peptide to form a nucleic acid transporter system. The lysis agent	
CC		forms an alpha-helical structure. The transporter system is used to	
CC		deliver nucleic acid to a cell and for treating humans by gene therapy.	
CC		By taking advantage of the characteristics of both the lysis agents	
CC		and the binding molecules, delivery of the nucleic acid is enhanced.	
CC		Specific lysis agents are capable of releasing the nucleic acid	
CC		into the cellular interior from the endosome. Release is efficient	
CC		without endosomal/lysosomal degradation. Once released the binding	
CC		complexes help target the nucleic acid to the nucleus.	
XX			
SQ		Sequence	9 AA;
		Query Match	36.4%, Score 4; DB 16; Length 9;
		Best Local Similarity	100.0%; Pred. No. 9, 4e-05;
		Matches	4; Conservative 0; Mismatches 0; Gaps 0;
Oy		I AKKK 4	
Db		I AKKK 6	
RESULT 48			
AAW78352			
ID		AAW78352 standard; peptide: 9 AA.	
XX			

[illegible][illegible]

XX WPI: 2000-292880/25.  
XX  
XX New antibodies useful in detecting apoptosis and diagnosis of  
PT conditions such as cancer, specifically recognize the new amino  
PT terminus of a protein cleaved by a protease during apoptosis.  
XX  
XX Claim 6; Page 40; 66pp; English.  
XX  
XX This sequence represents a fragment of the amino terminus sequence of  
CC poly ADP-ribose polymerase (PARP) after it has been cleaved during  
CC apoptosis. PARP is an enzyme associated with DNA repair. Cleavage of the  
CC PARP protein (by a caspase) into fragments contributes to the  
CC fragmentation of DNA that is characteristic of apoptosis. Identification  
CC of cells containing PARP fragments is an indication of apoptosis. The  
CC invention relates to an antibody that is immunoreactive with a neopeptide  
CC that produced in a cell undergoing apoptosis (e.g. a PARP fragment such as  
CC that represented by the present sequence). The antibody specifically  
CC recognises the new amino terminus of a protein cleaved at a cleavage site  
CC by a protease, and is not immunoreactive with the protein prior to  
CC cleavage. The antibodies are useful for detecting apoptosis in a cell or  
CC groups of cells, especially human leukaemia HL60 or Jurkat cells, by  
CC contacting the antibodies (optionally bound to a hapten, enzyme,  
CC radioactive, fluorescent or luminescent label) with a protein sample or a  
CC cell or tissue sample containing the neopeptide and detecting any binding  
CC activity. The antibody is also useful for diagnosing, from patient cell  
CC or tissue samples, disorders and diseases associated with apoptosis or  
CC the inability of cells to undergo apoptosis such as cancer,  
CC neurodegeneration, autoimmunity or heart disease. The antibodies are also  
CC useful for screening for inhibitors and/or inducers of apoptosis, by  
CC exposing two samples to conditions known to activate apoptosis,  
CC contacting the first sample with a test compound, contacting both samples  
CC with the antibody and detecting and comparing the binding of the antibody  
CC to the neopeptide in the two samples.  
XX  
XX  
SQ Sequence 9 AA:  
Query Match 36.4%; Score 4; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 36-95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AKKK 4  
Db 6 AKKK 9  
RESULT 40  
AAY51591  
ID AAY51591 standard; peptide; 9 AA.  
XX  
XX AAY51591:  
XX  
XX 25-MAY-2000 (first entry)  
XX  
XX HIV-1 derived gp120 peptide fragment #3.  
XX  
XX Plastic carrier surface; detection: gp120.  
XX  
XX Human immunodeficiency virus type 1.  
XX  
XX W0200005584-A1.  
XX  
XX 03-FEB-2000.  
XX  
XX 21-JUL-1999; 99WO-NL00470.  
XX  
XX 21-JUL-1998; 98NL-1009703.  
XX  
XX (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOEK.  
XX  
XX Puijk WC;  
XX  
XX WPI: 2000-182757/16.  
DR

XX  
PT Ultra flat plastic carrier surfaces by molding on to smooth  
PT non adhesive surfaces e.g. fused silica, and release, can carry  
PT active groups for biological and phys. also form substrate after size  
PT wells suitable for micro-printed techniques.  
XX  
XX Disclosure: Fig 9, 4pp; Eng. Lab.  
XX  
XX This invention describes a novel method for the manufacture of ultra  
CC flat plastic carrier surfaces, by molding on to a very smooth auxiliary  
CC surface, treating the plastic so that the surface roughness of the side  
CC facing the auxiliary is reduced, and removal coupling of chemical and  
CC biochemical analyses via excitation through active groups on the  
CC plastic surface. Surfaces of plastic suitable for microjet printing  
CC techniques. Examples of applications of the surface include  
CC investigations of biological materials: peptides, proteins, saccharides,  
CC cells, viruses, enzymes, and the reaction carrying polymers, e.g. DNA or  
CC RNA, or their fragments, or optically attached via linkers, detection  
CC and determination of various biological interest can be carried out as a  
CC standard procedure, e.g. in SA, fluorescence, color, or radiation, except  
CC that very small amounts can be detected, investigated, determined, etc.  
CC The surfaces can be used as a substrate for hemispheres of the varying  
CC size, hemispheres of varying size, hemispheres of the varying  
CC size, the hemispheres of the varying size, but it can find very small  
CC amounts of materials, e.g. peptides, which can be detected, polymerized,  
CC when also together, in the surface by microscopy and/or photo-  
CC e.g. a chemical scanning without interference from bumps and humps  
CC caused by the scanning. AAY51591/4 represent peptide fragments  
CC derived from the human immunodeficiency virus type 1 gp120 protein which  
CC are used to illustrate the method of the invention.  
XX  
XX Sequence 9 AA:  
Query Match 36.4%; Score 4; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 36-95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AKKK 4  
Db 6 AKKK 9  
RESULT 41  
AAB85065  
ID AAB85065 standard; peptide; 9 AA.  
XX  
XX AAB85065:  
XX  
XX 05-AUG-2000 (first entry)  
XX  
XX N-terminal S-benzyl-L-homoserine peptide #5.  
XX  
XX Copolymer amino-derivative hydroxy derivative, this ester, two other.  
XX  
XX Synthetic  
XX  
XX Key: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1599, 1600, 1601, 1602, 1603, 1604, 1605, 1606, 1607, 1608, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954,

PI Galt MJ, Stetsenko D;  
 DR WPI: 2001-367105/38.  
 XX Method for coupling molecules, e.g. peptides and oligonucleotides, and  
 PT new intermediates and reagents  
 XX Example 3; Page 27; 39pp; English.  
 PS The invention relates to methods for coupling molecules. One method of  
 CC linking an amine derivative with a hydroxy derivative comprises reacting  
 CC an alkyl or aryl thio ester with an amino thioether. The compounds of the  
 CC invention are useful e.g. for linking a peptide and an oligonucleotide.  
 CC Sequences AAB8501-59 represent peptide N-terminal S-benzyl thio esters.  
 XX Sequence 9 AA;  
 SQ

Query Match 36.4%; Score 4; DR 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 DB IIII  
 2 AKKK 5

RESULT 42  
 ID AAB67921  
 XX AC AAB6792: standard; peptide; 9 AA.  
 AC AAB67921;  
 DT 29-JUN-2001 (first entry)  
 XX DE Formula for heparin affinity regulatory peptide anionic peptides.  
 XX Heparin affinity regulatory peptide; HARP; anionic peptide; HIV;  
 KW immune response; cellular growth; cellular regeneration; muscle cell;  
 KW cicatrization; immunosuppressive disease; human immunodeficiency virus;  
 KW HIV infection; antiviral.  
 XX Synthetic.  
 QS

Key Location/Qualifiers  
 FT Misc-difference 1 /note- "any amino acid; represents 0-20, where the  
 FT sum of the residues represented by amino acids  
 FT 1 and 9 is 0-20, preferably 0-15, and most  
 FT preferably 0-10"  
 FT Misc-difference 9 /note- "any amino acid; represents 0-20, where the  
 FT sum of the residues represented by amino acids  
 FT 1 and 9 is 0-20, preferably 0-15, and most  
 FT preferably 0-10"  
 XX W0200127136-A2.  
 XX 19-APR-2001.  
 XX 06-OCT-2000; 2000WO-FR02786.  
 XX 12-OCT-1999; 99FR-0012714.  
 XX (CNRS ) CNRS CENT NAT RECH SCI  
 XX Barritault D, Achour A, Courty J;  
 XX WPI: 2001-281970/29.  
 XX New Heparin Affinity Regulatory Peptide anionic peptides, useful for  
 PT regenerating muscle cells, aiding cicatrization, detecting and  
 PT treating immunosuppressive diseases, stimulate immune response and  
 PT tissue regeneration

XX Claim 2; Page 32; 43pp; French.  
 PS The present sequence represents a formula for heparin affinity  
 XX regulatory peptide (HARP) anionic peptides that stimulate immune  
 CC response, cellular growth and regeneration. The peptides are useful  
 CC for regeneration cells, such as muscle cells, and in aiding  
 CC cicatrization as well as in the treatment of immunosuppressive  
 CC diseases. The peptide activity the replication of human immunodeficiency  
 CC virus (HIV) in vitro and are useful in the detection of HIV infected cells.  
 CC When used with an initial agent, they render the HIV more accessible  
 CC to the antiviral agent, and therefore are more easily destroyed.  
 XX Sequence 9 AA.  
 SQ

Query Match 36.4%; Score 4; DR 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKKK 4  
 DB IIII  
 3 AKKK 6

RESULT 43  
 ID AAB67922  
 XX AC AAB6792: standard; peptide; 9 AA.  
 AC AAB67922;  
 DT 29-JUN-2001 (first entry)  
 XX DE PEP2AA heparin peptide from human PAK 1.  
 XX Cytotoxic T lymphocyte associated protein; CD44;  
 KW protein phosphatase 2A; PEP2AA; immune response regulation; autoimmune  
 KW autoimmune disease; rheumatoid arthritis; myasthenia gravis;  
 KW autoimmune thyroiditis; systemic lupus erythematosus; Graves disease;  
 KW type 1 diabetes mellitus; multiple sclerosis; transplant  
 KW graft versus host disease; allergy; inflammatory disorder;  
 KW bacterial infection; viral infection; HIV; parasitic infection;  
 KW human immunodeficiency virus; hepatitis; human PAK 1.  
 XX Homo sapiens  
 QS

Key Location/Qualifiers  
 FT Misc-difference 45 A2.  
 FT W020025445 A2.  
 XX 24 AUG 2002  
 XX 15-FEB-2002; 2002WO-FR04344.  
 XX 16-FEB-2001; 2001US-2003722.  
 XX (CFMY ) GENETICS INC. 1107  
 XX (PREF ) PEP2AA 2ND 1ST 2ND 3RD 4TH 5TH 6TH 7TH 8TH 9TH  
 XX (HGM ) BETHAM & WILKINS HOSPITAL  
 XX Collins M, Madigan J, Courton R, Kellum V,  
 XX WPI: 2002-624642/22  
 XX Manual method for heparin peptides for treating a subject having a  
 DT condition that would benefit from down regulation of an immune  
 PT response, e.g. allergy, or diseases, comprises targeting the  
 PT interaction between CD44 and PEP2AA  
 XX Example 5; Page 44; English.  
 XX The invention relates to a method of an immune response comprising  
 CC contacting a cell expressing at least one protein having a  
 CC CD44 (cyto x1) cytoplasmic associated protein 4) lysine rich  
 CC motif, and at least one second molecule having a PEP2A (protein  
 CC phosphatase 2A regulatory subunit A) CD44 interacting domain with an

CC agent that modulates the interaction between the first molecule and the  
 CC second molecule. Also included are: (1) treating a subject having a  
 CC condition that would benefit from down-regulation of an immune response,  
 CC comprising administering an agent that inhibits the interaction between a  
 CC first molecule and a second molecule described above; (2) identifying a  
 CC compound that modulates the interaction of CTLA4 and PP2AA, and  
 CC (3) identifying a compound which modulates the interaction of a  
 CC molecule comprising at least one CTLA4 lysine rich motif and a PP2AA  
 CC molecule comprising a PP2AA CTLA4-interacting domain.  
 CC The methods are useful for modulating an immune response and  
 CC treating a subject having a condition that would benefit from  
 CC down-regulation of an immune response, such as autoimmune disorder  
 CC (e.g. rheumatoid arthritis, myasthenia gravis, autoimmune thyroiditis,  
 CC systemic lupus erythematosus, type 1 diabetes mellitus, Grave's  
 CC disease, or multiple sclerosis), a transplant (e.g. a bone marrow  
 CC transplant, a stem cell transplant, a heart transplant, a lung  
 CC transplant, or a liver transplant), a kidney transplant, a cornea  
 CC transplant, or an inflammatory disorder, graft versus host disease, an  
 CC allergy, or an inflammatory disorder. Enhancing an immune  
 CC response is useful in treating bacterial, viral (e.g. HIV 1 or 2,  
 CC human immunodeficiency virus, hepatitis B or C) or parasitic infections.  
 CC The present sequence is a PP2AA-binding peptide from human PAK-1.

XX Sequence 9 AA:

Query Matrix: 36.4% Score 4; Pos 23; Length 9;  
 Best Local Similarity 100.0%; Pos 1, 6-9;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 QY 2 KKE 5  
 DB 111  
 5 KKE 8

# RESULT 44

ABG32828  
 ID ARG32828 standard; Peptide: 9 AA.

XX AC ARG32828:

XX DT 29-NOV-2002 (first entry)

XX DE PP2AA-binding peptide from mouse HRX #2.

XX KW Cytotoxic T-lymphocyte associated protein; CTLA4;  
 KW protein phosphatase 2; PP2AA; immune response regulation; gene therapy;  
 KW autoimmune disorder; rheumatoid arthritis; myasthenia gravis;  
 KW autoimmune thyroiditis; systemic lupus erythematosus; Grave's disease;  
 KW type 1 diabetes mellitus; multiple sclerosis; transplant;  
 KW graft versus host disease; allergy; inflammatory disorder;  
 KW bacterial infection; viral infection; HIV; parasitic infection;  
 KW human immunodeficiency virus; hepatitis; mouse; HRX.

XX OS Mus musculus.

XX PN WO200266045-A2.

XX PO 29 AUG-2002.

XX PF 15-FEB-2002; 2002WO-US04459.

XX PR 16-FEB-2001; 2001US-269757P.

XX PA (GENY) GENETICS INST LLC.

XX PA (ROHF-) ROBERTS RES INST JOHN P.

XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX PI Collins M, Madrenas J, Carreno B, Kuchroo V;

XX WPI: 2002-674892/72.

PT Modulating an immune response, for treating a subject having a  
 PT condition that would benefit from down-regulation of an immune

IT response, and a method of down-regulating the interaction between the  
 XX interaction between CTLA4 and PP2AA

ES Example 5: E1 is edge motif.

XX the interaction between a molecule and an immune response comprising  
 CC containing a molecule comprising at least one first molecule having a  
 CC CTLA4 (cytotoxic T-lymphocyte associated protein 4) lysine rich  
 CC motif, and at least a second molecule having a PP2AA (protein  
 CC phosphatase 2A) regulating domain (A) CTLA4 interacting domain with the  
 CC agent that modulates the interaction between the first molecule and the  
 CC second molecule. Also included are: (1) treating a subject having a  
 CC condition that would benefit from down-regulation of an immune response,  
 CC comprising administering an agent that inhibits the interaction between a  
 CC first molecule and a second molecule described above; (2) identifying a  
 CC compound that modulates the interaction of CTLA4 and PP2AA, and  
 CC (3) identifying a compound which modulates the interaction of a  
 CC molecule comprising at least one CTLA4 lysine rich motif and a PP2AA  
 CC molecule comprising a PP2AA CTLA4-interacting domain.

XX The methods are useful for modulating an immune response and  
 CC treating a subject having a condition that would benefit from  
 CC down-regulation of an immune response, such as autoimmune disorder  
 CC (e.g. rheumatoid arthritis, myasthenia gravis, autoimmune thyroiditis,  
 CC systemic lupus erythematosus, type 1 diabetes mellitus, Grave's  
 CC disease, or multiple sclerosis), a transplant (e.g. a bone marrow  
 CC transplant, a stem cell transplant, a heart transplant, a lung  
 CC transplant, or a liver transplant), a kidney transplant, a cornea  
 CC transplant, or an inflammatory disorder, graft versus host disease, an  
 CC allergy, or an inflammatory disorder. Enhancing an immune  
 CC response is useful in treating bacterial, viral (e.g. HIV 1 or 2,  
 CC human immunodeficiency virus, hepatitis B or C) or parasitic infections.  
 CC The present sequence is a PP2AA-binding peptide from mouse HRX #2.

XX Sequence 9 AA:

Query Matrix: 36.4% Score 4; Pos 23; Length 9;  
 Best Local Similarity 100.0%; Pos 1, 6-9;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKE 5

DB 111

5 KKE 8

# RESULT 45

AAH24406

DE AAH24406 standard; Peptide: 9 AA

AC AAH24406:

DT 22-NOV-2002 (first entry)

DE Nucleon Proteasome subunit protein (RUS) #2.

XX Identifying a protein and RNA binding protein gene construct  
 KW target gene sequence, the sequence of a gene encoding a protein

XX E1 is edge motif

XX WO200244562 A2

XX 23 MAY-2002

XX 16-NOV-2001; 2001WO-US04459

XX 16-NOV-2001; 2001WO-US04459

XX (WISN) WISN LLC

XX (FIRM) FIRMUS LLC

XX WISE 02, 2002-674892/72

PT WPI: 2002-674892/72

XX Deriving DNA binding protein sequence binding to target regulatory  
PT sequence comprises selecting sequence for protein, mutating it, and  
PT providing to cell having reporter/seperator gene and screening for gene  
PT expression.  
XX  
XX  
XX Example 5: Page 47: 90pp: English.  
XX  
XX The invention relates to methods for identification and production of  
CC new DNA binding proteins that up or down regulate the expression of pre-  
CC determined target genes. Such genes include DNA sequences that encode  
CC proteins that regulate such target genes as well as gene constructs  
CC and biological materials that contain such DNA binding proteins and/  
CC or their DNA sequences. The method is useful for deriving a gene  
CC sequence of a new DNA binding protein that can bind to a target  
CC regulatory sequence where the gene sequence derived is useful as a  
CC tool for controlling gene expression and as therapeutics. The present  
CC sequence is a nuclear localisation signal (NLS) peptide used to  
CC illustrate the method of the invention.  
XX  
XX  
SQ Sequence 9 AA;

Query Match: 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 40-87;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AKKK 4  
DB 2 AKKK 5

RESULT 46  
AA018023  
ID AA018023 standard; Peptide: 9 AA.  
XX  
XX AA018024;  
XX 30-AUG-2002 (first entry)  
XX Human immunoglobulin E epitope SEQ ID No: 15;  
XX Allergy: immunoglobulin E; IgE; vaccine: immunogen; epitope: human;  
KW non-anaphylactogenic; anti-allergic.  
XX Homo sapiens.  
OS  
PN WO200234288-A2.  
XX  
XX 02-MAY-2002.  
XX 24-OCT-2001: 2001WO-EP12392.  
XX  
XX 27-OCT-2000: 2000GB-0026334.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Vinals Pe Bassols YC;  
PT  
XX  
XX WPI: 2002-479702/51.  
XX  
XX New peptides epitopes and mimotopes derived from (19E, 19Ea, 19E, or  
PT treating or preventing allergies, for typing allergic and 19E, or  
PT for diagnosing atopy .  
XX  
XX Claim 1: Page 5; 28pp: English.  
XX  
XX The present invention provides peptide epitopes derived from human  
CC immunoglobulin E (19E), which are non-anaphylactogenic and can be used  
CC as immunogens to diagnose and treat allergies. The present sequence is  
CC an epitope of the invention.  
XX  
XX  
SQ Sequence 9 AA;

Query Match: 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 40-87;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 KUN 9  
DB 2 KUN 9  
RESULT 47  
AA018024  
ID AA018024 standard; Peptide: 9 AA.  
XX  
XX AA018024;  
XX 02-SEP-2002 (first entry)  
XX  
XX Human IgE epitope SEQ ID No: 15; Peptide SEQ ID No: 309;  
XX Immunogen: human IgE; vaccine: immunogen; epitope: human;  
KW vaccine: anti-allergic.  
XX Homo sapiens.  
OS  
PN WO200234288-A2.  
XX  
XX 28-SEP-2002.  
XX 02-AUG-2001: 2001WO-EP12392.  
XX  
XX 22-MAY-2002 (first entry)  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX 02-MAY-2002 (first entry)  
XX WPI: 2002-479702/51;  
XX  
XX Computer for use in preparation for treatment of allergy, comprises  
XX a substrate having a peptide sequence and an immunogenic carrier  
XX  
XX 02-MAY-2002 (first entry)  
XX  
XX The present invention relates to epitopes suitable for use in vaccines,  
XX where the epitopes are peptides and a substrate on the cyclised peptide and an  
XX immunogenic carrier. The sequences can be used in the treatment of  
XX allergies. The present sequence is a cyclised peptide immunogen derived  
XX from human IgE (19E) suitable for use in the invention.  
XX  
XX Sequence 9 AA;  
Query Match: 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 40-87;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 KUN 1  
DB 2 KUN 1  
RESULT 48  
AA018026  
ID AA018026 standard; Peptide: 9 AA.  
XX  
XX AA018026;  
XX  
XX 02-SEP-2002 (first entry)  
XX  
XX Human IgE associated peptide SEQ ID No: 119.  
XX  
XX 02-SEP-2002 (first entry)  
KW 02-SEP-2002 (first entry)  
KW Human IgE associated peptide SEQ ID No: 119.  
KW 02-SEP-2002 (first entry)  
KW Human IgE associated peptide SEQ ID No: 119.





CC The present invention relates to the isolation of novel human genes  
 CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The  
 CC gene encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding  
 CC PHOR1-F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6  
 CC polynucleotide and polypeptide sequences are useful in diagnostic and  
 CC therapeutic methods, and compositions for various cancers such as  
 CC prostate cancer. The sequences are useful for inhibiting the growth of  
 CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating  
 CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof  
 CC can be used to elicit an immune response. AA091563-AA092962 represent  
 CC PHOR1-A11 or PHOR1-F5D6 peptides tested for HLA binding.

xx SQ Sequence 9 AA:

Query Match 36.4%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEOK 7  
 ||||  
 Db 5 KEOK 8

Search completed: September 30, 2003, 17:03:05  
 Job time : 86 secs









A:Molecule type: protein  
 A:Residues: 1-9 <ARN>  
 A:Experimental source: heart  
 C:Genetics:  
 A:Genome: nuclear  
 C:Function:  
 A:Pathway: oxidative phosphorylation; respiratory chain  
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 27.3% Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2,46-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQ 6  
 DB 1 KEQ 3

## RESULT 3

PC7076  
 spectrin alpha chain, non-erythroid - mouse (fragment)  
 N:Alternate names: fodrin alpha chain  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C:Accession: PC7076  
 R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
 Electrophoresis 21, 1853-1871, 2000  
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of  
 A:Reference number: PC7072  
 A:Accession: PC7076  
 A:Molecule type: protein  
 A:Residues: 1-9 <FS>  
 A:Experimental source: strain C57BL/6Cr Slc, male; brain; striatum  
 C:Keywords: brain

Query Match 27.3% Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2,46-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4  
 DB 6 KKK 8

## RESULT 4

PD0441  
 translation elongation factor TU-like protein p43, mitochondrial - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 21-Aug-1998  
 C:Accession: PD0441  
 R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsunoda, A.;  
 submitted to JEPID, August 1998  
 A:Description: Proteome analysis of mouse brain.  
 A:Reference number: PD0441  
 A:Accession: PD0441  
 A:Molecule type: protein  
 A:Residues: 1-11 <KAW>  
 A:Experimental source: striatum  
 C:Keywords: mitochondrion

Query Match 27.3% Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3,46-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 4 AKK 6

## RESULT 5

E64573  
 hypothetical protein HP0429 - Helicobacter pylori (strain 26695)  
 C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1997  
 C:Accession: E64573  
 R:Torby, J.P.; White, D.; Korlyakov, A.P.; Clayton, R.A.; Sutton, G.; Fleishman,  
 Peterson, S.; Lottus, P.; Rongerson, G.; Hedson, R.; Khalak, H.; Giledek, A.; M  
 son, J.D.; Kelley, J.M.; Collins, M.B.; Weidenbach, J.M.; Fujii, C.; Rokman, G.; Wafar  
 Nature 388, 539-547, 1997  
 A:Authors: Wallin, E.; Hayes, W.S.; Borzoborsky, M.; Karpk, P.D.; Smith, H.G.; Elise  
 A:Title: The complete amino acid sequence of the gastric pathogen Helicobacter pylori  
 A:Reference number: A64573 #text\_change 12-Sep-1997  
 A:Accession: E64573  
 A:Status: preliminary  
 A:Molecule type: RNA  
 A:Residues: 1-12  
 A:Experimental source: not shown

Query Match 27.3% Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3,46-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKK 6  
 DB 1 KKK 6

## RESULT 6

A40763  
 sucrose 6-phosphate hydrolase (EC 3.2.2.22)  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 13-May-1992 #sequence\_revision 13-May-1992 #text\_change 12-Sep-1997  
 C:Accession: A40763

R:Tagesson, J.; Nyberg, N.Y.; Strickell, L.L.; Dockersloot, J.A.

Electrophoresis 264, 1553-1557, 1997  
 A:Title: Transposon encoded surface metabolism in lactococcus lactis, fermenting  
 A:Reference number: A40763 #text\_change 12-Sep-1997  
 A:Accession: A40763

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-12

A:Keywords: 4-phosphosucrose hydrolase

Query Match 27.3% Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3,46-03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKK 9  
 DB 1 KKK 9

## RESULT 7

PI0063

protein GAT60022 - Arabidopsis thaliana (strain)

C:Species: Arabidopsis thaliana (mouse ear cross)

C:Date: 07-Feb-1996 #sequence\_revision 13-Apr-1996 #text\_change 06-Oct-1997

C:Accession: PI0063

R:Tsuzuki, A.; Kato, M.; Kikuchi, Y.

submitted to JEPID, August 1998

A:Description: Arabidopsis thaliana (mouse ear cross)

A:Reference number: PI0063

A:Accession: PI0063

A:Molecule type: protein

A:Residues: 1-12

A:Experimental source: not shown

Query Match 27.3% Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3,46-03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FOR 7  
 DB 1 FOR 9

RESULT 8  
 S23168  
 Z: protein - guinea pig (fragment)  
 C: Species: Cavia porcellus (guinea pig)  
 C: Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
 C: Accession: S23168  
 R: Nicollier, M.; Roblin, S.; Cypriani, B.; Remy-Martin, J.P.; Adessi, G.L.  
 Eur. J. Biochem. 205, 1137-1144, 1992  
 A: Title: Purification and characterization of a binding protein related to the Z class of  
 A: Reference number: S23168; MUID:92249119; PMID:1576997  
 A: Accession: S23168  
 A: Molecule type: protein  
 A: Residues: 1-12 <NIC>  
 A: Experimental source: liver  
 C: Function:  
 A: Description: binds dehydroepiandrosterone sulfate, estrone sulfate, oleic acid, chole  
 C: Keywords: liver; steroid binding  
  
 Query Match 27.3%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 OKQ 8  
 DB 10 OKQ 12  
  
 RESULT 9  
 A33208  
 calreticulin, hepatic - bovine (fragment)  
 C: Species: Bos primigenius taurus (cattle)  
 C: Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 31-Oct-1997  
 C: Accession: A33208  
 R: Milner, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance, J.E.; Opas  
 J. Biol. Chem. 266, 7155-7165, 1991  
 A: Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of sm  
 A: Reference number: A33208; MUID:91201375; PMID:2016321  
 A: Accession: A33208  
 A: Status: preliminary  
 A: Molecule type: protein  
 A: Residues: 1-13 <ML>  
 C: Superfamily: calreticulin  
 C: Keywords: liver  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 KEQ 6  
 DB 7 KEQ 9  
  
 RESULT 10  
 T08533  
 hypothetical protein X - Enterobacter aerogenes plasmid 8751  
 C: Species: Enterobacter aerogenes  
 C: Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
 C: Accession: T08533  
 R: Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.  
 Plasmid 46, 95-111, 1996  
 A: Title: Conservation of the genetic switch between replication and transfer genes of 13  
 A: Reference number: 216434; MUID:97118926; PMID:8954881  
 A: Accession: T08533  
 A: Status: preliminary; translated from GR/EMBL/DBJ  
 A: Molecule type: DNA  
 A: Residues: 1-13 <THO>  
 A: Cross-references: EMBL:U67194; NID:q1572549; FIEN:AA764477.1; PMID:q1572582  
 C: Genetics:  
 A: Genome: plasmid 8751  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 AKK 4  
 DB 6 AKK 8  
  
 RESULT 11  
 S22995  
 hypothetical protein X - Escherichia coli plasmid 4801  
 C: Species: Escherichia coli  
 C: Date: 11-Dec-1994 #sequence\_revision 24-Sep-1994 #text\_change 08-Dec-1995  
 C: Accession: S22995  
 R: Zedeck, G.; Falsgaard, W.; Strick, P.; Bolger, D.; Klever, M.; Knif, V.; Bakka  
 DNA Seq. 1, 303-320, 1991  
 A: Title: Nucleotide sequence and organization of genes flanking the transfer origin  
 A: Reference number: S22995; MUID:9205634; PMID:1665937  
 A: Accession: S22995  
 A: Molecule type: DNA  
 A: Residues: 1-13 <ZF>  
 A: Cross-references: EMBL:U67194; NID:q1572549; FIEN:AA764477.1; PMID:q1572582  
 C: Genetics:  
 A: Genome: plasmid  
 A: Status: preliminary  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 AKK 4  
 DB 6 AKK 8  
  
 RESULT 12  
 A80126  
 hypothetical protein X - Escherichia coli (strain 017-107, 8-10-1997)  
 C: Species: Escherichia coli  
 C: Date: 16-Feb-2000 #sequence\_revision 17-Feb-2000 #text\_change 12-Sep-2000  
 C: Accession: A80126  
 R: Perera, N.L.; Perera, L.L.; Perera, V.; Man, B.; Glasner, J.; Perera, S.; Perera, M.  
 J. Biol. Chem. 275, 529-534, 2000  
 A: Title: Genetic sequence of a novel low-molecular-weight protein, which is a  
 A: Reference number: A80126; MUID:97118926; PMID:11206541  
 A: Accession: A80126  
 A: Status: preliminary  
 A: Molecule type: DNA  
 A: Residues: 1-13 <SH>  
 A: Cross-references: EMBL:U67194; NID:q1572549; FIEN:AA764477.1; PMID:q1572582  
 A: Experimental source: Escherichia coli (strain 017-107, 8-10-1997)  
 C: Genetics:  
 A: Genome: 758kb  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 AKK 4  
 DB 6 AKK 8  
  
 RESULT 13  
 QM84V  
 mastoparan, yellow (linked) (Western blotting)  
 C: Species: Wistar-Kyoto  
 C: Date: 24-Sep-1994 #sequence\_revision 24-Sep-1994 #text\_change 08-Dec-1995  
 C: Accession: QM84V  
 R: Horiuchi, Y.; Yasunaga, T.; Yoshida, H.; Nakajima, T.; Fujima, M.; Kikuchi, M.  
 Chem. Pharm. Bull. 42, 1942-1944, 1994  
 A: Title: A new mastoparan-related peptide mastoparan 16: the sequence of Wistar-Kyoto  
 A: Reference number: QM84V; MUID:9205634; PMID:7543862

A:Accession: A01776  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 A>Note: the active peptide was also synthesized  
 C:Comment: This cytoactive peptide from wasp venom induces mast cell degranulation. The  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3: 68 1: Length 14:  
 Best Local Similarity 100.0%: Pred. No. 4e-03:  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 14  
 QMWHMM  
 mastoparan M - hornet (Vespa mandarinia)  
 N:Alternate names: mast cell-degranulating peptide  
 C:Species: Vespa mandarinia  
 C:Date: 04-Dec-1986 #sequence\_revision: 04-Dec-1986 #text\_change: 4 Dec-1996  
 C:Accession: A01777  
 R:Ritai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 Biomed. Res. 2, 447-449, 1981  
 A:Title: A new mast cell degranulating peptide, mastoparan M, is the venom of the hornet  
 A:Reference number: A01777  
 A:Accession: A01777  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation and  
 C:Superfamily: mastoparan  
 A:Reference number: A01777  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3: 68 1: Length 14:  
 Best Local Similarity 100.0%: Pred. No. 4e-03:  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 15  
 QMWHXX  
 mastoparan X - hornet (Vespa xanthoptera)  
 C:Species: Vespa xanthoptera  
 C:Date: 24-Sep-1987 #sequence\_revision: 24-Sep-1991 #text\_change: 08 Dec-1996  
 C:Accession: A01778  
 R:Ritai, Y.; Kuwada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 Chem. Pharm. Bull. 27, 1945-1946, 1979  
 A:Title: A new mast cell degranulating peptide homologous to mastoparan in the venom of  
 A:Reference number: A01778; MUID:80155338; PMID:540463  
 A:Accession: A01778  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3: 68 1: Length 14:  
 Best Local Similarity 100.0%: Pred. No. 4e-03:  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 16  
 QMWHZ  
 mastoparan Z - hornet (Vespa mandarinia)  
 C:Species: Vespa mandarinia  
 C:Date: 26-Sep-1996 #sequence\_revision: 26-Sep-1996 #text\_change: 08 Dec-1996  
 C:Accession: A01779  
 R:Ritai, Y.; Kuwada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 J. Biol. Chem. 271, 11331-11334, 1996  
 A:Title: Isolation and characterization of a new mast cell degranulating peptide from hornet venom  
 A:Reference number: A01779; MUID:80155338; PMID:8626654  
 A:Accession: A01779  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This peptide from hornet venom induces mast cell degranulation.  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end (leu) #status experimental  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3: 68 1: Length 14:  
 Best Local Similarity 100.0%: Pred. No. 4e-03:  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 17  
 QMWHZ  
 mastoparan Z - hornet (Vespa mandarinia)  
 C:Species: Vespa mandarinia  
 C:Date: 26-Sep-1996 #sequence\_revision: 26-Sep-1996 #text\_change: 08 Dec-1996  
 C:Accession: A01779  
 R:Ritai, Y.; Kuwada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 J. Biol. Chem. 271, 11331-11334, 1996  
 A:Title: Isolation and characterization of a new mast cell degranulating peptide from hornet venom  
 A:Reference number: A01779; MUID:80155338; PMID:8626654  
 A:Accession: A01779  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This peptide from hornet venom induces mast cell degranulation.  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end (leu) #status experimental  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3: 68 1: Length 14:  
 Best Local Similarity 100.0%: Pred. No. 4e-03:  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 18  
 S4662  
 xylose 1,4 beta xylosidase (EC 3.2.1.35)  
 A:Title: Thermophilus thermophilus xylosidase and beta xylosidase from Thermophilus sp. strain  
 C:Species: Thermophilus  
 A:Accession: A01780  
 C:Date: 24-Mar-1999 #sequence\_revision: 24-Mar-1999 #text\_change: 08 Dec-1996  
 A:Accession: A01780  
 R:Ritai, Y.; Kuwada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 J. Biol. Chem. 274, 11331-11334, 1999  
 A:Title: Thermophilus thermophilus xylosidase and beta xylosidase from Thermophilus sp. strain  
 A:Reference number: A01780; MUID:80155338; PMID:8626654  
 A:Accession: A01780  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This enzyme activity was apparently associated with xylosidase and xylosidase from Thermophilus sp. strain  
 C:Superfamily: xylosidase  
 A:Note: plays an important role in the release of end-product inhibitor of end-xylosidase

Query Match 27.3% Score 3: 68 1: Length 14:  
 Best Local Similarity 100.0%: Pred. No. 4e-03:  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3  
 III  
 DB 10 AKK 12



C:Keywords: glycosidase; hydrolase; polysaccharide dehydratase

## Query Match

Best Local Similarity 27.3%, Score 3; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3

DB 1 AKK 3

## RESULT 19

S13864

methyl coenzyme M reductase (EC 1.8.1.1) [1: alpha chain - Methanobacterium thermoautotrophicum]

C:Species: Methanobacterium thermoautotrophicum

A:Variety: Strain Marburg

C:Date: 14-Mar-1997 #sequence\_revision 13-Sep-1998 #text\_change 30-Oct-1998

C:Accession: S13864

R:Rospert, S.; Linder, D.; Ellermann, J.; Trauer, R.K.

Eur. J. Biochem. 194, 871-877, 1990

A:Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium thermophilum

A:Reference number: S13864; MUID:91098179; PMID:226416

A:Accession: S13864

A:Molecule type: protein

A:Residues: 1-14 <ROS>

A:Experimental source: strain Marburg

C:Keywords: methanogenesis; oxidoreductase

## Query Match

Best Local Similarity 27.3%, Score 3; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKK 4

DB 12 KKK 14

## RESULT 20

B34135

DNA-binding protein q - Crithidia fasciculata mitochondrion (fragment)

C:Species: mitochondrion Crithidia fasciculata

C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 37-Oct-1999

C:Accession: B34135

R:Tittawalla, I.

FEBS Lett. 260, 57-61, 1990

A:Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata

A:Reference number: B34135

A:Molecule type: protein

A:Residues: 1-14 <IT>

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC6

C:Keywords: mitochondrion

## Query Match

Best Local Similarity 27.3%, Score 3; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3

DB 6 AKK 8

## RESULT 21

S14336

mastoparan B - hornet (Vespa basalis)

C:Species: Vespa basalis

C:Date: 14-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 30-Apr-1999

C:Accession: S14336

R:Ho, C.H.; Hwang, L.L.

Biochem. J. 274, 453-456, 1991

A:Title: Structure and biological activities of a new mastoparan isolated from the venom

A:Reference number: S14336

A:Accession: S14336

A:Molecule type: protein

A:Residues: 1-14 <ROS>

A:Experimental source: venom

C:Keywords:

A:Description: possesses a potent formyl peptide receptor activity which acts in synergy with the formyl peptide receptor antagonist, N-ethylmaleimide, to inhibit the chemotactic response of neutrophils to formyl peptides

A:Key words: mastoparan B; mastoparan B (MB); #status: experimental

Query Match

Best Local Similarity 27.3%, Score 3; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3

DB 1 AKK 14

## RESULT 22

S21717

non-mammalian myelin basic protein (MBP) [1: 1-111] (cytochrome P-450)

C:Species: myelin basic protein (MBP) [1: 1-111] (cytochrome P-450)

A:Title: Myelin basic protein (MBP) [1: 1-111] (cytochrome P-450)

A:Accession: S21717

A:Molecule type: protein

A:Residues: 1-111 <ROS>

A:Experimental source: myelin

C:Keywords: myelin basic protein (MBP)

A:Title: Myelin basic protein (MBP) [1: 1-111] (cytochrome P-450)

A:Reference number: S21717

A:Accession: S21717

A:Molecule type: protein

A:Residues: 1-111 <ROS>

A:Experimental source: myelin

C:Keywords: myelin basic protein (MBP)

Query Match

Best Local Similarity 27.3%, Score 3; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KKK 3

DB 2 KKK 4

## RESULT 23

B34208

cytochrome P-450 (CYP1A1)

C:Species: cytochrome P-450 (CYP1A1)

A:Title: Cytochrome P-450 (CYP1A1)

A:Accession: B34208

A:Molecule type: protein

A:Residues: 1-111 <ROS>

A:Experimental source: myelin

C:Keywords: myelin basic protein (MBP)

Query Match

Best Local Similarity 27.3%, Score 3; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

## RESULT 24

A63156

cellulase (EC 3.2.1.4)

A:Title: Cellulase (EC 3.2.1.4)

A:Reference number: S14336

A:Accession: S14336





Mol. Biochem. Parasitol. 2, 135-150, 1981  
 A:Title: glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-term  
 A:Reference number: A61512; MUID:81172836; PMID:6163983  
 A:Accession: C61512

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <HOL>

A:Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NA 11

DB 4 NA 5

RESULT 36

A21440

variant surface glycoprotein pSLcl - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei

C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Mar 1998

C:Accession: A21440

R:Parsons, M.; Nelson, R.G.; Watkins, K.F.; Agabian, N.

Cell 38, 309-316, 1984

A:Title: trypanosome mRNAs share a common 5' spliced leader sequence.

A:Reference number: A90853; MUID:84282716; PMID:6088073

A:Accession: A21440

A:Molecule type: mRNA

A:Residues: 1-8 <PAR>

A:Cross-references: GB:K02195; NID:q162150; PID:q162151

C:Keywords: glycoprotein

Query Match

18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KE 5

DB 4 KE 5

RESULT 37

B27867

homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)

C:Species: Drosophila melanogaster

C>Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 23-Feb-1997

C:Accession: B27867

R:Saari, G.; Bientz, M.

EMBO J. 6, 1775-1778, 1987

A:Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.

A:Reference number: A91072

A:Accession: B27867

A:Molecule type: mRNA

A:Residues: 1-8 <SAA>

C:Genetics:

A:Gene: FlyBase:Ubx

A:Cross-references: FlyBase:FBgn0003944

C:Keywords: DNA binding; nucleus; transcription regulation

Query Match

18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQ 6

DB 6 EQ 7

RESULT 38

A61467

penalbumin - Adelle penguin (fragment)

C:Species: pygoscolis adelle (Adelle penguin)

C>Date: 07-Oct-1994 #sequence\_revision 04-Nov-1994 #text\_change 04-Sep-1995

C:Accession: A61467

R:Seegal, D.L.; Amundsen, R.; De Vries, Y.K.; Allison, R.J.; Peckey, P.E.

Protein Chem. 2, 43-52, 1993

A:Title: Sulfhydryl proteins of penaeid egg white: ovalbumin and penalbumin. Penae

A:Reference number: A61467

A:Accession: A61467

A:Molecule type: protein

A:Residues: 1-8 <ST>

C:Title: Penalbumin as a major protein component of egg whites and penalbumin

C:Keywords: egg white; flycatcher

Query Match

18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NA 11

DB 7 NA 5

RESULT 39

P14234

heavy chain (fragment) - human (fragment)

C:Species: Homo sapiens (human)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-Aug-1999

C:Accession: P14234

R:Yamada, M.; Wasserman, K.L.; Redburn, R.A.; Skane, S.; Catlett, A.J.; Roeder, G.

J. Exp. Med. 173, 435-402, 1991

A:Title: Proteolytic modification of specific immunoglobulin heavy chain diversity

A:Reference number: P14234; PMID:1895102

A:Accession: P14234

A:Molecule type: DNA

A:Residues: 1-8 <YAR>

A:Experimental source: lymphocyte

C:Keywords: immunoglobulin; immunoglobulin

Query Match

18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQ 5

DB 7 EQ 6

RESULT 40

I46434

apolipoprotein A2 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1990 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: I46434

R:Ko, M.S.; Wang, X.; Bickel, C.; Bickel, M.; Takahashi, N.; Mizutani, T.; Radwin

Mamm. Genome 5, 344-355, 1994

A:Title: Gene structure of the mouse apolipoprotein A2

A:Reference number: I46434; PMID:6543949

A:Accession: I46434

A:Status: preliminary

A:Molecule type: cDNA

A:Residues: 1-8 <PES>

A:Cross-references: EMBL:J05011; MIM:146000; F01660; F01661; F01662

Query Match

18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2

DB 7 AK 5

RESULT 41

A54823  
 Olfactory receptor 17 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 28-Apr-1995 #sequence\_revision 28 Apr-1995 #text\_change 17-Mar-1999  
 C:Accession: A54823  
 R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 78, 823-834, 1994  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A:Reference number: A54823; MUID:94373818; PMID:8087849  
 A:Accession: A54823  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <CH>

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 II

DB 4 RN 5  
 II

RESULT 42  
 PN0043  
 phosphatidylethanolamine-binding protein - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 20-Oct-1997 #sequence\_revision 29-sep-1997 #text\_change 23-Jan-1998  
 C:Accession: PN0043  
 R:Kato, H.  
 Kawasaki 19kkaishi 22, 245-259, 1996  
 A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro  
 A:Reference number: PN0041  
 A:Accession: PN0043  
 A:Molecule type: protein  
 A:Residues: 1-8 <KAT>  
 A:Experimental source: neuroblastoma cell  
 C:Comment: The molecular mass is 23.500 and the pI is 4.4. The amino-terminus is blocked  
 C:Keywords: Brain

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQ 6  
 II  
 3 EQ 4

DB 3 EQ 4

RESULT 43  
 148935  
 apolipoprotein A-II - western wild mouse (fragment)  
 C:Species: Mus spretus (western wild mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: 148935  
 R:KO, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takabayashi, N.; Maeyaki, Y.; Nadeau, J.H.  
 Mamm. Genome 5, 349-355, 1994  
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
 A:Reference number: 148934; MUID:94319082; PMID:8043449  
 A:Accession: 148935  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <RES>  
 A:Cross-references: EMBL:005692; NID:q497011; FIDN:AK604743; FID:q42827

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2  
 II  
 7 AK 8

DB 7 AK 8

RESULT 44  
 B64823  
 Olfactory receptor 17 - western wild mouse (fragment)  
 C:Species: Mus spretus (western wild mouse)  
 C>Date: 28-Apr-1995 #sequence\_revision 02-Jul-1996 #text\_change 07-Mar-1999  
 C:Accession: B64823  
 R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 78, 823-834, 1994  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression  
 A:Reference number: A4823; MUID:94373818; PMID:8087849  
 A:Accession: B64823  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <CH>

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 II

DB 4 RN 5  
 II

RESULT 45  
 A63137  
 Cytochrome P450 A - rat (fragment)  
 C:Species: Rattus norvegicus (brown rat)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
 C:Accession: A63137  
 R:Shimono, H.; Kudo, A.; Ogata, S.; Nadeau, J.H.; Axel, R.  
 J Biol Chem 269, 257-261, 1994  
 A:Title: Purification and characterization of liver microsomal cy  
 A:Reference number: A63137; MUID:94373818; PMID:1676625  
 A:Accession: A63137  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <SH>

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KF 3  
 II  
 6 KF 2

DB 6 KF 2

RESULT 46  
 147642  
 apolipoprotein A-II - rat (fragment)  
 C:Species: Rattus sp. (rat)  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: 147642  
 R:Raney-Rehman, S.; Nadeau, J.H.  
 J Biol Chem 271, 296-300, 1996  
 A:Title: cDNA clones and sequences of rat apolipoprotein A-II cDNA  
 A:Reference number: 147642; MUID:94373818; PMID:841429  
 A:Accession: 147642  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RES>  
 A:Cross-references: EMBL:005692; NID:q497011; FIDN:AK604743; FID:q42827

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 II

DB 9 RN 10

DB 6 RN 7

## RESULT 47

YFPG

thymic factor - pig  
 N:Alternate names: FTS (facteur thymique serique)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 13-Jul-1981 #sequence\_revision 13 Jul-1981 #ext\_change 07 May-1999  
 C:Accession: A01523; A60983  
 R:Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.  
 J. Biol. Chem. 252, 8045-8047, 1977  
 A:Title: Structural study of circulating thymic factors: a peptide isolated from pig sera  
 A:Reference number: A01523; MUID:78026571; PMID:913462  
 A:Accession: A01523  
 A:Molecule type: protein  
 A:Residues: 1-9 <PLE>  
 R:Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.  
 Nature 266, 55-57, 1977  
 A:Title: Biochemical characterisation of a serum thymic factor  
 A:Reference number: A60983; MUID:77123829; PMID:306145  
 A:Accession: A60983  
 A:Molecule type: protein  
 A:Residues: 1-9 <BAC>  
 C:Comment: This peptide induces DNA synthesis in immature T-lymphocytes, but not peripheral in a variety of immunoassays.  
 C:Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modified  
 C:Superfamily: thymic factor  
 C:Keywords: pyroglutamic acid  
 F1/Modified site: pyrrolidone carboxylic acid (Glu) #status expert manual

## Query Match

18.28; Score 24; DB 1; Length 9;

Best Local Similarity 100.00; Pred. No. 2; Mismatches 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2

11

DB 2 AK 3

## RESULT 48

AKLOIM

locustamyl-inhibiting peptide - migratory locust  
 C:Species: Locusta migratoria (migratory locust)  
 C>Date: 31-Mar-1993 #sequence\_revision 31 Mar-1993 #ext\_change 26 Mar-1997  
 C:Accession: A60065  
 R:Schmidt, L.; Holman, G.M.; Hayes, T.K.; Natchem, R.L.; De Loof, A.  
 Regul. Pept. 36, 111-119, 1991  
 A:Title: Isolation, identification and synthesis of locustamyl-inhibiting peptide (LIMP)  
 A:Reference number: A60065; MUID:92173466; PMID:1736174  
 A:Accession: A60065  
 A:Molecule type: protein  
 A:Residues: 1-9 <SCH>  
 C:Comment: This peptide hormone suppresses sporophores overproductions of the hindgut and  
 C:Superfamily: locustamyl-inhibiting peptide  
 C:Keywords: amidated carboxyl end; hormone  
 F1/Modified site: amidated carboxyl end (Trp) #status expert manual

## Query Match

18.28; Score 24; DB 1; Length 9;

Best Local Similarity 100.00; Pred. No. 2; Mismatches 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NA 11

11

DB 6 NA 7

## RESULT 49

S59902

glutathione transferase (EC 2.5.1.18) P - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 20 Jul-1996 #sequence\_revision 13-Mar-1997 #ext\_change 17 Mar-1999  
 C:Accession: S59902

R.Mishchuk, J. R. P. J. Biol. Chem. 266, 10445-10448, 1991  
 R.Mishchuk, J. R. P. J. Biol. Chem. 266, 10445-10448, 1991  
 A:Title: The effect of protein A on the activity of glutathione transferase  
 A:Reference number: S59902; MUID:7574228  
 A:Accession: S59902  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <NIS>  
 C:Superfamily: glutathione transferase  
 C:Keywords: glutathione transferase

## Query Match

18.28; Score 24; DB 1; Length 9;

Best Local Similarity 100.00; Pred. No. 2; Mismatches 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 4

11

DB 6 NA 7

## RESULT 50

S60440

N:Alternate names: Amino acid oxidase  
 C:Species: Homo sapiens (human)  
 C>Date: 31-Mar-1993 #sequence\_revision 31 Mar-1993 #ext\_change 26 Mar-1997  
 C:Accession: A60065  
 R:Schmidt, L.; Holman, G.M.; Hayes, T.K.; Natchem, R.L.; De Loof, A.  
 Regul. Pept. 36, 111-119, 1991  
 A:Title: Isolation, identification and synthesis of locustamyl-inhibiting peptide (LIMP)  
 A:Reference number: A60065; MUID:92173466; PMID:1736174  
 A:Accession: A60065  
 A:Molecule type: protein  
 A:Residues: 1-9 <SCH>  
 C:Comment: This peptide hormone suppresses sporophores overproductions of the hindgut and  
 C:Superfamily: locustamyl-inhibiting peptide  
 C:Keywords: amidated carboxyl end; hormone  
 F1/Modified site: amidated carboxyl end (Trp) #status expert manual

## Query Match

18.28; Score 24; DB 1; Length 9;

Best Local Similarity 100.00; Pred. No. 2; Mismatches 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 1

11

DB 4 NA 7

## Search completed: September 01, 1999, 17:04:12

Job time: 49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 17:01:41 : Search time 23 Seconds

(without alignments)  
22.491 Million cell updates/sec

Title: US-09-787-443-20

Perfect score: 11

Sequence: 1 AKKEQKORNA 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 707

Minimum OR seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	9	1 COXE_THUOB	P80975 trunnus obe
2	3	27.3	9	1 FARS_PANRE	P82661 panagrellus
3	3	27.3	10	1 XN8_DICB4	P80717 dictyoglomu
4	3	27.3	12	1 RS19_GLYEP	Q46490 clover yeli
5	3	27.3	13	1 CRIC_BOVIN	P28489 bos taurus
6	3	27.3	14	1 MAST_VESBA	P21654 vespa basai
7	3	27.3	14	1 MAST_VESCR	P01516 vespa cratr
8	3	27.3	14	1 MAST_VESLE	P01514 vespa lew
9	3	27.3	14	1 MAST_VESMA	P04205 vespa manda
10	3	27.3	14	1 MCRX_METTM	P01515 vespa xanth
11	3	27.3	14	1 MCRX_METTM	P58815 methanobact
12	3	27.3	14	1 TKM_PANNA	P40951 rana margar
13	3	27.3	15	1 COX1_THUOB	P83478 thunnus obe
14	3	27.3	15	1 G78_HORSE	P01392 equus cabal
15	3	27.3	15	1 UC08_MAIZE	P80614 zea mays (m
16	2	18.2	8	1 B44K_PORGI	P81886 porphyromon
17	2	18.2	8	1 FARI_PENMO	P81316 penaeus mon
18	2	18.2	8	1 FARI_HOMAM	P41486 homarus ame
19	2	18.2	8	1 FARI_HOMAM	P41487 homarus ame
20	2	18.2	8	1 NPB_HOVIN	P1507 bos taurus
21	2	18.2	8	1 NS1_MYCTU	P81152 mycobacteri
22	2	18.2	8	1 RS1_ERMCH	P37985 erwinia chr
23	2	18.2	9	1 CCAP_CARMA	P85556 carcinus ma
24	2	18.2	9	1 CONO_CONGE	P05486 conus geogr
25	2	18.2	9	1 CONO_CONST	P05487 conus stria
26	2	18.2	9	1 FARM_MACRS	P63279 macrobrachi
27	2	18.2	9	1 LMIP_LOCHI	P31799 locusta mig
28	2	18.2	9	1 LPCA_STAAT	P36884 staphylococ
29	2	18.2	9	1 NEUO_CAVPO	P34966 cavia porce
30	2	18.2	9	1 OXYT_EISFO	P42998 eisenia foe
31	2	18.2	9	1 OXYT_OCTVU	P80027 octopus vul
32	2	18.2	9	1 RS10_SERMA	O68936 serratia ma
33	2	18.2	9	1 RT33_BOVIN	P82926 bos taurus

34	2	18.2	9	1 COXE_PLT	P01250 sus scro fa
35	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
36	2	18.2	9	1 FARS_SHEEP	P81205 ov a aries
37	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
38	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
39	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
40	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
41	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
42	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
43	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
44	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
45	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
46	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
47	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
48	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
49	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
50	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
51	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
52	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
53	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
54	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
55	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
56	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
57	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
58	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
59	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
60	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
61	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
62	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
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64	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
65	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
66	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
67	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
68	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
69	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
70	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
71	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
72	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
73	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
74	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
75	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
76	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
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78	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
79	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
80	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
81	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
82	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
83	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
84	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
85	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
86	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
87	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
88	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
89	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
90	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
91	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
92	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
93	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
94	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
95	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
96	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
97	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
98	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
99	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
100	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
101	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
102	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
103	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
104	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
105	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien
106	2	18.2	9	1 O_AZ_HUMAN	P51920 homo sapien

107	2	18.2	15	1	EF1A_MICCR	P81266 microplis	180	9.1	1	PLM_RGVIN	P82929 tes tauris
108	2	18.2	15	1	FIBA_ANAPL	P12501 anas platyr	181	9.1	1	FL26_MALFE	P8632 zea mays (m
109	2	18.2	15	1	LEC2_PSOSC	P22585 psophocarp	182	9.1	1	FL26_MALFE	P8632 zea mays (m
110	2	18.2	15	1	MAT1_BACIO	P80722 bacillus th	183	9.1	1	FL26_MALFE	P8632 zea mays (m
111	2	18.2	15	1	MCA2_RHOOP	P56870 rhodococcus	184	9.1	1	FL26_MALFE	P8632 zea mays (m
112	2	18.2	15	1	MCRA_METTE	P22948 methanosarc	185	9.1	1	FL26_MALFE	P8632 zea mays (m
113	2	18.2	15	1	MM01_RAT	P81563 rattus norv	186	9.1	1	FL26_MALFE	P8632 zea mays (m
114	2	18.2	15	1	NIS1_ANAVA	C44507 anabaena va	187	9.1	1	FL26_MALFE	P8632 zea mays (m
115	2	18.2	15	1	NUO3_SOLTU	P80263 solanum tub	188	9.1	1	FL26_MALFE	P8632 zea mays (m
116	2	18.2	15	1	NUO8_SOLTU	P80731 solanum tub	189	9.1	1	FL26_MALFE	P8632 zea mays (m
117	2	18.2	15	1	ONC1_ONCMY	P83287 oncorhynch	190	9.1	1	FL26_MALFE	P8632 zea mays (m
118	2	18.2	15	1	PGK1_PHPYA	P80659 physcomitre	191	9.1	1	FL26_MALFE	P8632 zea mays (m
119	2	18.2	15	1	PGS5_PELAC	P80504 pelobacter	192	9.1	1	FL26_MALFE	P8632 zea mays (m
120	2	18.2	15	1	R13A_SPIOL	P82454 spiculus ol	193	9.1	1	FL26_MALFE	P8632 zea mays (m
121	2	18.2	15	1	RS10_BACST	P59683 bacillus st	194	9.1	1	FL26_MALFE	P8632 zea mays (m
122	2	18.2	15	1	RS20_BACST	P59681 bacillus st	195	9.1	1	FL26_MALFE	P8632 zea mays (m
123	2	18.2	15	1	RT32_BOVIN	P82927 bos taurus	196	9.1	1	FL26_MALFE	P8632 zea mays (m
124	2	18.2	15	1	THL1_CLOPA	P81347 clostridium	197	9.1	1	FL26_MALFE	P8632 zea mays (m
125	2	18.2	15	1	UC01_MAIZE	P83637 zea mays (m	198	9.1	1	FL26_MALFE	P8632 zea mays (m
126	2	18.2	15	1	UC13_MAIZE	P83619 zea mays (m	199	9.1	1	FL26_MALFE	P8632 zea mays (m
127	2	18.2	15	1	UC17_MAIZE	P83623 zea mays (m	200	9.1	1	FL26_MALFE	P8632 zea mays (m
128	2	18.2	15	1	UC27_MAIZE	P83633 zea mays (m	201	9.1	1	FL26_MALFE	P8632 zea mays (m
129	2	18.2	15	1	UN01_PINPS	P81106 pinus pinas	202	9.1	1	FL26_MALFE	P8632 zea mays (m
130	2	18.2	15	1	UN04_PINPS	P81673 pinus pinas	203	9.1	1	FL26_MALFE	P8632 zea mays (m
131	2	18.2	15	1	URE2_MORMO	P17338 morganella	204	9.1	1	FL26_MALFE	P8632 zea mays (m
132	2	18.2	15	1	VORE_METTM	P80907 methanobact	205	9.1	1	FL26_MALFE	P8632 zea mays (m
133	1	9.1	8	1	ACL1_THUAL	P18691 thymus alb	206	9.1	1	FL26_MALFE	P8632 zea mays (m
134	1	9.1	8	1	ACT1_CARMA	P80709 carcinus ma	207	9.1	1	FL26_MALFE	P8632 zea mays (m
135	1	9.1	8	1	AKH2_GRYBI	P13086 gryllus bim	208	9.1	1	FL26_MALFE	P8632 zea mays (m
136	1	9.1	8	1	AKH1_EIBAU	P25418 ciellula a	209	9.1	1	FL26_MALFE	P8632 zea mays (m
137	1	9.1	8	1	AKH1_MEIML	P25423 melolontha	210	9.1	1	FL26_MALFE	P8632 zea mays (m
138	1	9.1	8	1	AKH1_TABAT	P14595 tabanus atr	211	9.1	1	FL26_MALFE	P8632 zea mays (m
139	1	9.1	8	1	AL12_CARMA	P81615 carcinus ma	212	9.1	1	FL26_MALFE	P8632 zea mays (m
140	1	9.1	8	1	AL15_CARMA	P81918 carcinus ma	213	9.1	1	FL26_MALFE	P8632 zea mays (m
141	1	9.1	8	1	AL17_CARMA	P81920 carcinus ma	214	9.1	1	FL26_MALFE	P8632 zea mays (m
142	1	9.1	8	1	ALL1_CYDPO	P82152 cydia pomon	215	9.1	1	FL26_MALFE	P8632 zea mays (m
143	1	9.1	8	1	ALL3_CYDPO	P82154 cydia pomon	216	9.1	1	FL26_MALFE	P8632 zea mays (m
144	1	9.1	8	1	ALL4_CALVO	P41840 calliphora	217	9.1	1	FL26_MALFE	P8632 zea mays (m
145	1	9.1	8	1	ALL4_CYDPO	P82155 cydia pomon	218	9.1	1	FL26_MALFE	P8632 zea mays (m
146	1	9.1	8	1	ALL5_CYDPO	P82156 cydia pomon	219	9.1	1	FL26_MALFE	P8632 zea mays (m
147	1	9.1	8	1	ALL6_CYDPO	P82157 cydia pomon	220	9.1	1	FL26_MALFE	P8632 zea mays (m
148	1	9.1	8	1	ALL7_CARMA	P81839 carcinus ma	221	9.1	1	FL26_MALFE	P8632 zea mays (m
149	1	9.1	8	1	ALL8_CARMA	P81811 carcinus ma	222	9.1	1	FL26_MALFE	P8632 zea mays (m
150	1	9.1	8	1	ALL9_CARMA	P81812 carcinus ma	223	9.1	1	FL26_MALFE	P8632 zea mays (m
151	1	9.1	8	1	ANG2_BOTJA	P19582 botriopsis ja	224	9.1	1	FL26_MALFE	P8632 zea mays (m
152	1	9.1	8	1	CAD1_ENTFA	P14268 entelococcu	225	9.1	1	FL26_MALFE	P8632 zea mays (m
153	1	9.1	8	1	CLP1_THICU	P80488 tiliobacilli	226	9.1	1	FL26_MALFE	P8632 zea mays (m
154	1	9.1	8	1	COXG_RAT	P82430 rattus norv	227	9.1	1	FL26_MALFE	P8632 zea mays (m
155	1	9.1	8	1	FAR1_PANKE	P41872 panagrelus	228	9.1	1	FL26_MALFE	P8632 zea mays (m
156	1	9.1	8	1	FAR2_MACRS	P84275 macrobrachi	229	9.1	1	FL26_MALFE	P8632 zea mays (m
157	1	9.1	8	1	FAR2_MACRS	P84277 macrobrachi	230	9.1	1	FL26_MALFE	P8632 zea mays (m
158	1	9.1	8	1	FAR2_ASCSU	P43171 ascaris su	231	9.1	1	FL26_MALFE	P8632 zea mays (m
159	1	9.1	8	1	FAR2_CALVO	P43583 calliphora	232	9.1	1	FL26_MALFE	P8632 zea mays (m
160	1	9.1	8	1	FUSS_FUSSO	P81910 fusarium so	233	9.1	1	FL26_MALFE	P8632 zea mays (m
161	1	9.1	8	1	GLUR_HUMAN	P82729 homo sapien	234	9.1	1	FL26_MALFE	P8632 zea mays (m
162	1	9.1	8	1	HTE1_PBRAM	P84548 periplaneta	235	9.1	1	FL26_MALFE	P8632 zea mays (m
163	1	9.1	8	1	HTE2_PBRAM	P84549 periplaneta	236	9.1	1	FL26_MALFE	P8632 zea mays (m
164	1	9.1	8	1	HTE1_TENKI	P25419 tenobrio mc	237	9.1	1	FL26_MALFE	P8632 zea mays (m
165	1	9.1	8	1	ICK1_LEUMA	P21140 leucophaea	238	9.1	1	FL26_MALFE	P8632 zea mays (m
166	1	9.1	8	1	ICK3_LEUMA	P21142 leucophaea	239	9.1	1	FL26_MALFE	P8632 zea mays (m
167	1	9.1	8	1	ICK4_LEUMA	P21143 leucophaea	240	9.1	1	FL26_MALFE	P8632 zea mays (m
168	1	9.1	8	1	ICK6_LEUMA	P19088 leucophaea	241	9.1	1	FL26_MALFE	P8632 zea mays (m
169	1	9.1	8	1	ICK7_LEUMA	P19089 leucophaea	242	9.1	1	FL26_MALFE	P8632 zea mays (m
170	1	9.1	8	1	ICK8_LEUMA	P19090 leucophaea	243	9.1	1	FL26_MALFE	P8632 zea mays (m
171	1	9.1	8	1	LMT2_LOCHI	P22396 leocusta miq	244	9.1	1	FL26_MALFE	P8632 zea mays (m
172	1	9.1	8	1	LPK1_LEUMA	P13049 leucophaea	245	9.1	1	FL26_MALFE	P8632 zea mays (m
173	1	9.1	8	1	LPM5_STAEP	P82121 staphylococ	246	9.1	1	FL26_MALFE	P8632 zea mays (m
174	1	9.1	8	1	ORMY_ORCHI	P82455 oriconectes	247	9.1	1	FL26_MALFE	P8632 zea mays (m
175	1	9.1	8	1	PLP_BRANA	P81707 brassica na	248	9.1	1	FL26_MALFE	P8632 zea mays (m
176	1	9.1	8	1	PPK2_PBRAM	P82692 periplaneta	249	9.1	1	FL26_MALFE	P8632 zea mays (m
177	1	9.1	8	1	PPK1_PBRAM	P82618 periplaneta	250	9.1	1	FL26_MALFE	P8632 zea mays (m
178	1	9.1	8	1	RPCH_PANBO	P83939 pandalus bo	251	9.1	1	FL26_MALFE	P8632 zea mays (m
179	1	9.1	8	1	RS7_MYCIT	P83564 mycobacteri	252	9.1	1	FL26_MALFE	P8632 zea mays (m









RA Vance J.E., Opas M., Michalak M.:  
 RT "Calreticulin, and not calsequestrin, is the major calcium-binding  
 RT protein of smooth sarcoplasmic reticulum and other endoplasmic  
 RT reticulum".  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 CC -|- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -|- SUBUNIT: Monomer (By similarity).  
 CC -|- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -|- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 DR PIR: A33208.  
 DR InterPro: IPR001580; Calreticulin.  
 DR PROSITE: PS00803; CALRETICULIN\_1; PARTIAL.  
 DR PROSITE: PS00804; CALRETICULIN\_2; PARTIAL.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; PARTIAL.  
 KW Endoplasmic reticulum; Calcium-binding.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA: 1557 MW: C85DDA6990CA1339 CR'64.

Query Match 27.3% Score 3; LR 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+00;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 REQ 6  
 DB 7 REQ 9

## RESULT 6

MAST\_VESHA  
 ID MAST\_VESBA STANDARD: PRT: 14 AA  
 AC P21654  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan B.  
 OS Vespa basalis (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eurytomia;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespidae;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID:7444;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Venom;  
 RX MEDLINE=91174755; PubMed=2006909;  
 RA Lo C.-L., Hwang L.-L.;  
 RT "Structure and biological activities of a new mastoparan isolated  
 RT from the venom of the hornet Vespa basalis".  
 RL Biochem. J. 274:453-456(1991).  
 CC -|- FUNCTION: Mast cell degranulating peptide. Activates B proteins  
 CC that couple to phospholipase C.  
 DR PIR: S14336; S14336.  
 DR Mast cell degranulation; Amidation.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 14 AA: 1613 MW: D35944CAL9A19A2 CR'64.

Query Match 27.3% Score 3; LR 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.0e+00;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 10 AKK 12

## RESULT 7

MAST\_VESCR  
 ID MAST\_VESCR STANDARD: PRT: 14 AA  
 AC P01516;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan C.

MAST\_VESCR  
 ID MAST\_VESCR STANDARD: PRT: 14 AA  
 AC P01516;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan C.  
 OS Vespa cralpa (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eurytomia;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespidae;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID:7444;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Venom;  
 RX MEDLINE=8428944; PubMed=2006909;  
 RA Aoki T., Aoki T., Aoki T.;  
 RT "Isolation and characterization of a new mastoparan-like peptide  
 RT from the venom of the hornet Vespa cralpa".  
 RL Biochem. J. 274:453-456(1991).  
 CC -|- FUNCTION: Mast cell degranulating peptide. Activates B proteins  
 CC that couple to phospholipase C.  
 DR PIR: A33208; A33208.  
 DR Mast cell degranulation; Amidation.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 14 AA: 1557 MW: C85DDA6990CA1339 CR'64.

Query Match 27.3% Score 3; LR 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.0e+00;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 10 AKK 12

MAST\_VESLE  
 ID MAST\_VESLE STANDARD: PRT: 14 AA  
 AC P21654  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan B.  
 OS Vespa basalis (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eurytomia;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespidae;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID:7444;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Venom;  
 RX MEDLINE=91174755; PubMed=2006909;  
 RA Lo C.-L., Hwang L.-L.;  
 RT "Structure and biological activities of a new mastoparan isolated  
 RT from the venom of the hornet Vespa basalis".  
 RL Biochem. J. 274:453-456(1991).  
 CC -|- FUNCTION: Mast cell degranulating peptide. Activates B proteins  
 CC that couple to phospholipase C.  
 DR PIR: S14336; S14336.  
 DR Mast cell degranulation; Amidation.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 14 AA: 1613 MW: D35944CAL9A19A2 CR'64.

Query Match 27.3% Score 3; LR 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.0e+00;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 10 AKK 12

MAST\_VESMA  
 ID MAST\_VESMA STANDARD: PRT: 14 AA  
 AC P01516;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan C.



RA Zhu Y.Q., Zou G., Tsou K.:  
 RT "Isolation and structure of ranamargarin, a new tachykinin from the  
 RL skin of Chinese frog *Rana margaratae*.";  
 RN Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 32:570-574(1989).  
 (2)

RP SYNTHESIS.  
 RX MEDLINE:90253600; PubMed:2340087;  
 RA Lu Y.A., Peng J.L., Zhu Y.Q., Wu S.X., Tang Y.Q., Tian S.H., Zou G.:  
 RT "Synthesis and biological activity of a new frog skin peptide,  
 RL ranamargarin.";  
 RN Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 33:170-177(1990).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR InterPro: IPR002040; Tachykinin.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 14 14 AMIDATION.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 14 AA; 1617 MW; D4593AE406C3673D CR 64:

Query Match 27.3%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 7 AKK 9

## RESULT 13

COX1\_THUOB  
 ID COX1\_THUOB STANDARD; PRT: 15 AA.  
 AC P80978;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIC-2 (EC 1.9.3.1) (Fragments).  
 OS Thunnus obesus (Bigeye tuna).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Perculiformes; Scombridae;  
 OC Scombridae; Thunnus.  
 OX NCB1\_TaxID=8241;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE:97454291; PubMed:9310366;  
 RA Arnold S., Lee I., Kim M., Song E., Binder E., Gottspesch E.,  
 RA Kadenbach B.:  
 RT "The subunit structure of cytochrome c oxidase from tuna heart and  
 RL liver.";  
 RL Eur. J. Biochem. 248:99-103(1997).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane  
 CC PIR: S77987; S77987.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_CUNS 8 9  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1656 MW; 4C4C966C73A0294 CR 64:

Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 7 AKK 9

RESULT 14

GR7H\_HKSE SHANANAN; PRT: 15 AA

AC P16492;  
 DT 01-AUG-1996 (Rel. 35, Created)  
 DT 01-AUG-1996 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE 74 kDa glucose regulated protein (GRP 78) (Immunoglobulin heavy chain  
 DE binding protein) (NBI) (P01654).  
 GN USP45 OR GRP78.  
 OS Equis Caballus (Horse).  
 CC Eukaryota; Metazoa; Vertebrata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 CC NCB1\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE:9147911; PubMed:1699130;  
 RA Gries R., Boyd N.:  
 RT "Isolation and characterization of a polypeptide in the Hsp 70 family  
 RT that binds stress proteins.";  
 RE Biochem. Biophys. Res. Commun. 166:676-682(1990).  
 CC -!- FUNCTION: Protein plays a role in facilitating the assembly of  
 CC molecular chaperone complexes with the ER  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -!- SIMILARITY: BELONGS TO THE HSP70 PROTEIN FAMILY.  
 ER Eukaryotic proteins.  
 DR PROSITE: PS00277; HSP70; 1; PARTIAL.  
 DR PROSITE: PS00277; HSP70; 1; PARTIAL.  
 DR PROSITE: PS00277; HSP70; 1; PARTIAL.  
 KW Amidation; Endoplasmic reticulum.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 15 AA; 1643 MW; 411661161240P CR 64:

Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 7 AKK 9

## RESULT 15

GR7H\_HKSE SHANANAN; PRT: 15 AA

AC P16492;  
 DT 01-AUG-1996 (Rel. 35, Created)  
 DT 01-AUG-1996 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE 74 kDa glucose regulated protein (GRP 78) (Immunoglobulin heavy chain  
 DE binding protein) (NBI) (P01654).  
 GN USP45 OR GRP78.  
 OS Equis Caballus (Horse).  
 CC Eukaryota; Metazoa; Vertebrata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 CC NCB1\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE:9147911; PubMed:1699130;  
 RA Gries R., Boyd N.:  
 RT "Isolation and characterization of a polypeptide in the Hsp 70 family  
 RT that binds stress proteins.";  
 RE Biochem. Biophys. Res. Commun. 166:676-682(1990).  
 CC -!- FUNCTION: Protein plays a role in facilitating the assembly of  
 CC molecular chaperone complexes with the ER  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -!- SIMILARITY: BELONGS TO THE HSP70 PROTEIN FAMILY.  
 ER Eukaryotic proteins.  
 DR PROSITE: PS00277; HSP70; 1; PARTIAL.  
 DR PROSITE: PS00277; HSP70; 1; PARTIAL.  
 DR PROSITE: PS00277; HSP70; 1; PARTIAL.  
 KW Amidation; Endoplasmic reticulum.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 15 AA; 1643 MW; 411661161240P CR 64:

QY 1 AKK 3  
 DB 7 AKK 9

Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR Maize-2DPAGE: P80614; COLEOPTILE.

DR MaizeUB: 123934; -

FT NON\_TER 1

FT NON\_TER 15

SQ SEQUENCE 15 AA: 1785 MW: 1978B1D6AB41D0F8E CR664

#### Query Match

Best Local Similarity 27.3%; Score 3; DB 1; Length 15;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RNA 11

DB 4 RNA 6

#### RESULT 16

B44K\_P0RG1

ID B44K\_P0RG1 STANDARD: PRT: # AA:

AC P81485;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 44 kDa immunogenic protein (Fragment).

OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales.

OC Porphyromonadaceae; Porphyromonadaceae.

OX NCBI\_TaxID=837;

RN 11

RP SEQUENCE.

RC STRAIN=VEB 3492;

RX MEDLINE=20198497; PubMed=10731616;

RA Norris J.M., Love D.N.;

RT "Serum antibody responses of cats to soluble whole cell antigens of

RT feline Porphyromonas gingivalis."

RL Vet. Microbiol. 73:37-49(2000).

CC -i- SIMILARITY: P.P.GINGIVALIS HEMAGGLUTININ A

KW Antigen.

FT NON\_TER

SQ SEQUENCE 8 AA: 989 MW: 9554540326CH475D CR664;

#### Query Match

Best Local Similarity 18.2%; Score 2; DB 1; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OK 7

DB 4 OK 5

#### RESULT 17

FAP1\_PENMI

ID FAP1\_PENMI STANDARD: PRT: # AA:

AC P81316;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE FMRFamide-like neuropeptide FLPL (GPRNR-like analog).

OS Penaeus monodon (Penaeid shrimp).

OC Fukuyota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Decapodiformata; Penaeoidea;

OC Penaeidae; Penaeus.

OX NCBI\_TaxID=6687;

RN 11

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Eyestalk;

RX MEDLINE=21956277; PubMed=11959015;

RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.;

RA Chaivuthangkura P., Sithigorngul W., Petsom A.;

RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk

RT of the giant tiger prawn Penaeus monodon."

RL Comp. Biochem. Physiol. 131B:325-337(2002).

CC -i- SUBCELLULAR LOCATION: Secreted.

CC -i- MASS SPECTROMETRY: MW-1024.8; METHOD=MALDI.

CC -i- SIMILARITY: P.P.PEN. 1; 100% (FMRFAMIDE RELATED PEPTIDE)

KW Neuropeptide

FT NON\_TER 8

SQ SEQUENCE 8 AA: 14 MW: 1237.2003-45AAR CR664

#### Query Match

Best Local Similarity 100.0%; Score 4; DB 1; Length 8;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 OK 4

DB 4 OK 4

#### RESULT 18

FAP1\_PENMI

ID FAP1\_PENMI STANDARD: PRT: # AA:

AC P81316;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE FMRFamide-like neuropeptide FLPL (GPRNR-like analog).

OS Penaeus monodon (Penaeid shrimp).

OC Fukuyota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Decapodiformata; Penaeoidea;

OC Penaeidae; Penaeus.

OX NCBI\_TaxID=6687;

RN 11

RP SEQUENCE.

RC TISSUE=Eyestalk;

RX MEDLINE=21956277; PubMed=11959015;

RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.;

RA Chaivuthangkura P., Sithigorngul W., Petsom A.;

RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk

RT of the giant tiger prawn Penaeus monodon."

RL Comp. Biochem. Physiol. 131B:325-337(2002).

CC -i- SUBCELLULAR LOCATION: Secreted.

CC -i- MASS SPECTROMETRY: MW-1024.8; METHOD=MALDI.

#### Query Match

Best Local Similarity 100.0%; Score 4; DB 1; Length 8;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 OK 4

DB 4 OK 4

RT substances from the lobster nervous system: isolated and sequenced.  
 RL analysis of two closely related peptides." J. Comp. Neurol. 266:15-26(1987).  
 CC -1- FUNCTION: CAN ACT AS A MODULATOR OF EXCITATORY AMINOACETIC ACID NEUROTRANSMISSION.  
 CC -1- SIMILARITY: BELONGS TO THE FAPR (PENTAPEPTIDE REPEAT PEPTIDE) FAMILY.

KW Neuropeptide: Amidation.  
 FT MOD\_RES 8 AA: 1067 MW: 10672964540451 (P0004).  
 SQ SEQUENCE 8 AA: 1067 MW: 10672964540451 (P0004).

Query Match: 18.2% Score 21: 1P 11: 10445.61  
 Best Local Similarity 100.0% Pred. No. 1: 4-05  
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps

QY 9 RN 1C  
 11  
 DB 3 RN 4

RESULT 20  
 NPB\_BOVIN STANDARD: PRT: 8 AA  
 AC P15507  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropeptide B.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae;  
 CC Ruminantia; Bovidae; Bos.  
 CC NCBI\_TaxID:9913;  
 RN [1]  
 RP SEQUENCE  
 RX TISSUE=Brain;  
 KW MEDLINE=86067985; PubMed=3865193;  
 RA Yang H.-Y.T., Pratta W., Majano E.A., Costa E.  
 RT Isolation, sequencing, synthesis, and pharmacological  
 RT characterization of two brain neuropeptides that modulate the action  
 RT of morphine.  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7757-7761(1995)  
 CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.  
 DR PIR: B24749; B24749.  
 KW Neuropeptide: Amidation.  
 FT MOD\_RES 8 AA: 1062 MW: 10621677696729 (P0004).  
 SQ SEQUENCE 8 AA: 1062 MW: 10621677696729 (P0004).

Query Match: 18.2% Score 21: 1P 11: 10445.61  
 Best Local Similarity 100.0% Pred. No. 1: 4-05  
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps

QY 8 OR 9  
 11  
 DB 6 OR 7

RESULT 21  
 NS3\_MYCTU STANDARD: PRT: 8 AA  
 AC P11152  
 DT 15-JUN-1999 (Rel. 38, Created)  
 DT 15-JUN-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 40 kDa non-secretory protein 3 (Fragment)  
 OS Mycobacterium tuberculosis  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetiales;  
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;  
 CC NCBI\_TaxID:1773;  
 RN [1]  
 RP SEQUENCE  
 RC STRAIN=H37RV;  
 RA Prasad H.K., Annapurna P.S.,

RT substances from the lobster nervous system: isolated and sequenced.  
 RL analysis of two closely related peptides." J. Comp. Neurol. 266:15-26(1987).  
 CC -1- FUNCTION: CAN ACT AS A MODULATOR OF EXCITATORY AMINOACETIC ACID NEUROTRANSMISSION.  
 CC -1- SIMILARITY: BELONGS TO THE FAPR (PENTAPEPTIDE REPEAT PEPTIDE) FAMILY.

KW Neuropeptide: Amidation.  
 FT MOD\_RES 8 AA: 1067 MW: 10672964540451 (P0004).  
 SQ SEQUENCE 8 AA: 1067 MW: 10672964540451 (P0004).

Query Match: 18.2% Score 21: 1P 11: 10445.61  
 Best Local Similarity 100.0% Pred. No. 1: 4-05  
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps

QY 1 AR 4  
 11  
 DB 3 AR 4

RESULT 22  
 PEST\_FISH STANDARD: PRT: 8 AA  
 AC P15507  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropeptide B.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae;  
 CC Ruminantia; Bovidae; Bos.  
 CC NCBI\_TaxID:9913;  
 RN [1]  
 RP SEQUENCE  
 RX TISSUE=Brain;  
 KW MEDLINE=86067985; PubMed=3865193;  
 RA Yang H.-Y.T., Pratta W., Majano E.A., Costa E.  
 RT Isolation, sequencing, synthesis, and pharmacological  
 RT characterization of two brain neuropeptides that modulate the action  
 RT of morphine.  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7757-7761(1995)  
 CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.  
 DR PIR: B24749; B24749.  
 KW Neuropeptide: Amidation.  
 FT MOD\_RES 8 AA: 1062 MW: 10621677696729 (P0004).  
 SQ SEQUENCE 8 AA: 1062 MW: 10621677696729 (P0004).

Query Match: 18.2% Score 21: 1P 11: 10445.61  
 Best Local Similarity 100.0% Pred. No. 1: 4-05  
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps

QY 1 AR 4  
 11  
 DB 3 AR 4

RESULT 23  
 NS3\_MYCTU STANDARD: PRT: 8 AA  
 AC P11152  
 DT 15-JUN-1999 (Rel. 38, Created)  
 DT 15-JUN-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 40 kDa non-secretory protein 3 (Fragment)  
 OS Mycobacterium tuberculosis  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetiales;  
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;  
 CC NCBI\_TaxID:1773;  
 RN [1]  
 RP SEQUENCE  
 RC STRAIN=H37RV;  
 RA Prasad H.K., Annapurna P.S.,



OS Spodoptera eridania (Southern armyworm);  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Brachyura; Portunoidae; Portunidae; Carcinus;  
 OX NCBI\_TaxID=6759, 7130, 7067, 37547;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=C.maenas; TISSUE=Pericardial organs;  
 RA Stangier J., Hilbich C., Beyreuther K., Keller K.  
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
 RT shore crab Carcinus maenas";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987)  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=M.sexata;  
 RA MEDLINE=93050243; PubMed=1426284;  
 RX Cheung C.C., Loi P.K., Sylvester A.W., Lee T.P., Tuller N.J.,  
 RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Barker M.,  
 RA Schooley D.A.;  
 RT "Isolation and identification of a cardioactive peptide from tobacco  
 RT moth and Spodoptera eridania";  
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993)  
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INH. AND CHR. IN THE C.  
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
 CC INTO THE HEMOLYPH.  
 DR PIR: A26363; A26363;  
 DR PIR: S27233; S27233;  
 KW Neuropeptide; Amidation.  
 FT DISULFID 3 9  
 FT MID.RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA: 959 MW: 65A861A9C7D44EB9 3694;  
 Query Match 18.28, Score 24, DB 1, Length 9  
 Best Local Similarity 100.00, Prod. No. 1, No. seqs 1  
 Matches 2: Conservative 0; Mismatches 0; Labels 0  
 QY 10 NA 1;  
 DB 4 NA 5  
 RESULT 24  
 CONO\_CONGE STANDARD: PRT: 1 AA;  
 AC P05446;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lys-conopressin G.  
 OS Conus geographus (Geography cone)  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Mollusca; Trochophora;  
 OC Apogastropoda; Caenogastropoda; Sorogastropoda; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus  
 OX NCBI\_TaxID=6401;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=88058932; PubMed=3680288;  
 RA Cruz L.J., de Santos V., Zafaralla G., Ramirez G.A., Zeikus R.D.,  
 RA Gray W.K., Olivera B.M.;  
 RT "Invertebrate vasopressin/oxytocin homologs: characterization of  
 RT peptides from Conus geographus and Conus striatus venoms";  
 RL J. Biol. Chem. 262:15821-15824(1987)  
 RN [2]  
 RP REVIEW.  
 RX MEDLINE=89024586; PubMed=3052286;  
 RA Gray W.K., Olivera B.M., Cruz L.J.

PI "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
 RC shore crab Carcinus maenas";  
 RA Stangier J., Hilbich C., Beyreuther K., Keller K.  
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
 RT shore crab Carcinus maenas";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987)  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=M.sexata;  
 RA MEDLINE=93050243; PubMed=1426284;  
 RX Cheung C.C., Loi P.K., Sylvester A.W., Lee T.P., Tuller N.J.,  
 RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Barker M.,  
 RA Schooley D.A.;  
 RT "Isolation and identification of a cardioactive peptide from tobacco  
 RT moth and Spodoptera eridania";  
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993)  
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INH. AND CHR. IN THE C.  
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
 CC INTO THE HEMOLYPH.  
 DR PIR: A26363; A26363;  
 DR PIR: S27233; S27233;  
 KW Neuropeptide; Amidation.  
 FT DISULFID 3 9  
 FT MID.RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA: 959 MW: 65A861A9C7D44EB9 3694;  
 Query Match 18.28, Score 24, DB 1, Length 9  
 Best Local Similarity 100.00, Prod. No. 1, No. seqs 1  
 Matches 2: Conservative 0; Mismatches 0; Labels 0  
 QY 10 NA 1;  
 DB 4 NA 5  
 RESULT 24  
 CONO\_CONGE STANDARD: PRT: 1 AA;  
 AC P05446;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lys-conopressin G.  
 OS Conus geographus (Geography cone)  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Mollusca; Trochophora;  
 OC Apogastropoda; Caenogastropoda; Sorogastropoda; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus  
 OX NCBI\_TaxID=6401;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=88058932; PubMed=3680288;  
 RA Cruz L.J., de Santos V., Zafaralla G., Ramirez G.A., Zeikus R.D.,  
 RA Gray W.K., Olivera B.M.;  
 RT "Invertebrate vasopressin/oxytocin homologs: characterization of  
 RT peptides from Conus geographus and Conus striatus venoms";  
 RL J. Biol. Chem. 262:15821-15824(1987)  
 RN [2]  
 RP REVIEW.  
 RX MEDLINE=89024586; PubMed=3052286;  
 RA Gray W.K., Olivera B.M., Cruz L.J.

```

ID PAR6_MACRS STANDARD: PRT: 9 AA:
AC P83279:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLIP6 (DAGANFLFF amide)
OS Macrobrachium rosenbergii (giant freshwater prawn)
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyotalia; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium
ON NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Eye stalk;
RX MEDLINE=21107394; PubMed=1117912;
RA Sithigornquai P., Sarathchandra W., Longyear S., Panchan N.,
RA Sithigornquai W., Panchan A.;
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eye stalk of the giant freshwater prawn Macrobrachium rosenbergii."
RL Peptides 22:191-197(2001)
CC -1- MASS SPECTROMETRY: MW=1080.7; METH=0-MAI01
CC -1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide related peptide)
CC FAMILY.
DR G0: G0300C218; P-neuropeptide signaling pathway; IUA;
KW Neuropeptide; Amidation.
FT MGD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1081 MW: 2680072904540878 CP0644;

Query Match 18.2% Score 2; ID 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10
DB 4 RN 5

RESULT 27
ID LMIP_L0CMI STANDARD: PRT: 9 AA:
AC P31799;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locustamininhibiting peptide (LOM-MIP)
OS Locusta migratoria (Migratory locust)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta;
ON NCBI_TaxID=7004;
RN [1]
RP SEQUENCE
RX MEDLINE=92179466; PubMed=1796179;
RA Schoofs L., Holman G.M., Hayes T.K., Natchian R.J., de laet A.;
RT "Isolation, identification and synthesis of locustamininhibiting
RT peptide (LOM-MIP), a novel biologically active neuropeptide from
RT Locusta migratoria."
RL Regul. Pept. 36:111-119(1991)
CC -1- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HYPOTHALAMIC
CC INDUCTION.
CC -1- TISSUE SPECIFICITY: NEURONS LOCATED IN THE VENTRAL CELL CLUSTERS
CC IN THE SUBESOPHAGEAL GANGLION
DR PIR: A60065; AKLOIM.
KW Amidation; Neuropeptide.
FT MGD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1060 MW: 3870700447248654 CP0644;

Query Match 18.2% Score 2; ID 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NA 11
DB 11

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ID PAR6_MACRS STANDARD: PRT: 9 AA:
AC P83279:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLIP6 (DAGANFLFF amide)
OS Macrobrachium rosenbergii (giant freshwater prawn)
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyotalia; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium
ON NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Eye stalk;
RX MEDLINE=21107394; PubMed=1117912;
RA Sithigornquai P., Sarathchandra W., Longyear S., Panchan N.,
RA Sithigornquai W., Panchan A.;
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eye stalk of the giant freshwater prawn Macrobrachium rosenbergii."
RL Peptides 22:191-197(2001)
CC -1- MASS SPECTROMETRY: MW=1080.7; METH=0-MAI01
CC -1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide related peptide)
CC FAMILY.
DR G0: G0300C218; P-neuropeptide signaling pathway; IUA;
KW Neuropeptide; Amidation.
FT MGD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1081 MW: 2680072904540878 CP0644;

Query Match 18.2% Score 2; ID 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10
DB 4 RN 5

RESULT 27
ID LMIP_L0CMI STANDARD: PRT: 9 AA:
AC P31799;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locustamininhibiting peptide (LOM-MIP)
OS Locusta migratoria (Migratory locust)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta;
ON NCBI_TaxID=7004;
RN [1]
RP SEQUENCE
RX MEDLINE=92179466; PubMed=1796179;
RA Schoofs L., Holman G.M., Hayes T.K., Natchian R.J., de laet A.;
RT "Isolation, identification and synthesis of locustamininhibiting
RT peptide (LOM-MIP), a novel biologically active neuropeptide from
RT Locusta migratoria."
RL Regul. Pept. 36:111-119(1991)
CC -1- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HYPOTHALAMIC
CC INDUCTION.
CC -1- TISSUE SPECIFICITY: NEURONS LOCATED IN THE VENTRAL CELL CLUSTERS
CC IN THE SUBESOPHAGEAL GANGLION
DR PIR: A60065; AKLOIM.
KW Amidation; Neuropeptide.
FT MGD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1060 MW: 3870700447248654 CP0644;

Query Match 18.2% Score 2; ID 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NA 11
DB 11

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```

QY      2 KK 3
DB      11
      2 KK 3

RESULT 29
NEUO_CAVPO
ID      NEUO_CAVPO      STANDARD;      PRT;      9 AA.
AC      P34966;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Neuromedin U-9 (NMU-9).
GN      NMU.
OS      Cavia porcellus (Guinea pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX      NCBI_TaxID=10141;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Small intestine;
RX      MEDLINE=90341105; PubMed=2381877;
RA      Murphy K., Turner C.A., Furness J.B., Parker L., Giraud A.J.
RT      "Isolation and microsequence analysis of a novel form of neuromedin U
RT      from guinea pig small intestine."
RL      Peptides 11:613-617(1990).
CC      -!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES
CC      -!- SELECTIVE VASOCONSTRICTION.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: BELONGS TO THE NMU FAMILY.
DR      InterPro: IPR001942; NMU.
DR      Pfam: PF02070; NMU; 1.
DR      PROSITE: PS00967; NMU; 1.
KW      Antidation; Hormone.
FT      MOD_RES      9 AA: 1169 MW; IECF177409K72938 (Rel. 41);
SQ      SEQUENCE      9 AA: 1169 MW; IECF177409K72938 (Rel. 41);

Query Match:      18.2% Score 21 DB 1; Length 9;
Best local Similarity 100.0%; Pred. No. 1, 0-05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 RN 10
DB      11
      8 RN 9

RESULT 30
OXYT_ELSFO
ID      OXYT_ELSFO      STANDARD;      PRT;      9 AA.
AC      P42968;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      Arginine.
OS      Eisenia foetida (Common brandling worm) (Common dung worm).
OC      Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplocladia;
OC      Lumbricina; Lumbricidae; Eisenia.
OX      NCBI_TaxID=6396;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Intestine;
RX      MEDLINE=94121650; PubMed=8292046;
RA      Gumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Matsukata H.,
RA      Nomoto K.
RT      "Anetocin: an oxytocin-related peptide isolated from the earthworm,
RT      Eisenia foetida."
RL      Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC      -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC      PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC      NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC      NEPHRIDIAL FUNCTION.
CC      -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR      PIR: PC2021; PC2021.

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DR      InterPro: IPR001941; Neuromedin;
DR      Pfam: PF0220; Neuromedin;
DR      PROSITE: PS00264; NEURAVIPPTS (HMM; FALSE_NEG.
KW      Hormones; Antidation.
FT      DISULFID      1
FT      MOD_RES      9 AA: 1169 MW; IECF177409K72938 (Rel. 41);
SQ      SEQUENCE      9 AA: 1169 MW; IECF177409K72938 (Rel. 41);

Query Match:      18.2% Score 21 DB 1; Length 9;
Best local Similarity 100.0%; Pred. No. 1, 0-05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 RN 10
DB      4 RN 5

RESULT 31
OXYT_ELSFO
ID      OXYT_ELSFO      STANDARD;      PRT;      9 AA.
AC      P42968;
DT      01-MAR-1992 (Rel. 32, Created)
DT      01-MAR-1992 (Rel. 32, Last sequence update)
DT      01-NOV-1995 (Rel. 41, Last annotation update)
DE      Arginine.
OS      Oxytropis magdalenae (Papilionaceae).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Cyprinodontiformes; Cyprinodontidae; Poeciliidae;
OX      NCBI_TaxID=10141;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Neuroendocrine;
RX      MEDLINE=94121650; PubMed=8292046;
RA      Gumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Matsukata H.,
RT      "Anetocin: an oxytocin-related peptide isolated from the earthworm,
RT      Eisenia foetida."
RL      Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC      -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC      PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC      NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC      NEPHRIDIAL FUNCTION.
CC      -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR      PIR: PC2021; PC2021.

```

RL Submitted (APR-1998) to the EMBL/GenBank/DBSJ databases.  
 CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF058451; AAC14294.1; -;  
 DR HAHAH; MF\_00508; -; 1;  
 DR INTERPRO: IPR001848; Ribosomal\_S10.  
 DR PROSITE: PS00361; RIBOSOMAL\_S10; PARTIAL.  
 KW Ribosomal protein.  
 FT NON\_TER 9  
 FT SEQUENCE 9 AA; 1214 MW; DE3944004410456 CKE64;

Query Match 18.2% Score 2; FR 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QR 9  
 DB 4 QR 5

RESULT 33  
 RT33\_BOVIN  
 ID RT33\_BOVIN STANDARD; PRI: 9 AA.  
 AC P82926;  
 DT 28-FEB-2003 (rel. 41, Created)  
 DT 28-FEB-2003 (rel. 41, Last sequence update)  
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MPP-S34) (fragment).  
 GN MRPS33.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCRL\_TaxID=99113;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=21276436; PubMed=11279123;  
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Sprommler L.L.;  
 RT "The small subunit of the mammalian mitochondrial ribosome:  
 RT Identification of the full complement of ribosomal proteins present."  
 RL J. Biol. Chem. 276:19363-19374(2001).  
 CC -!- SUBUNIT: Component of a mitochondrial ribosome small subunit  
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 1  
 FT NON\_TER 9  
 FT SEQUENCE 9 AA; 1032 MW; D341D73776D80589 CKE64.

Query Match 18.2% Score 2; FR 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AK 2  
 DB 8 AK 9

RESULT 34  
 THYF\_PIG  
 ID THYF\_PIG STANDARD; PRI: 9 AA.  
 AC P01255;

DT 21 JUL-1998 (rel. 41, Created)  
 DT 21 JUL-1998 (rel. 41, Last sequence update)  
 DT 28 FEB-2003 (rel. 41, Last annotation update)  
 DE Thymic factor.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Suidae; Sus  
 CC NCRL\_TaxID=99113;  
 RN [1]  
 RP SEQUENCE.  
 KX MEDLINE=7602671; PubMed=944442;  
 RA Fleury J.M., Lardoux M., Bloch Y., Bach J.-F.;  
 RT "Structural study of thymic thymic factor: a peptide isolated  
 RT from pig thymus. II. Amino acid sequence."  
 RL J. Biol. Chem. 268:6066-6070(1993).  
 CC -!- MISCELLANEOUS: HEAVY METAL ION SENSITIVE AND PHYSIOLOGICAL  
 CC ACTIVITIES OF THE THYMIC FACTOR HAVE NOT BEEN DETERMINED.  
 DR FIP; A01620; YF03;  
 KW Peptide; Thymic factor; Thymus; Thymocyte; Thymic factor; Thymic  
 FT NON\_TER 1  
 FT SEQUENCE 9 AA; 1199 MW; D1941363422 CKE64;

Query Match 18.2% Score 2; FR 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AK 2  
 DB 2 AK 4

RESULT 35  
 HLA\_HUMAN  
 ID HLA\_HUMAN STANDARD; PRI: 9 AA.  
 AC P31429;  
 DT 01 JUL-1993 (rel. 23, Created)  
 DT 01 JUL-1993 (rel. 23, Last sequence update)  
 DE Unknown protein from 2L page of liver tissue (Spot 106) (Fragment)  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catartiodactyla; Hominiidae; Homo.  
 OX NCPI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94147900; PubMed=841676;  
 RA Hughes G.J., Burkhardt W., Blackburn K., Moseley A., Sprommler L.L.;  
 RA "The small subunit of the mammalian mitochondrial ribosome:  
 RT Identification of the full complement of ribosomal proteins present."  
 RL J. Biol. Chem. 276:19363-19374(2001).  
 CC -!- SUBUNIT: Component of a mitochondrial ribosome small subunit  
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 1  
 FT NON\_TER 9  
 FT SEQUENCE 9 AA; 1199 MW; D1941363422 CKE64;

Query Match 18.2% Score 2; FR 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AK 3  
 DB 6 AK 1

RESULT 36  
 CATH\_SHEEP  
 ID CATH\_SHEEP STANDARD; PRI: 10 AA.  
 AC P84255;  
 DT 15 SEP-2003 (rel. 42, Created)  
 DT 15 SEP-2003 (rel. 42, Last sequence update)  
 DT 15 SEP-2003 (rel. 42, Last annotation update)

DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).  
GN CISH.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Artiodactyla; Bovidae; Bovinae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID:9940;  
RN [1]  
RP SEQUENCE.  
RC TISSUE: Placenta;  
RX MEDLINE:22394055; PubMed:12563852;  
RA El Amir B., Remy B., Sousa N.M., Doris R., editors N. El Amir B.,  
KA "Isolation and partial characterization of three protease-associated  
RT glycoproteins from the ewe placenta.";  
RL Mol. Reprod. Dev. 64:199-206(2004).  
CC 1-1- FUNCTION: Thiol protease which is believed to participate in  
CC intracellular degradation and turnover of proteins; has also been  
CC implicated in tumor invasion and metastasis;  
CC 1-1- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
CC for peptide bonds. Preferentially cleaves Arg-Arg-Xaa bonds in  
CC small molecule substrates (thus differing from cathepsin B). In  
CC addition to being an endopeptidase, shows peptidyl dipeptidase  
CC activity, liberating C-terminal dipeptides.  
CC 1-1- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked  
CC by a disulfide bond (by similarity).  
CC 1-1- SUBCELLULAR LOCATION: Lysosomal (by similarity).  
CC 1-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 11.  
DR InterPro: IPR000169; Shprot\_acsite.  
DR PROSITE: PS00640; THIOL\_PROTEASE\_ASN; PARTIAL.  
DR PROSITE: PS00139; THIOL\_PROTEASE\_CYS; PARTIAL.  
DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; PARTIAL.  
KW Hydrolase; Thiol protease; Lysosome.  
FT NON-TER 10 10  
SQ SEQUENCE 10 AA: 1177 MW: 879578.10DAAAGTSEA CR664;  
Query Match 18.2% Score 21.38 E-10 Length 192  
Best Local Similarity 100.0% Pred. No. 1,10,44  
Matches 2: Conservative G: Mismatches 6: Indels 0: Gaps 0:  
QY 5 EQ 6  
Db 1  
FC 10  
RESULT 47  
COXA\_OXNMY STANDARD: PRT: 10 AA.  
ID COXA\_OXNMY  
AC P60428;  
DT 01-OCT-1994 (rel. 30, Created)  
DT 01-OCT-1994 (rel. 30, Last sequence update)  
DT 30-MAY-2000 (rel. 39, Last annotation update)  
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment)  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Procaranopterygii; Salmoniformes; Salmonidae; Oncorhynchus;  
OX NCBI\_TaxID:8022;  
RN [1]  
RP SEQUENCE.  
RC TISSUE: Liver;  
RX MEDLINE:94217150; PubMed:8181469;  
RA Freund R., Kadenbach B.;  
RT "Identification of tissue-specific isoforms for subunits VB and VIIa  
RT of cytochrome c oxidase isolated from rainbow trout.";  
RL Eur. J. Biochem. 221:1111-1116(1994).  
CC 1-1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT  
CC 1-1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferrioxycyclochrome  
CC c + 2 H(2)O.  
CC 1-1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
CC 1-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
DR PIR: S43625; S43625.

KW Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
FT NON-TER 10 10  
SQ SEQUENCE 10 AA: 1177 MW: 879578.10DAAAGTSEA CR664;  
Query Match 18.2% Score 21.38 E-10 Length 192  
Best Local Similarity 100.0% Pred. No. 1,10,44  
Matches 2: Conservative G: Mismatches 6: Indels 0: Gaps 0:  
QY 5 EQ 6  
Db 1  
FC 10  
RESULT 47  
COXA\_OXNMY STANDARD: PRT: 10 AA.  
ID COXA\_OXNMY  
AC P60428;  
DT 01-OCT-1994 (rel. 30, Created)  
DT 01-OCT-1994 (rel. 30, Last sequence update)  
DT 30-MAY-2000 (rel. 39, Last annotation update)  
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment)  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Procaranopterygii; Salmoniformes; Salmonidae; Oncorhynchus;  
OX NCBI\_TaxID:8022;  
RN [1]  
RP SEQUENCE.  
RC TISSUE: Liver;  
RX MEDLINE:94217150; PubMed:8181469;  
RA Freund R., Kadenbach B.;  
RT "Identification of tissue-specific isoforms for subunits VB and VIIa  
RT of cytochrome c oxidase isolated from rainbow trout.";  
RL Eur. J. Biochem. 221:1111-1116(1994).  
CC 1-1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT  
CC 1-1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferrioxycyclochrome  
CC c + 2 H(2)O.  
CC 1-1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
CC 1-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
DR PIR: S43625; S43625.









```
RN SEQUENCE.
RP STRAIN-L2/434/Bu;
RA Bini L., Santucci A., Maqi B., Martocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christlanen G., Birkelund S., Viireto E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
DR Siena-2DPAGE: P38007;
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1243 MW: DAD39A333048539 CRC64:

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
DB 7 KK 8

RESULT 50
ASL2_BACSE
1D ASL2_BACSE STANDARD: PRT: 11 AA.
AC P83147;
DT 28 FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN-H-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.-S., Kim D.-H.;
RT *Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6, its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA: 1195 MW: D79D897C7AA451AD CRC64:

Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QR 9
DB 10 QR 11
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 17:03:12 : Search time 92 Seconds  
(without alignments)  
10.854 Million cell updates/sec

Title: US-09-787-443-20

Perfect score: 11

Sequence: 1 AKKEQKQRNA 11

Scoring table: OLIGO  
Gapox 60.0, Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1454

Minimum DB seq length: 8  
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database:

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriapi:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	15	4 Q90C17	Q90C17 homo sapien
2	4	36.4	15	10 Q90U16	Q90U16 ariza sativ
3	3	27.3	9	11 Q90M63	Q90M63 mus muscul
4	3	27.3	11	4 Q90H45	Q90H45 homo sapien
5	3	27.3	12	2 Q90VX8	Q90VX8 thelmus the
6	3	27.3	12	16 Q25179	Q25179 helicobacte
7	3	27.3	13	2 Q50117	Q50117 mycobacteri
8	3	27.3	13	4 Q90HC1	Q90HC1 homo sapien
9	3	27.3	13	8 Q90T569	Q90T569 zea mays (m
10	3	27.3	13	16 Q8X4F5	Q8X4F5 escherichia
11	3	27.3	14	1 Q90WM2	Q90WM2 pyrococcus
12	3	27.3	14	2 Q56750	Q56750 western x p
13	3	27.3	14	2 Q46291	Q46291 canadian pc
14	3	27.3	14	4 Q96Q50	Q96Q50 homo sapien
15	3	27.3	14	4 Q15222	Q15222 homo sapien
16	3	27.3	14	13 P82831	P82831 rana luteiv

17	3	27.3	15	2 Q90C12	Q90C12 escherichia
18	3	27.3	15	4 Q90B85	Q90B85 rhoa sapien
19	3	27.3	15	4 Q90B62	Q90B62 homo sapien
20	3	27.3	16	4 Q90V20	Q90V20 homo sapien
21	3	27.3	16	5 Q90W04	Q90W04 r11111114 1
22	3	27.3	16	5 Q90V49	Q90V49 homo sapien
23	3	27.3	16	5 Q90B46	Q90B46 homo sapien
24	3	27.3	16	15 Q90S81	Q90S81 zea mays (m
25	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
26	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
27	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
28	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
29	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
30	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
31	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
32	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
33	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
34	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
35	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
36	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
37	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
38	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
39	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
40	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
41	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
42	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
43	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
44	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
45	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
46	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
47	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
48	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
49	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
50	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
51	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
52	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
53	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
54	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
55	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
56	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
57	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
58	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
59	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
60	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
61	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
62	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
63	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
64	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
65	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
66	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
67	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
68	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
69	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
70	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
71	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
72	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
73	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
74	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
75	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
76	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
77	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
78	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
79	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
80	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
81	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
82	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
83	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
84	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
85	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
86	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
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88	3	27.3	16	16 Q90A11	Q90A11 r11111114 1
89	3	27.3	16	16 Q90A11	Q90A11 r11111114 1

90	2	18.2	10	2	Q8VNE5	Q8VNE5 bacillibacter	1.3	2	13.3	1	Q8VNE5	Q8VNE5 bacillibacter
91	2	18.2	10	2	Q8X3M2	Q8X3M2 bacillibacter	1.4	2	13.4	1	Q8X3M2	Q8X3M2 bacillibacter
92	2	18.2	10	2	Q8Y217	Q8Y217 bacillibacter	1.5	2	13.5	1	Q8Y217	Q8Y217 bacillibacter
93	2	18.2	10	2	Q8RSU1	Q8RSU1 bacillibacter	1.6	2	13.6	1	Q8RSU1	Q8RSU1 bacillibacter
94	2	18.2	10	2	Q8S336	Q8S336 bacillibacter	1.7	2	13.7	1	Q8S336	Q8S336 bacillibacter
95	2	18.2	10	2	Q8Q194	Q8Q194 bacillibacter	1.8	2	13.8	1	Q8Q194	Q8Q194 bacillibacter
96	2	18.2	10	2	Q8Q192	Q8Q192 bacillibacter	1.9	2	13.9	1	Q8Q192	Q8Q192 bacillibacter
97	2	18.2	10	2	Q8S5N1	Q8S5N1 bacillibacter	2.0	2	14.0	1	Q8S5N1	Q8S5N1 bacillibacter
98	2	18.2	10	2	Q8S5N3	Q8S5N3 bacillibacter	2.1	2	14.1	1	Q8S5N3	Q8S5N3 bacillibacter
99	2	18.2	10	2	Q8Q464	Q8Q464 bacillibacter	2.2	2	14.2	1	Q8Q464	Q8Q464 bacillibacter
100	2	18.2	10	2	Q8S182	Q8S182 bacillibacter	2.3	2	14.3	1	Q8S182	Q8S182 bacillibacter
101	2	18.2	10	2	Q8JNC5	Q8JNC5 bacillibacter	2.4	2	14.4	1	Q8JNC5	Q8JNC5 bacillibacter
102	2	18.2	10	2	Q8RTT1	Q8RTT1 bacillibacter	2.5	2	14.5	1	Q8RTT1	Q8RTT1 bacillibacter
103	2	18.2	10	2	Q8AE19	Q8AE19 bacillibacter	2.6	2	14.6	1	Q8AE19	Q8AE19 bacillibacter
104	2	18.2	10	2	Q8Q619	Q8Q619 bacillibacter	2.7	2	14.7	1	Q8Q619	Q8Q619 bacillibacter
105	2	18.2	10	2	Q8S163	Q8S163 bacillibacter	2.8	2	14.8	1	Q8S163	Q8S163 bacillibacter
106	2	18.2	10	2	Q8J062	Q8J062 bacillibacter	2.9	2	14.9	1	Q8J062	Q8J062 bacillibacter
107	2	18.2	10	2	Q8NKC9	Q8NKC9 bacillibacter	3.0	2	15.0	1	Q8NKC9	Q8NKC9 bacillibacter
108	2	18.2	10	2	Q8UMK9	Q8UMK9 bacillibacter	3.1	2	15.1	1	Q8UMK9	Q8UMK9 bacillibacter
109	2	18.2	10	2	Q8UCS3	Q8UCS3 bacillibacter	3.2	2	15.2	1	Q8UCS3	Q8UCS3 bacillibacter
110	2	18.2	10	2	Q8QD28	Q8QD28 bacillibacter	3.3	2	15.3	1	Q8QD28	Q8QD28 bacillibacter
111	2	18.2	10	2	Q8Q019	Q8Q019 bacillibacter	3.4	2	15.4	1	Q8Q019	Q8Q019 bacillibacter
112	2	18.2	10	2	Q8NKC6	Q8NKC6 bacillibacter	3.5	2	15.5	1	Q8NKC6	Q8NKC6 bacillibacter
113	2	18.2	10	2	Q8X3S5	Q8X3S5 bacillibacter	3.6	2	15.6	1	Q8X3S5	Q8X3S5 bacillibacter
114	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	3.7	2	15.7	1	Q8NCP1	Q8NCP1 bacillibacter
115	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	3.8	2	15.8	1	Q8NCP1	Q8NCP1 bacillibacter
116	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	3.9	2	15.9	1	Q8NCP1	Q8NCP1 bacillibacter
117	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.0	2	16.0	1	Q8NCP1	Q8NCP1 bacillibacter
118	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.1	2	16.1	1	Q8NCP1	Q8NCP1 bacillibacter
119	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.2	2	16.2	1	Q8NCP1	Q8NCP1 bacillibacter
120	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.3	2	16.3	1	Q8NCP1	Q8NCP1 bacillibacter
121	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.4	2	16.4	1	Q8NCP1	Q8NCP1 bacillibacter
122	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.5	2	16.5	1	Q8NCP1	Q8NCP1 bacillibacter
123	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.6	2	16.6	1	Q8NCP1	Q8NCP1 bacillibacter
124	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.7	2	16.7	1	Q8NCP1	Q8NCP1 bacillibacter
125	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.8	2	16.8	1	Q8NCP1	Q8NCP1 bacillibacter
126	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	4.9	2	16.9	1	Q8NCP1	Q8NCP1 bacillibacter
127	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.0	2	17.0	1	Q8NCP1	Q8NCP1 bacillibacter
128	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.1	2	17.1	1	Q8NCP1	Q8NCP1 bacillibacter
129	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.2	2	17.2	1	Q8NCP1	Q8NCP1 bacillibacter
130	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.3	2	17.3	1	Q8NCP1	Q8NCP1 bacillibacter
131	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.4	2	17.4	1	Q8NCP1	Q8NCP1 bacillibacter
132	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.5	2	17.5	1	Q8NCP1	Q8NCP1 bacillibacter
133	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.6	2	17.6	1	Q8NCP1	Q8NCP1 bacillibacter
134	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.7	2	17.7	1	Q8NCP1	Q8NCP1 bacillibacter
135	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.8	2	17.8	1	Q8NCP1	Q8NCP1 bacillibacter
136	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	5.9	2	17.9	1	Q8NCP1	Q8NCP1 bacillibacter
137	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.0	2	18.0	1	Q8NCP1	Q8NCP1 bacillibacter
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139	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.2	2	18.2	1	Q8NCP1	Q8NCP1 bacillibacter
140	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.3	2	18.3	1	Q8NCP1	Q8NCP1 bacillibacter
141	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.4	2	18.4	1	Q8NCP1	Q8NCP1 bacillibacter
142	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.5	2	18.5	1	Q8NCP1	Q8NCP1 bacillibacter
143	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.6	2	18.6	1	Q8NCP1	Q8NCP1 bacillibacter
144	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.7	2	18.7	1	Q8NCP1	Q8NCP1 bacillibacter
145	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.8	2	18.8	1	Q8NCP1	Q8NCP1 bacillibacter
146	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	6.9	2	18.9	1	Q8NCP1	Q8NCP1 bacillibacter
147	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.0	2	19.0	1	Q8NCP1	Q8NCP1 bacillibacter
148	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.1	2	19.1	1	Q8NCP1	Q8NCP1 bacillibacter
149	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.2	2	19.2	1	Q8NCP1	Q8NCP1 bacillibacter
150	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.3	2	19.3	1	Q8NCP1	Q8NCP1 bacillibacter
151	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.4	2	19.4	1	Q8NCP1	Q8NCP1 bacillibacter
152	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.5	2	19.5	1	Q8NCP1	Q8NCP1 bacillibacter
153	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.6	2	19.6	1	Q8NCP1	Q8NCP1 bacillibacter
154	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.7	2	19.7	1	Q8NCP1	Q8NCP1 bacillibacter
155	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.8	2	19.8	1	Q8NCP1	Q8NCP1 bacillibacter
156	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	7.9	2	19.9	1	Q8NCP1	Q8NCP1 bacillibacter
157	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	8.0	2	20.0	1	Q8NCP1	Q8NCP1 bacillibacter
158	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	8.1	2	20.1	1	Q8NCP1	Q8NCP1 bacillibacter
159	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	8.2	2	20.2	1	Q8NCP1	Q8NCP1 bacillibacter
160	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	8.3	2	20.3	1	Q8NCP1	Q8NCP1 bacillibacter
161	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	8.4	2	20.4	1	Q8NCP1	Q8NCP1 bacillibacter
162	2	18.2	10	2	Q8NCP1	Q8NCP1 bacillibacter	8.5	2	20.5	1	Q8NCP1	Q8NCP1 bacillibacter



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427 Q8KY46 12 13 Q8KY46 18.2 2
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429 Q9RF24 12 13 Q9RF24 18.2 2
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445 Q9TWK3 12 13 Q9TWK3 18.2 2
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450 Q812E2 12 13 Q812E2 18.2 2
451 Q81085 12 13 Q81085 18.2 2
452 Q81084 12 13 Q81084 18.2 2
453 Q81083 12 13 Q81083 18.2 2
454 Q9BDQ8 12 13 Q9BDQ8 18.2 2

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Q99NX8 dinomys bra
Q9QZY4 mus musculus
Q99NY1 heterocephala
Q99NZ0 castor cana
Q99NY3 arethizon d
Q99NX7 arethizon tacz
Q99NY0 cavia tachu
Q99NZ1 tamias stri
Q99NY4 hystrix bra
Q99NY8 pedetes cap
Q8CJ30 mus musculus
Q89243 woodchuck h
Q66202 transmissib
Q84038 influenzavi
Q9PVC2 gadus morhu
Q9PVC3 lampris sp
Q9PVC0 muqil cepha
Q9PVC1 lothaus sp
Q9PVB9 cryzias lat
Q9PVC6 plicoglossu
Q9PVB8 hemiramphus
Q9PVC7 esox lucius
Q9PVC4 harpadon sp
Q8AUP8 salmo trutt
Q8AUP7 salmo salar
Q98VN6 human immun
Q85631 avian carci
Q12036 caprine art
Q98R89 human immun
Q9RG00 human immun
Q9X376 mycoplasma
Q9X376 prochloroco
Q50476 mycobacteri
Q34770 borrelia af
Q47601 escherichia
Q47601 escherichia
Q8RSG9 uncultured
Q9X3E1 prochloroco
Q9X386 prochloroco
P97140 borrelia bu
Q47693 escherichia
Q50038 mycobacteri
Q8KY46 enterococcu
Q34622 borrelia bu
Q9RF24 mycoplasma
Q9RF27 actinobacil
Q9R2F8 escherichia
P82560 streptococc
Q8GBU2 vibrio harv
Q9BEE2 homo sapien
Q9PBB6 homo sapien
Q9PBB6 homo sapien
Q9U3S1 homo sapien
Q9UM46 homo sapien
Q9U352 homo sapien
Q9PBB6 homo sapien
P82276 homo sapien
Q9U7D6 neospora ca
Q9W5Q6 drosophila
Q9TWK4 titius serr
Q9TWK3 locusta miq
Q97122 toxoplasma
Q8MM57 heliconius
Q818F2 drosophila
Q818F2 drosophila
Q812E2 plasmodium
Q81085 drosophila
Q81084 drosophila
Q81083 drosophila
Q9BDQ8 sus scrofa

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## ALIGNMENTS

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RESULT 1
Q99NY7 10 Q99NY7 PROCLIMINAPYD 150 15 AA
AC Q99NY7
BT Q1 MAY-2000 (F11EM0100) 14 (Unreleased)
BT Q1 MAY-2000 (F11EM0100) 14 (Last Sequence Update)
BT Q1 DEP-2000 (F11EM0100) 14 (Last amino acid update)
DE M1K100 (F11EM0100)
OS Bacteria (F11EM0100)
OC Bacteria (F11EM0100)
OC Bacteria (F11EM0100)
CX NCBI_TaxID 9606
RN 1
RP SEQUENCE
FX MEDLINE 44069423 PubMed 44069423
RA Novotny W.F., Maffi T., Medina P.L., Milner P.G.
RT Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.
RL Arterioscler. Thromb. Vasc. Biol. 1995;15(4):
SQ SEQUENCE 15 AA: 1527 MW: 13406.9927047440 CRC64:
Query Match 10.4% Score 4: 10.4 10.4 15:

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Best Local Similarity 100.0%; Pred. No. 9,1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
Db 2 AKKK 5

## RESULT 2

Q9SQ16 PRELIMINARY; PRT: 15 AA.  
AC Q9SQ16  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
DE Translation elongation factor (Fraumeni).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzoideae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li Z.-Y., Chen S.-Y.;  
RT "Inducible expression of translation elongation factor 1A gene in rice seedlings in response to environmental stresses.";  
RL Acta Bot. Sin. 41:800-806(1999).  
DR EMBL: AF067195; AAC79991.1; -;  
DR Gramene: Q9SQ16; -;  
KW Elongation factor.  
FT NON\_TER  
SQ SEQUENCE 15 AA: 1514 MW: 95E5C46F069C9775 CRC64:

Query Match 36.4%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9,1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
Db 12 AKKK 15

## RESULT 3

Q99MG3 PRELIMINARY; PRT: 9 AA.  
AC Q99MG3  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE NCAM protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA More M.I., Kirsch F.P., Rathjen F.G.;  
RT "Targeted ablation of Nrcam and ankyrin-B results in disorganized lens fibres leading to cataract formation.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF346472; AAK25814.1; -;  
FT NON\_TER  
SQ SEQUENCE 9 AA: 1039 MW: 32FCB721E3333327 CRC64:

Query Match 27.3%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8,3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4  
Db 3 KKK 5

## RESULT 4

Q9H4H5 PRELIMINARY; PRT: 11 AA.  
AC Q9H4H5  
DT 01-MAR-2001 (TRENBLrel. 20, Created)  
DT 01-MAR-2001 (TRENBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 23, Last annotation update)  
DE 23611.2012 (NCBI TaxID=4530) domain and SNF2 N-terminal domain conserved in the human (Homo sapiens).  
GN Ljz2011.1  
OS Homo sapiens (Homo).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Skolnik A.;  
KL Submitted (01-MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AAF01111; -;  
FT NON\_TER  
SQ SEQUENCE 11 AA: 111 MW: 11122.254 CRC64:

Query Match 36.4%; Score 4; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9,1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 6  
Db 7 KKK 9

## RESULT 5

Q9VXXB PRELIMINARY; PRT: 12 AA.  
AC Q9VXXB  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE LYSYL-PNA Synthesase (Friedmann).  
GN LYSN  
OS Thermobus thermophilus  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Thermobacteriaceae; Thermobacterium.  
OC Thermobus.  
OX NCBI\_TaxID=2144;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Straub K.R.;  
RA Spada S.;  
KL "Cloning and characterization of a wild-type gene from T. thermophilus.";  
KL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AAF01111; -;  
FT NON\_TER  
SQ SEQUENCE 12 AA: 1212 MW: 6226.627 CRC64:

Query Match 27.3%; Score 3; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8,3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 6  
Db 4 KKK 6

## RESULT 6

Q25179 PRELIMINARY; PRT: 12 AA.  
AC Q25179  
DT 01-JAN-1998 (TRENBLrel. 05, Created)  
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Hypothetical protein HP0429.  
GN HP0429.  
OS Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=26695 / ATCC 700392;  
RX MESLINE=97394467; PubMed=9252185;  
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.B.,  
RA Feiselman K.D., Ketchum K.A., Klock H.-P., Gill S., Dougherty R.A.,  
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,  
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,  
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Beckey E.K.,  
RA Berg D.E., Gocayne J.D., Utterback T.K., Peterson J.D., Kelley J.M.,  
RA Colton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin F.,  
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,  
RA Venter J.C.;  
RT \*The complete genome sequence of the gastric pathogen Helicobacter  
RT pylori.\*;  
RL Nature 388:539-547(1997).  
DR EMBL: AE005559; AA007512.1;  
DR TIGR: HP0429;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 12 AA; 1375 MW; 20959A84E21333B CRC64;  
  
Query Match 27.38; Score 3; DB 16; Length 12;  
Best Local Similarity 100.0%; Pred. No. Hov. 3;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KKK 5  
DB 111  
6 KKE 8  
  
RESULT 7  
Q50117 PRELIMINARY; PRT; 13 AA.  
ID Q50117  
AC Q50117;  
DT 01-NOV-1996 (TrEMBLrel. 0); Created)  
DT 01-NOV-1996 (TrEMBLrel. 0); Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23; last annotation update)  
DE U650w.  
OS Mycobacterium leprae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Smith D.R.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Robinson K.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U15184; AAA63055.1;  
SQ SEQUENCE 13 AA; 1503 MW; CAABF1429DE5412 CRC64;  
  
Query Match 27.38; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. Hov. 3;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 RNA 11  
DB 111  
7 RNA 9  
  
RESULT 8  
Q9H4C1 PRELIMINARY; PRT; 13 AA.  
ID Q9H4C1  
AC Q9H4C1;  
DT 01-MAR-2001 (TrEMBLrel. 16; Created)

DE MAY 2001 (EMBLrel. 1); Last sequence update)  
DT 01-SEP-2001 (EMBLrel. 1); Last annotation update)  
LE ANGIOTENSIN II (Angiotensin II)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Hominidae; Hominidae; Homo  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC METLIN=271044; PubMed=11111111;  
RA Villalaz A., Villalaz A., Villalaz A., Villalaz A., Villalaz A.,  
RA Villalaz A., Villalaz A., Villalaz A., Villalaz A., Villalaz A.,  
RT \*Genomic structure of the human angiotensin II receptor gene  
RT 2.\*  
RL Human; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
RL EMBL: AL444444.1; GenBank: U00000.1; F00000.1;  
RT NCBI\_TaxID=9606;  
SQ SEQUENCE 14 AA; 1503 MW; 20959A84E21333B CRC64;  
  
Query Match 27.38; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. Hov. 3;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KKK 5  
DB 111  
6 KKE 8  
  
RESULT 9  
Q50117 PRELIMINARY; PRT; 13 AA.  
ID Q50117  
AC Q50117;  
DT 01-MAY-2001 (EMBLrel. 1); Last sequence update)  
DT 01-MAY-2001 (EMBLrel. 1); Last annotation update)  
DE Mitochondrial cytochrome c oxidase subunit 2 (Mitochondrial)  
OS Saccharomyces cerevisiae  
OC Eukaryota; Eukaryota; Fungi; Ascomycota; Basidiomycota; Tardicophyta; Tardicophyta;  
OC Spectrin; Mitochondrial; Mitochondrial; Mitochondrial; Mitochondrial;  
OC PANTHER: PANTHER:000000; Angiotensin II;  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TIGR: S00000;  
RA TIGR: S00000;  
PT \*Transcription of the 22 kDa mitochondrial cytochrome c  
RL Plant Mitochondrial; Mitochondrial; Mitochondrial;  
DR EMBL: M16092; AAA63055.1;  
KW Mitochondrial;  
RN [2]  
RP SEQUENCE FROM N.A.  
SQ SEQUENCE 14 AA; 1503 MW; 20959A84E21333B CRC64;  
  
Query Match 27.38; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. Hov. 3;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KKK 5  
DB 111  
6 KKE 8  
  
RESULT 10  
Q9H4C1 PRELIMINARY; PRT; 13 AA.  
ID Q9H4C1  
AC Q9H4C1;  
DT 01-MAR-2002 (TrEMBLrel. 23; Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 23; Last annotation update)  
DE Eukaryotic protein; Mitochondrial;  
GN 75884.  
OS Escherichia coli O157:H7

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=0157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Petrá N.T., Plunkett G. III, Burland V., Mau R., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor G., Kirkpatrick B.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Stoeck Y., Miller S.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.F., Potamocitis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RL \*Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.\*;  
 RL Nature 409:529-533(2001).  
 KW EMBL: AE005659; AAG59469.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE: 13 AA; 1520 MW; 4145922/4484187/3694.

Query Match 27.3% Score 3; ID 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8; E=0.0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKK 3  
 DB 8 AKK 10

RESULT 11  
 Q9UWM2  
 ID Q9UWM2 PRELIMINARY; PRT; 14 AA.  
 AC Q9UWM2;  
 DT 01-MAY-2000 (TrEMBLrel. 13; Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13; Last sequence update)  
 DE L-glutamate:NAD(P)+ oxidoreductase (EC 1.4.1.4) (Fragment).  
 OS Pyrococcus furiosus.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID=2261;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92247806; PubMed=1576153;  
 RA Robb F.T., Park J.B., Adams M.W.;  
 RT \*Characterization of an extremely thermostable glutamate  
 RT dehydrogenase; a key enzyme in the primary metabolism of the  
 RT hyperthermophilic archaeobacterium, Pyrococcus furiosus.\*;  
 RL Biochim. Biophys. Acta 1120:267-272(1992).  
 SQ SEQUENCE: 14 AA; 1684 MW; 1E8F0506R25550B CR664;

Query Match 27.3% Score 3; ID 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8; E=0.0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KEQ 5  
 DB 2 KEQ 4

RESULT 12  
 Q56750  
 ID Q56750 PRELIMINARY; PRT; 14 AA.  
 AC Q56750;  
 DT 01-NOV-1996 (TrEMBLrel. 01; Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 01; Last annotation update)  
 DE Ribosomal protein S19 (Fragment).  
 OS Western x phytoplasmata.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Phytoplasma.  
 OX NCBI\_TaxID=37704;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=4306707; PubMed=11206551;  
 RA Gundersen D.P., Davis K.E., Kinoshita T.;  
 RT \*Polygeny of mycoplasma-like organisms (phytoplasmas): a basis for  
 RT their classification.\*;  
 RL J. Bacteriol. 176:114-124(1994).  
 DE EMBL: L23047; AAA55414;  
 DE NON-TEP;  
 SQ SEQUENCE: 14 AA; 1520 MW; 334181F4E1F8A3 CR664;  
 Query Match 27.3% Score 3; ID 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8; E=0.0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKK 3  
 DB 8 AKK 10  
 RESULT 13  
 Q56750  
 ID Q56750 PRELIMINARY; PRT; 14 AA.  
 AC Q56750;  
 DT 01-NOV-1996 (TrEMBLrel. 01; Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)  
 DE L-glutamate:NAD(P)+ oxidoreductase (EC 1.4.1.4) (Fragment).  
 OS Pyrococcus furiosus.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID=2261;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92247806; PubMed=1576153;  
 RA Robb F.T., Park J.B., Adams M.W.;  
 RT \*Characterization of an extremely thermostable glutamate  
 RT dehydrogenase; a key enzyme in the primary metabolism of the  
 RT hyperthermophilic archaeobacterium, Pyrococcus furiosus.\*;  
 RL Biochim. Biophys. Acta 1120:267-272(1992).  
 SQ SEQUENCE: 14 AA; 1684 MW; 1E8F0506R25550B CR664;

Query Match 27.3% Score 3; ID 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8; E=0.0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKK 3  
 DB 8 AKK 10

RESULT 14  
 Q56750  
 ID Q56750 PRELIMINARY; PRT; 14 AA.  
 AC Q56750;  
 DT 01-NOV-1996 (TrEMBLrel. 01; Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 01; Last annotation update)  
 DE Ribosomal protein S19 (Fragment).  
 OS Western x phytoplasmata.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Phytoplasma.  
 OX NCBI\_TaxID=37704;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2142915; PubMed=11206551;  
 RA Komachi N., Saito T., Yoshida M., Kurihara M., Hara S.,  
 RA Katsunaga K., Iwaki T.;  
 RT \*The human enterohemorrhagic E. coli O157:H7 ribosomal protein genes: Mapping of homologues  
 RT to the ribosomes and implications for human disorders.\*;  
 RL Genes 27:15-26(2001).  
 DE EMBL: AB01623; BAB1565.1;  
 KW Ribosomal Protein.





Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQ 6  
DB 13 KEQ 15

## RESULT 19

ID Q9UCN2 PRELIMINARY: PRT: 15 AA.  
AC Q9UCN2; 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)  
DE Fructose-1,6-bisphosphate aldolase A (EC 4.1.2.13) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92353128; PubMed=1353685;  
RA Lee K.N., Maxwell M.D., Patterson M.K.Jr., Birckbichler P.J.,  
RA Conway E.;  
RT "Identification of transglutaminase substrates in HT29 colon cancer  
RT cells: use of 5-(biotinamido)pentylamine as a transglutaminase-  
RT specific probe."  
RL Biochim. Biophys. Acta 1135:12-16(1992).  
DR HSSP: P04075; 2ALD.  
SQ SEQUENCE 15 AA; 1805 MW; 8D07536D1FC03F61 CRC64;

Query Match 27.38; Score 3; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 9, Re+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKE 5  
DB 12 KKE 14

## RESULT 20

ID Q81Z00 PRELIMINARY: PRT: 15 AA.  
AC Q81Z00;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DE Protein kinase A catalytic subunit beta (Fragment).  
GN PKACR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wu K.-J., Mattioli M., Morse H.C., Galla-Ravera R.;  
RT "c-MYC activates protein kinase A (PKA) by direct transcriptional  
RT activation of the PKA catalytic subunit beta (PAA- $\beta$ ) gene."  
RL Oncogene 0:0-0(2002).  
DR EMBL: AF538872; AAN16454.1;  
KW Kinase.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1480 MW; 52FE5695C19R70A CRC64;

Query Match 27.38; Score 3; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 9, Re+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
DB 7 AKK 9

## RESULT 21

ID Q9TW34 PRELIMINARY: PRT: 15 AA.  
AC Q9TW34;  
DT 01-MAY-2000 (TRENBLrel. 14, Created)  
DT 01-MAY-2000 (TRENBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
DE KINA-binding protein (Fragment).  
OS Crithidia fasciculata.  
OC Eukaryota; Excavata; Kinetoplastida; Trypanosomatidae; Crithidia.  
OX NCBI\_TaxID=5656;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=9324912; PubMed=852395;  
RA Tiliawalla I.;  
RT "Identification of cDNA encoding proteins in the parasitic protozoan  
RT Crithidia fasciculata and evidence for their association with the  
RT mitochondrial genome."  
RC EXP. CELL. RES. 234:115-121(1998).  
SQ SEQUENCE 15 AA; 1453 MW; 3D9452569B270 CRC64;

Query Match 27.38; Score 3; DB 5; Length 15;

Best Local Similarity 100.0%; Pred. No. 9, Re+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
DB 13 AKK 15

## RESULT 22

ID Q82Z07 PRELIMINARY: PRT: 15 AA.  
AC Q82Z07;  
DT 01-ET-2001 (TRENBLrel. 14, Created)  
DT 01-ET-2001 (TRENBLrel. 14, Last sequence update)  
DT 01-ET-2001 (TRENBLrel. 14, Last annotation update)  
DE Unknown protein from dog-pup (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Artiodactyla; Ruminantia; Insecta; Procyonida;  
OC Neoptera; Euphorbia; Lepidoptera; Glossata; Diptera; Hymenoptera;  
OC Bombyx mori; Bombyx.  
OX NCBI\_TaxID=7943;  
RN [1]  
RP SEQUENCE.  
RX STRAIN XINGANG X KEMING; TISSUE Body wall, and Fat body;  
RC MEDLINE=317443; PubMed=1280994;  
RA Zhou H.X.;  
RT "Protein database for several tissues derived from five instar of  
RT silkworm."  
RL J. Mol. Biol. 272:27-27(1997).  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1433 MW; 68F6B4766A750 CRC64;

Query Match 27.38; Score 3; DB 5; Length 15;

Best Local Similarity 100.0%; Pred. No. 9, Re+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KEQ 8  
DB 3 KEQ 7

## RESULT 23

ID Q9TR45 PRELIMINARY: PRT: 15 AA.  
AC Q9TR45;  
DT 01-MAY-2000 (TRENBLrel. 14, Created)  
DT 01-MAY-2000 (TRENBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
DE Apoliteris tomolox (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID-9913;
RN [1]
RP SEQUENCE.
RX MEDLINE-96029671; PubMed-7592757;
RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
RA Nagashima M., Lundh E.R., Vijay S., Niecek D.,
RT "The receptor for advanced glycation end products (RAGE) is a cellular
RT binding site for amphoterin. Mediation of neurite outgrowth and co-
RT expression of rage and amphoterin in the developing nervous system.";
RL J. Biol. Chem. 270:25752-25761(1995).
SQ SEQUENCE 15 AA; 1757 MW; 390B9679501CE020 CRC64;

Query Match 27.38; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4
DB 11 KKK 13

RESULT 24
Q9S8F1 PRELIMINARY; PRT; 15 AA.
AC Q9S8F1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Glutathione S-transferase isoform II (EC 2.5.1.16) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID-4577;
RN [1]
RP SEQUENCE.
RX MEDLINE-95322859; PubMed-7599527;
RA Holt D.C., Lay V.J., Clarke E.D., Dinsmore A., Jepson I., Bright S.W.,
RA Greenland A.J.;
RT "Characterization of the safener-induced glutathione S-transferase
RT isoform II from maize.";
RL Planta 196:295-302(1995).
SQ SEQUENCE 15 AA; 1530 MW; 2F105C48F7CD3A56 CRC64;

Query Match 27.38; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQ 6
DB 13 KEQ 15

RESULT 25
P82431 PRELIMINARY; PRT; 15 AA.
AC P82431;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 100 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID-4097;
RN [1]
RP SEQUENCE.
RC STRAIN-cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Rolwell G.P.;

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37 "Proteomic study of secondary cell wall proteins from transformed
37 tobacco cultured.";
37 Planta 196:303-309(1995).
37 CC 01 SUBCELLULAR LOCATION: CELL WALL.
37 CC 01 TISSUE SPECIFICITY: XYLEM.
37 KW CELL WALL.
37 FT NON-TER 15
37 SQ SEQUENCE 15 AA; 1530 MW; 5400254E147626 CRC64;

Query Match 27.38; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4
DB 4 KKK 4

RESULT 26
P82431 PRELIMINARY; PRT; 15 AA.
AC P82431;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 100 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID-4097;
RN [1]
RP SEQUENCE.
RC STRAIN-cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Rolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco cultured.";
RL Planta 196:303-309(1995).
SQ SEQUENCE 15 AA; 1530 MW; 5400254E147626 CRC64;

Query Match 27.38; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4
DB 11 KKK 13

RESULT 27
Q9R712 PRELIMINARY; PRT; 15 AA.
AC Q9R712;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Hypothetical 100 kDa protein (Fragment).
OS Yeast.
OC Eukaryota; Eukaryota; Eukaryota; Eukaryota; Eukaryota;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID-562;
RN [1]
RP SEQUENCE FROM N A
RC STRAIN-K12;
RX Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RX Wojtaszek P., Rolwell G.P.;

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RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kawai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.,  
 RT "A 718-kb DNA Sequence of *Escherichia coli* K-12 Genome Corresponding  
 RT to the 12.7-28.0 min Region on the Linkage Map";  
 RL DNA Res. 3:137-155(1996);  
 DR EMBL: D90705; BAA35310.1;  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 964 MW; DF133B1F0045476A GC64;

Query Match 18.2%; Score 2; ID 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KE 5  
 DB 7 KE 8

## RESULT 28

## Q9AGP4

ID Q9AGP4 PRELIMINARY; PRT; 8 AA.

AC Q9AGP4

DT 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Serine hydroxymethyltransferase (Fragment).

GN GLYA.

OS *Arthrobacter* sp. LIN.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Micrococcineae; Micrococcaceae; *Arthrobacter* sp.

OX NCBI\_TaxID=153502;

RN [1]

RP SEQUENCE FROM N.A.

RA Meskys R., Harris R.J., Casalta V., Hassan J., Scrutton N.S.,  
 RT "Genetic organization of the genes involved in dimethylglycine and  
 RT sarcosine degradation in *Arthrobacter* spp.: implications for glycine  
 RT betaine catabolism";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF329478; AAK16486.1;

KW Methyltransferase; Transferase.

FT NON\_TER

SQ SEQUENCE 8 AA; 898 MW; 5B1870533372457 GC64;

Query Match 18.2%; Score 2; ID 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 DB 4 KE 5

## RESULT 29

## Q93SR0

ID Q93SR0 PRELIMINARY; PRT; 8 AA.

AC Q93SR0

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE Beta-lactamase repressor Blal (Fragment).

GN BLAI

OS *Staphylococcus epidermidis*.

OG Plasmid pS76.

OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.

OX NCBI\_TaxID=1282;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=6;

RA Slime M.S., Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 RT "Genetic organization of the genes involved in dimethylglycine and  
 RT sarcosine degradation in *Arthrobacter* spp.: implications for glycine  
 RT betaine catabolism";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases  
 DR EMBL: AF329478; AAK16486.1;  
 KW Methyltransferase; Transferase.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 964 MW; DF133B1F0045476A GC64;

Query Match 18.2%; Score 2; ID 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KE 5  
 DB 7 KE 8

## RESULT 30

## Q9XKX1

ID Q9XKX1 PRELIMINARY; PRT; 8 AA.

AC Q9XKX1

DT 01-NOV-2001 (TRENBLrel. 12, Created)

DT 01-NOV-2001 (TRENBLrel. 12, Last sequence update)

DT 01-NOV-2001 (TRENBLrel. 12, Last annotation update)

DE *Streptococcus* sp. (Sequence)

GN EF15.

OS *Prothiobacter* sp.

OC Bacteria; *Prothiobacter* sp.

OC Prothiobacter

OX NCBI\_TaxID=1223

RN [1]

RP SEQUENCE FROM N.A.

RA "Genetic diversity in *Prothiobacter* populations from a  
 RT sorted from the same site. See also "Stream";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF078144; AA24024.1;

FT NON\_TER

SQ SEQUENCE 8 AA; 100 MW; 1000805672960D GC64;

Query Match 18.2%; Score 2; ID 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KE 8  
 DB 1 KE 2

## RESULT 31

## Q56429

ID Q56429 PRELIMINARY; PRT; 8 AA.

AC Q56429

DT 01-NOV-1996 (TRENBLrel. 4, Created)

DT 01-NOV-1996 (TRENBLrel. 4, Last sequence update)

DT 01-SEP-2001 (TRENBLrel. 19, Last annotation update)

DE *SAR* (Fragment)

OS *Staphylococcus aureus*

OC Bacteria; *Staphylococcus aureus*; Enterococci; Enterococcales; Enterococci

OX NCBI\_TaxID=221

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=84

EX MEDLINE:8902522; PubMed:652437

RA Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.

RT "Nucleotide sequence of the phosphoglycerate kinase gene from the

RT extreme thermophile, *Thermoplasma* sp.

RL Biochem. J. 254:567-574(1988)

DR EMBL: X12474; CAA31065.1

FT NON\_TER

SQ SEQUENCE 8 AA; 885 MW; 50A7333372457B GC64;





DR EMBL: AJ488208; CAD32561.1; -  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;

Query Match 18.2% Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 II  
 DB 5 RN 5

## RESULT 41

Q8MUN6 PRELIMINARY: PRT; 8 AA.  
 AC Q8MUN6  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN MPI.  
 OS Heliconius melpomene melpomene.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius  
 OX NCBI\_TaxID=171917;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-STRI-B-441-Mpi-2;  
 RA Bull V., Beltran M., Birmingham E., Jiggins C., McMillan C.,  
 RA Mallet J.;  
 RT "Molecular evidence for gene flow between species of Heliconius."  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR FMBL: AF516247; AAM61933.1;  
 KW Isomerase.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 977 MW; 16E736DB100:EA3 CRC64;

Query Match 18.2% Score 2; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQ 6  
 II  
 DB 5 EQ 6

## RESULT 42

Q9N6M5 PRELIMINARY: PRT; 8 AA.  
 AC Q9N6M5  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Dihydrofolate reductase thymidylate synthase (Fragment).  
 GN POLI.  
 OS Toxoplasma gondii.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;  
 OC Toxoplasma.  
 OX NCBI\_TaxID=5811;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RH, COUGAR TC751034, SEA OTTER TC82801, and BEVERLEY;  
 RA Lehmann T., Blackston C.R., Parmlay S.F., Remington J.S., Dubey J.P.;  
 RT "Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and  
 RT Housekeeping Genes."  
 RL J. Parasitol. 0:0-0(2000).  
 DR EMBL: AF249695; AAF79153.1;  
 DR EMBL: AF249692; AAF79150.1;  
 DR EMBL: AF249693; AAF79151.1;  
 DR EMBL: AF249694; AAF79152.1;

FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1030 MW; 44AAAA50B13544 CRC64;

Query Match 14.2% Score 2; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EQ 5  
 II  
 DB 4 EQ 4

## RESULT 43

Q18854 PRELIMINARY: PRT; 8 AA.  
 AC Q18854  
 DT 01-OCT-2002 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 15, Last annotation update)  
 DE Eukaryotic Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OS Canis familiaris (dog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteleostomi; Carnivora; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC 130 P. 130; S. 130; H. 130; K. 130; M. 130; J. 130; G. 130;  
 RA "A human PCR/PCR product of the canine T cell antigen gene."  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF044171; AAF04417.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 862 MW; 20CAAAHFF125A7 CRC64;

Query Match 14.2% Score 2; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EQ 5  
 II  
 DB 4 EQ 4

## RESULT 44

Q45M24 PRELIMINARY: PRT; 8 AA.  
 AC Q45M24  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Na+/K+ ATPase alpha subunit (EF 4.6.1.37) (Fragment).  
 GN ATPAL.  
 OS Sus scrofa (pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteleostomi; Artiodactyla; Suidae; Sus.  
 OX NCBI\_TaxID=4823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Pi3131;  
 RA Blazkova P., Stratil A., Pecher R., Van Poucke M., Reiner G.,  
 RA Geldermann H., Kopecky M.;  
 RT "PH mapping of the porcine ATPAL, ATPAL1, V-ATPase, IVL genes and  
 RT linkage assignments of ATPAL and IVL to chromosome 4."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ441381; FAF44138.1;  
 KW Hydrolase  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 1137 MW; 6C4H41AR133R02D3 CRC64;

Query Match 14.2% Score 2; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KE 5  
DB 4 KE 5

## RESULT 45

O19957 PRELIMINARY; PRT; 8 AA.  
AC O19957;  
DT 01-JAN-1998 (TRENBLrel. 05, Created)  
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Ribosomal protein L16 (Fragment).  
GN RPL16.  
OS Gossypium hirsutum (Upland cotton).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
OX NCBI\_TaxID=3635;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;  
RT "The tortoise and the hare: choosing between noncoding plastome and  
RT nuclear Adh sequences for phylogeny reconstruction in a recently  
RT diverged plant group."  
RL Am. J. Bot. 85:1301-1315(1998).  
DR EMBL: AF031452; AAC63546.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 971 MW; 7185B73404540327 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 9 RN 10  
DB 3 RN 4

## RESULT 46

O36898 PRELIMINARY; PRT; 8 AA.  
AC O36898;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE RPS19' protein (Fragment).  
GN RPS19'.  
OS Nicotiana glauca, and  
OS Nicotiana glauca (Bigelov's tobacco).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=49453; 4088;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.R.;  
RL Mol. Gen. Genet. 0:0-0(1996).  
DR EMBL: 271234; CAA94933.1; -.  
DR EMBL: 271225; CAA94921.1; -.  
KW Chloroplast.  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 977 MW; FD43333735A411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 KK 5  
DB 6 KK 7

## RESULT 47

O41002 PRELIMINARY; PRT; 8 AA.  
AC O41002;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
DE Cytochrome c oxidase subunit 1 (Fragment).  
GN COX1.  
OS Terranatos dolichopterus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neoptera; Teleostei; Euteleostei; Neopteleostei;  
OC Actinopterygii; Atherinomorpha; Atherinomorpha; Atherinomorpha;  
OX NCBI\_TaxID=61800;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Urbek T., Larsen A.;  
RT "The evolution of cytochrome c oxidase in the killifish family Rivulidae  
RT (Atherinomorpha): implications for molecular phylogenetics and  
RT biogeographic interpretation."  
RL Evolution 53:329-333(1999).  
DR EMBL: AF024221; AAC00441.1; -.  
KW Mitochondrion.  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 1062 MW; E099040B44056 CRC64;

Query Match 14.2%; Score 2; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 15 NA 11

DB 4 NA 4

## RESULT 48

O37854 PRELIMINARY; PRT; 8 AA.  
AC O37854;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-MAY-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 17, Last annotation update)  
DE Coliphage genome of unknown function, 5' end (Fragment).  
OX Bacteriophage P1.  
OC Viruses; ssRNA positive-sense, no DNA stage; Leviviridae;  
OX NCBI\_TaxID=12126;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 7124467; PubMed: 4447230.  
RA Bering J.P.E.;  
RT "A sequence of 5000 bp from the Coliphage P1  
RT genome."  
PL Bering J.P., Bering J.P. (1973).  
DR EMBL: M24261; AAA22765.1; -.  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 967 MW; E0454120E72726 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 9 RN 10

DB 6 RN 7



## RESULT 49

Q99NX9 PRELIMINARY: PRT: 8 AA.  
 AC Q99NX9;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Amyloid beta protein (fragment).  
 GN APP.  
 OS Hydrochoerus hydrochaeris (Capybara) (Carpincho).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;  
 OC Hydrochaeris.  
 OX NCBI\_TaxID=10149;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals."  
 RL Nature 409:614-618(2001).  
 DR FMBL; AY011342; AAG47377.1;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1071 MW; 13560686DB19C9C3 56K64;

Query Match 18.2%; Score 2; DB 11; Length 8;

Best local Similarity 100.0%; Pred. No. 6, 3e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6

Db 4 EQ 5

## RESULT 50

Q62721 PRELIMINARY: PRT: 8 AA.  
 AC Q62721;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Prohibitin (fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Fisher;  
 RX MEDLINE=95331633; PubMed=7607556;  
 RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.L., Friedman V.,  
 RA Henderson T., Owens G.A., Danner D.H., Jope E.B., DelGioco R.T.,  
 RA McClung J.K.;  
 RT "Regions of evolutionary conservation between the rat and human  
 RT prohibitin-encoding genes."  
 RL Gene 158:291-294(1995).  
 DR FMBL; U17178; AAA86692.1;  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 1150 MW; EFD3237H05A41376 38K64;

Query Match 18.2%; Score 2; DB 11; Length 8;

Best local Similarity 100.0%; Pred. No. 6, 3e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8

Db 7 KQ 8

Search completed: September 30, 2003, 17:24:05  
 Job time : 110 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 17:21:07 : Search time 28 seconds  
(without alignments)  
16,622 Million cell updates/sec

Title: US-09-787-443-20  
Perfect score: 11  
Sequence: 1 AKKEOKORNA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext: 50.0

Searched: 328717 seqs, 4210853 residues

Word size: 0

Total number of hits satisfying chosen parameters: 38454

Minimum DH seq length: 8  
Maximum DH seq length: 15

Post-processing: Listing first 500 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 2: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 3: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 4: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 5: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 6: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	4	36.4	8	3	US-08-160-604 7
2	4	36.4	8	3	US-08-160-604 8
3	4	36.4	8	3	US-08-160-604 9
4	4	36.4	8	3	US-08-160-604 10
5	4	36.4	8	3	US-08-160-604 11
6	4	36.4	8	3	US-08-160-604 12
7	4	36.4	8	3	US-08-160-604 13
8	4	36.4	8	3	US-08-160-604 14
9	4	36.4	8	3	US-08-160-604 15
10	4	36.4	8	3	US-08-160-604 16
11	4	36.4	8	3	US-08-160-604 17
12	4	36.4	8	3	US-08-160-604 18
13	4	36.4	8	3	US-08-160-604 19
14	4	36.4	8	3	US-08-160-604 20
15	4	36.4	8	3	US-08-160-604 21
16	4	36.4	8	3	US-08-160-604 22
17	4	36.4	8	3	US-08-160-604 23
18	4	36.4	8	3	US-08-160-604 24
19	4	36.4	8	3	US-08-160-604 25
20	4	36.4	8	3	US-08-160-604 26
21	4	36.4	8	3	US-08-160-604 27
22	4	36.4	8	3	US-08-160-604 28
23	4	36.4	8	3	US-08-160-604 29
24	4	36.4	8	3	US-08-160-604 30
25	4	36.4	8	3	US-08-160-604 31
26	4	36.4	8	3	US-08-160-604 32
27	4	36.4	8	3	US-08-160-604 33

[illegible]

247	3	27.3	9	2	US-08-124-981A-35	Sequence 35, Appl	120	1	27.3	4	US 08 124 981A 35	Sequence 4, Appl
248	3	27.3	9	2	US-07-829-461A-1	Sequence 1, Appl1	121	1	27.3	4	US 07 829 461A 1	Sequence 12, Appl
249	3	27.3	9	2	US-08-440-409B-23	Sequence 23, Appl	122	1	27.3	4	US 08 440 409B 23	Sequence 1, Appl
250	3	27.3	9	2	US-08-621-803-203	Sequence 203, Appl	123	1	27.3	4	US 08 621 803 203	Sequence 2, Appl
251	3	27.3	9	2	US-08-462-498-5	Sequence 5, Appl1	124	1	27.3	4	US 08 462 498 5	Sequence 1, Appl
252	3	27.3	9	2	US-08-733-505A-41	Sequence 41, Appl	125	1	27.3	4	US 08 733 505A 41	Sequence 36, Appl
253	3	27.3	9	2	US-08-621-259A-176	Sequence 176, Appl	126	1	27.3	4	US 08 621 259A 176	Sequence 15, Appl
254	3	27.3	9	2	US-08-503-226B-5	Sequence 5, Appl1	127	1	27.3	4	US 08 503 226B 5	Sequence 6, Appl
255	3	27.3	9	2	US-08-637-759B-187	Sequence 187, Appl	128	1	27.3	4	US 08 637 759B 187	Sequence 27, Appl
256	3	27.3	9	2	US-08-637-759B-17	Sequence 17, Appl	129	1	27.3	4	US 08 637 759B 17	Sequence 3, Appl1
257	3	27.3	9	2	US-08-586-764-2	Sequence 2, Appl1	130	1	27.3	4	US 08 586 764 2	Sequence 41, Appl
258	3	27.3	9	2	US-08-679-865-8	Sequence 8, Appl1	131	1	27.3	4	US 08 679 865 8	Sequence 37, Appl
259	3	27.3	9	2	US-08-680-876-8	Sequence 8, Appl1	132	1	27.3	4	US 08 680 876 8	Sequence 43, Appl
260	3	27.3	9	2	US-08-894-139-1	Sequence 1, Appl1	133	1	27.3	4	US 08 894 139 1	Sequence 29, Appl
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## ALIGNMENTS

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RESULT 1
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? Sequence 7, Applicant: US/08/006,604
? Patent No. 6,242,022
? GENERAL INFORMATION
? APPLICANT: Barley, John
? APPLICANT: Jones, Judith A
? TITLE OF INVENTION: METHOD OF DETECTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY
? NUMBER OF SEQUENCES: 127
? PRESUMED TO BE A: YES
? ADDRESS: 10111 1st St
? STREET: 10111 1st St, Suite 2800
? CITY: Atlanta
? STATE: Georgia
? COUNTRY: SA
? ZIP: 30309-1001
? CYCLES REACHED: 100
? METHOD: NIE, LARRY, LUK
? COMMENTS: FOR INFORMATION
? OPERATING SYSTEM: LINUX/MS-DOS
? SOFTWARE: PROTEO RELEASE #1.0, VERSION #1.25
? CURRENT APPLICATION NUMBER: US/08/160,604
? FILING DATE: 03 NOV 1999
? CLASSIFICATION: 4-3
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/863,419
? FILING DATE: 13 APR 1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/648,205
? FILING DATE: 03 JAN 1991
? PRIOR APPLICATION DATA:
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1 APPLICATION NUMBER: US 07/472,947  
2 FILING DATE: 31-JAN-1990  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Pabst, Patrea L.  
5 REGISTRATION NUMBER: 31,284  
6 REFERENCE/DOCKET NUMBER: OMRP114CIP(3)  
7 TELEPHONE: (404)-815-6508  
8 TELEFAX: (404)-815-6555  
9 INFORMATION FOR SEQ ID NO: 7:  
10 SEQUENCE CHARACTERISTICS:  
11 LENGTH: 8 amino acids  
12 TYPE: amino acid  
13 STRANDEDNESS: single  
14 TOPOLOGY: linear  
15 MOLECULE TYPE: peptide  
16 HYPOTHETICAL: NO  
17 ANTI-SENSE: NO  
18 FRAGMENT TYPE: N-terminal  
19 US-08-160-604-7

Query Match: 36.4%, Score 4, 165 A, Length 8;  
Best Local Similarity 100.0%; Pred. No. 2, 564, 45;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 KEQK 8

RESULT 2  
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1 Sequence 8, Application US/08160604  
2 Patent No. 6232522  
3 GENERAL INFORMATION:  
4 APPLICANT: Harley, John  
5 APPLICANT: James, Judith A.  
6 APPLICANT: Scofield, R. H.  
7 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
8 NUMBER OF SEQUENCES: 127  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESSEE: Patrea L. Pabst  
11 STREET: 1100 Peachtree Street, Suite 2830  
12 CITY: Atlanta  
13 STATE: Georgia  
14 COUNTRY: USA  
15 ZIP: 30309-4530  
16 COMPUTER READABLE FORM:  
17 MEDIUM TYPE: Floppy disk  
18 COMPUTER: IBM PC compatible  
19 OPERATING SYSTEM: PC-DOS/MS-DOS  
20 SOFTWARE: PatentIn Release #1.0, Version #1.25  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/08/160,604  
23 FILING DATE: 30-NOV-1993  
24 CLASSIFICATION: 424  
25 PRIOR APPLICATION DATA:  
26 APPLICATION NUMBER: US 07/867,819  
27 FILING DATE: 13-APR-1992  
28 PRIOR APPLICATION DATA:  
29 APPLICATION NUMBER: US 07/648,205  
30 FILING DATE: 31-JAN-1991  
31 PRIOR APPLICATION DATA:  
32 APPLICATION NUMBER: US 07/472,947  
33 FILING DATE: 31-JAN-1990  
34 ATTORNEY/AGENT INFORMATION:  
35 NAME: Pabst, Patrea L.  
36 REGISTRATION NUMBER: 31,284  
37 REFERENCE/DOCKET NUMBER: OMRP114CIP(3)  
38 TELEPHONE: (404)-815-6508  
39 TELEFAX: (404)-815-6555  
40 INFORMATION FOR SEQ ID NO: 8:

1 SEQUENCE CHARACTERISTICS  
2 LENGTH: 8 amino acids  
3 TYPE: amino acid  
4 STRANDEDNESS: single  
5 TOPOLOGY: linear  
6 MOLECULE TYPE: peptide  
7 HYPOTHETICAL: NO  
8 ANTI-SENSE: NO  
9 FRAGMENT TYPE: N-terminal  
10 US-08-160-604-8  
11 Query Match: 36.4%, Score 4, 165 A, Length 8;  
12 Best Local Similarity 100.0%; Pred. No. 2, 564, 45;  
13 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
14 QY 4 KEQK 7  
15 111  
16 Db 5 KEQK 8  
17 RESULT 3  
18 US-08-160-604-9  
19 Sequence 9, Application US/08160604  
20 Patent No. 6232522  
21 GENERAL INFORMATION:  
22 APPLICANT: Harley, John  
23 APPLICANT: James, Judith A.  
24 APPLICANT: Scofield, R. H.  
25 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
26 NUMBER OF SEQUENCES: 127  
27 CORRESPONDENCE ADDRESS:  
28 ADDRESSEE: Patrea L. Pabst  
29 STREET: 1100 Peachtree Street, Suite 2830  
30 CITY: Atlanta  
31 STATE: Georgia  
32 COUNTRY: USA  
33 ZIP: 30309-4530  
34 COMPUTER READABLE FORM:  
35 MEDIUM TYPE: Floppy disk  
36 COMPUTER: IBM PC compatible  
37 OPERATING SYSTEM: PC-DOS/MS-DOS  
38 SOFTWARE: PatentIn Release #1.0, Version #1.25  
39 CURRENT APPLICATION DATA:  
40 APPLICATION NUMBER: US/08/160,604  
41 FILING DATE: 30-NOV-1993  
42 CLASSIFICATION: 424  
43 PRIOR APPLICATION DATA:  
44 APPLICATION NUMBER: US 07/867,819  
45 FILING DATE: 13-APR-1992  
46 PRIOR APPLICATION DATA:  
47 APPLICATION NUMBER: US 07/648,205  
48 FILING DATE: 31-JAN-1991  
49 PRIOR APPLICATION DATA:  
50 APPLICATION NUMBER: US 07/472,947  
51 FILING DATE: 31-JAN-1990  
52 ATTORNEY/AGENT INFORMATION:  
53 NAME: Pabst, Patrea L.  
54 REGISTRATION NUMBER: 31,284  
55 REFERENCE/DOCKET NUMBER: OMRP114CIP(3)  
56 TELEPHONE: (404)-815-6508  
57 TELEFAX: (404)-815-6555  
58 INFORMATION FOR SEQ ID NO: 9:  
59 SEQUENCE CHARACTERISTICS  
60 LENGTH: 8 amino acids  
61 TYPE: amino acid  
62 STRANDEDNESS: single  
63 TOPOLOGY: linear  
64 MOLECULE TYPE: peptide  
65 HYPOTHETICAL: NO  
66 ANTI-SENSE: NO  
67 FRAGMENT TYPE: N-terminal  
68 US-08-160-604-9

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RESULT 4  
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 : Patent No. 6232522  
 : GENERAL INFORMATION:  
 : APPLICANT: Harley, John  
 : APPLICANT: James, Judith A.  
 : APPLICANT: Scofield, R. H.  
 : TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOPHAGNITIVATION  
 : NUMBER OF SEQUENCES: 127  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Patricia L. Paest  
 : STREET: 1100 Peachtree Street, Suite 2800  
 : CITY: Atlanta  
 : STATE: Georgia  
 : COUNTRY: USA  
 : ZIP: 30309-4530  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
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 : SOFTWARE: Patent In Release #17, Version #1.25  
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 : APPLICATION NUMBER: US/08/160,604  
 : FILING DATE: 30-NOV-1993  
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 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/667,819  
 : FILING DATE: 13-APR-1992  
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 : APPLICATION NUMBER: US 07/668,205  
 : FILING DATE: 31-JAN-1991  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/472,947  
 : FILING DATE: 31-JAN-1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Padst, Patricia L.  
 : REGISTRATION NUMBER: 31,284  
 : REFERENCE/DOCKET NUMBER: OMRF114CIP(3)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (404)-815-6508  
 : TELEFAX: (404)-815-6555  
 : INFORMATION FOR SEQ ID NO: 10:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
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 : US-08-160-604-10

Query Match 36.4%; Score 4: 04 00 Length 10  
 Best Local Similarity 100.0%; Pred. No. 2 6005;  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-08-160-604-10  
 : Sequence 10, Application US/08:604  
 : Patent No. 6232522  
 : GENERAL INFORMATION:  
 : APPLICANT: Harley, John  
 : APPLICANT: James, Judith A.  
 : APPLICANT: Scofield, R. H.  
 : TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOPHAGNITIVATION  
 : NUMBER OF SEQUENCES: 127  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Patricia L. Paest  
 : STREET: 1100 Peachtree Street, Suite 2800  
 : CITY: Atlanta  
 : STATE: Georgia  
 : COUNTRY: USA  
 : ZIP: 30309-4530  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
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 : APPLICATION NUMBER: US/08/160,604  
 : FILING DATE: 30-NOV-1993  
 : CLASSIFICATION: 424  
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 : APPLICATION NUMBER: US 07/667,819  
 : FILING DATE: 13-APR-1992  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/668,205  
 : FILING DATE: 31-JAN-1991  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/472,947  
 : FILING DATE: 31-JAN-1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Padst, Patricia L.  
 : REGISTRATION NUMBER: 31,284  
 : REFERENCE/DOCKET NUMBER: OMRF114CIP(3)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (404)-815-6508  
 : TELEFAX: (404)-815-6555  
 : INFORMATION FOR SEQ ID NO: 10:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : HYPOTHEtical: NO  
 : ANTI-SENSE: NO  
 : FRAGMENT TYPE: N-terminal  
 : US-08-160-604-10  
 : Query Match 36.4%; Score 4: 04 00 Length 10  
 : Best Local Similarity 100.0%; Pred. No. 2 6005;  
 : Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEOK 7  
 1111  
 DB 2 KEOK 5

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/160,604  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,819  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/948,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMRF114-P(4)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404)-815-6568  
 TELEFAX: (404)-815-6555  
 INFORMATION FOR SEQ ID NO: 40:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-160-604-40

Query Match 36.4%, Score 4, LH 3, Length 8:  
 Best Local Similarity 100.0%, Pred. No. 2,54,000  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
 DB 4 KORN 7

RESULT 7  
 US-08-160-604-41  
 Sequence 41, Application US/08160604  
 Patent No. 6232522  
 GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: James, Judith A.  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY: CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09-787-443-20  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,819  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/948,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMRF114-P(4)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404)-815-6568  
 TELEFAX: (404)-815-6555  
 INFORMATION FOR SEQ ID NO: 40:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-160-604-41

Query Match 36.4%, Score 4, LH 3, Length 8:  
 Best Local Similarity 100.0%, Pred. No. 2,54,000  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
 DB 4 KORN 7

RESULT 8  
 US-08-160-604-42  
 Sequence 42, Application US/08160604  
 Patent No. 6232522  
 GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: James, Judith A.  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY: CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08160604  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,819  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:



APPLICATION NUMBER: US 07/648,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,547  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMR114CIP(3)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404)-815-6508  
 TELEFAX: (404)-815-6555  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-160-604-42

Query Match 36.4% Score 43 BB 43 Length 8  
 Best Local Similarity 100.0% Prod. No. 2 60-05  
 Matches 4: Conservative 9; Mismatches 0; Indels 0

QY 7 KORN 10  
 DB 2 KORN 5

## RESULT 9

US-08-160 604-43  
 Sequence 43, Application US/08160604  
 Patent No. 6232522

GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30109-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/160,604  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,619  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/648,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMR114CIP(3)  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (404)-815-6508  
 TELEFAX: (404)-815-6555  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-09-787-443-20

Query Match 100.0% Score 43 BB 43 Length 8  
 Best Local Similarity 100.0% Prod. No. 2 60-05  
 Matches 4: Conservative 9; Mismatches 0; Indels 0

QY 7 KORN 10  
 DB 2 KORN 5

## RESULT 10

US-09-787-443-20  
 Sequence 43, Application US/09787443-20  
 Patent No. 6415550

GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30109-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/787,443-20  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,619  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/648,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMR114CIP(3)  
 TELECOMMUNICATION INFORMATION:

US-09-787-443-20

Query Match 100.0% Score 43 BB 43 Length 8  
 Best Local Similarity 100.0% Prod. No. 2 60-05  
 Matches 4: Conservative 9; Mismatches 0; Indels 0

QY 7 KORN 10  
 DB 2 KORN 5

## RESULT 11

US-09-787-443-20  
 Sequence 43, Application US/09787443-20  
 Patent No. 6415550

GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30109-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/787,443-20  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,619  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/648,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMR114CIP(3)  
 TELECOMMUNICATION INFORMATION:

QY 7 KORN 10  
 DB 2 KORN 5

Query Match 100.0% Score 43 BB 43 Length 8  
 Best Local Similarity 100.0% Prod. No. 2 60-05  
 Matches 4: Conservative 9; Mismatches 0; Indels 0

QY 7 KORN 10  
 DB 2 KORN 5

```

RESULT 12
US-09-100-930A-24
: Sequence 24, Application US/09100930A
: Patent No. 6248549
: GENERAL INFORMATION:
: APPLICANT: Van Eyk, Jennifer E.
: APPLICANT: Ma, Alan S.
: APPLICANT: Cote, Graham P.
: TITLE OF INVENTION: Methods of Modulating Muscle Contraction
: CURRENT APPLICATION NUMBER: US/09/100,930A
: CURRENT FILING DATE: 1998-06-22
: PRIOR APPLICATION NUMBER: 60/050,478
: PRIOR FILING DATE: 1997-06-23
: PRIOR APPLICATION NUMBER: 60/089,505
: PRIOR FILING DATE: 1998-06-16
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 24
: LENGTH: 9
: TYPE: PPT
: ORGANISM: Unknown
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: (1)..(9)
: OTHER INFORMATION: Residues 25 to 38 of In1
: NAME/KEY: PEPTIDE
: LOCATION: (9)
: OTHER INFORMATION: Targeted Ser phospho-amino acid
US-09-100-930A-24

Query Match          36.48; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4
   IIII
Db 5 AKKK 8

RESULT 13
US-09-445-615-4
: Sequence 4, Application US/09445615
: Patent No. 6350452
: GENERAL INFORMATION:
: APPLICANT: Kiss, Terry
: TITLE OF INVENTION: APOPTOSIS MARKER ANTIBODIES AND METHODS OF USE
: FILE REFERENCE: 16026,9033
: CURRENT APPLICATION NUMBER: US/09/445,615
: CURRENT FILING DATE: 1999-12-08
: PRIOR APPLICATION NUMBER: 60/101,920
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 9
: TYPE: PPT
: ORGANISM: Homo sapiens
US-09-445-615-4

Query Match          36.48; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4
   IIII
Db 6 AKKK 9

RESULT 14
US-08-213-897A-18

```

```

: Sequence 18, Application US/08213897A
: Patent No. 5618731
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Anticase Modulated Drug Delivery System
: NUMBER OF SEQUENCES: 18
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: DOS/MS-DOS
: SOFTWARE: PatentIn Ver. 2.1; Version: 2.1.0 (Beta)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/213,897A
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/06,867
: FILING DATE: 07/01/2000
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/06,867
: FILING DATE: 07/01/2000
: INFORMATION FOR SEQUENCES:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-213-897A-18

Query Match          40.48; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4
   I
Db 1 AKKK 4

RESULT 15
US-08-082-2840-3
: Sequence 4, Application US/08-422693
: Patent No. 677127
: GENERAL INFORMATION:
: APPLICANT: Kohn, Michael
: APPLICANT: Bock, Thomas
: APPLICANT: Ault, David
: TITLE OF INVENTION: Polymers and Compositions for Calculating Polysaccharides
: NUMBER OF SEQUENCES: 4
: CURRENT APPLICATION DATA:
: ADDRESS: 16000 E. 1st Ave., Suite 100
: STREET: 4849 E. 1st Ave. Suite 100
: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80152-9414
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: PatentIn Ver. 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/082,269
: FILING DATE: 08/01/2000
: CLASSIFICATION: 135
: ALTERNATIVE INFORMATION:
: NAME: Bock, Thomas; Ault, David
: REGISTRATION NUMBER: 42,123
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 465-8800
: TELEFAX: (303) 344-6004
: INFORMATION FOR SEQUENCES:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: Amino Acid

```



```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,947
; FILING DATE: 31-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF1401P(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N terminal
; US-08-165-604 6

```

```

Query Match          36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Prod. No. 20-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

```

QY 4 KEOK 7
DB 5 KEOK 8

```

```

RESULT 20
US-09-025-596-34
; Sequence 34, Application US/09025596
; Patent No. 6340463
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIBIOTIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/09/025,596
; CURRENT FILING DATE: 1998-02-18
; EARLIER APPLICATION NUMBER: 08/911,593
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 65/023,921
; EARLIER FILING DATE: 1996-08-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PPT
; ORGANISM: Chlamydia pneumoniae
; US-09-025-596-34

```

```

Query Match          36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Prod. No. 20-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

```

QY 1 AKKK 4
DB 3 AKKK 6

```

```

RESULT 21
US-09-579-664B-33
; Sequence 33, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja

```

```

; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: KINASE INHIBITORS
; FILE REFERENCE: US/09/025,596
; CURRENT APPLICATION NUMBER: US/09/025,596
; CURRENT FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 11
; TYPE: PPT
; ORGANISM: Chlamydia pneumoniae
; OTHER INFORMATION:
; OTHER INFORMATION:
; US-09-579-664B-34

```

```

Query Match          36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Prod. No. 20-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

```

QY 4 KEOK 7
DB 5 KEOK 8

```

```

RESULT 22
US-08-165-604 6
; Sequence 6, Application US/08165604 6
; Patent No. 6340463
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIBIOTIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/08/165,604
; CURRENT FILING DATE: 1998-02-18
; EARLIER APPLICATION NUMBER: 08/911,593
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 65/023,921
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PPT
; ORGANISM: Chlamydia pneumoniae
; OTHER INFORMATION:
; OTHER INFORMATION:
; US-08-165-604 6

```

```

Query Match          36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Prod. No. 20-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

```

QY 1 AKKK 4
DB 3 AKKK 6

```

```

RESULT 23
US-09-579-664B-33
; Sequence 33, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; TITLE OF INVENTION: KINASE INHIBITORS
; FILE REFERENCE: US/09/025,596
; CURRENT APPLICATION NUMBER: US/09/025,596
; CURRENT FILING DATE: 1998-02-18
; EARLIER APPLICATION NUMBER: 08/911,593
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 65/023,921
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13

```

```

; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Optimized
; OTHER INFORMATION: substrate for Abl
US-09-480-993-13

Query Match          36.4%   Score 4: 05 4: Length 12:
Best Local Similarity 100.0%   Pred. No. 2,200(2)
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AKKK 4
DB 9 AKKK 12

RESULT 24
US-09-167-065A-13
; Sequence 19, Application US/09367065A
; Patent No. 6390821
; GENERAL INFORMATION:
; APPLICANT: Shokat, Kevan M.
; TITLE OF INVENTION: Engineered Protein Kinases which can Utilize Modified
; TITLE OF INVENTION: Nucleotide Triphosphate Substrates
; FILE REFERENCE: 51538-5002-US
; CURRENT APPLICATION NUMBER: US/06/167,065A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: US 06/797,542
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: US 60/046,727
; PRIOR FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: PCT/US96/32522
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Optimized
; OTHER INFORMATION: enzyme inhibitor for Abl
US-09-367-065A-18

Query Match          36.4%   Score 4: 05 4: Length 12:
Best Local Similarity 100.0%   Pred. No. 2,200(2)
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AKKK 4
DB 9 AKKK 12

RESULT 25
US-09-579-664B-35
; Sequence 35, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Optimized
US-09-579-664B-35

Query Match          36.4%   Score 4: 05 4: Length 12:
Best Local Similarity 100.0%   Pred. No. 2,200(2)
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AKKK 4
DB 9 AKKK 12

RESULT 26
US-09-579-664B-35
; Sequence 35, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
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APPLICATION NUMBER: PCT/US95/00147  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,570  
FILING DATE: JANUARY 7, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A., Jr.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-0042PFC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
PCT-US95-00147-88

Query Match 36.4% Score 4: (8 5) Length 12:  
Best Local Similarity 100.0% Pred. No. 2,49-02:  
Matches 4: Conservative 0; Mismatches 0; Gaps 0;

Oy 1 AKKK 4  
DB 9 AKKK 12

RESULT 28  
US-08-342-101-2  
Sequence 2, Application US/08342101  
Patent No. 5756882  
GENERAL INFORMATION:  
APPLICANT: Wicks, Richard W.  
APPLICANT: Zartman, Leslie O.  
APPLICANT: Vargas, Annette M.  
APPLICANT: Tortelli, Stacy A.  
TITLE OF INVENTION: ASSAY FOR CARDIAC TROPONIN I  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,101  
FILING DATE: 18-NOV-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/063,166  
FILING DATE: 17-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-342-101-2  
Query Match 36.4% Score 4: (8 5) Length 12:  
Best Local Similarity 100.0% Pred. No. 2,49-02:  
Matches 4: Conservative 0; Mismatches 0; Gaps 0;

Oy 1 AKKK 4  
DB 9 AKKK 12

RESULT 28  
US-08-342-101-2  
Sequence 2, Application US/08342101  
Patent No. 5756882  
GENERAL INFORMATION:  
APPLICANT: Wicks, Richard W.  
APPLICANT: Zartman, Leslie O.  
APPLICANT: Vargas, Annette M.  
APPLICANT: Tortelli, Stacy A.  
TITLE OF INVENTION: ASSAY FOR CARDIAC TROPONIN I  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,101  
FILING DATE: 18-NOV-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/063,166  
FILING DATE: 17-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

APPLICANT: Petesch  
TITLE OF INVENTION: PROCESS FOR PREPARING A SYNTHETIC  
CALIBRATOR FOR USE IN SANDWICH  
IMMUNOASSAYS, WHICH CALIBRATOR  
CONSISTS OF AN ANTIBODY AGAINST ONE  
OF THE ANTIBODIES USED IN THE ASSAY  
AND OF A SEQUENCE OF THE ANALYTE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPRUNG KRAMER SCHAEFER & BRISCHKE  
STREET: 660 White Plains Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-5144  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
MEDIUM TYPE: storage  
COMPUTER: NEC Powermate 1 Plus  
OPERATING SYSTEM: DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/98/763,374  
FILING DATE: 13-DEC-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19548028  
FILING DATE: 21-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurt G. Briscoe  
REGISTRATION NUMBER: 33,141  
REFERENCE/DOCKET NUMBER: Bayer 9763-KGR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 332-1700  
TELEFAX: (914) 332-1844  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-763-374-1

Query Match 36.4% Score 4: DB 2: Length 13:  
Best Local Similarity 100.0% Pred. No. 2.4e+02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4  
DB 9 AKKK 12

RESULT 31  
US-09-325-601-30  
Sequence 30: Application US/09325601  
Patent No. 6573045  
GENERAL INFORMATION:  
APPLICANT: Karn  
APPLICANT: Prescott  
TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds  
FILE REFERENCE: 3950/81235  
CURRENT APPLICATION NUMBER: US/09/325,601  
CURRENT FILING DATE: 1999-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide from K,  
Q, R-pentapeptide library  
US-09-325-601-30

Query Match 36.4% Score 4: DB 4: Length 13:  
Best Local Similarity 100.0% Pred. No. 2.4e+02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 AKKK 9  
DB 9 AKKK 9

RESULT 42  
US-08-4-05449-2  
Sequence 4: Application US/08-4-05449  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: ASSAYS FOR DETECTING A  
NUMBER OF SEQUENCES: 1  
DEPENDENT PATENT:  
ALPHESEE: 2003-08-01  
STATE: 1: 2: 3: 4: 5: 6: 7: 8: 9: 10: 11: 12: 13: 14: 15: 16: 17: 18: 19: 20: 21: 22: 23: 24: 25: 26: 27: 28: 29: 30: 31: 32: 33: 34: 35: 36: 37: 38: 39: 40: 41: 42: 43: 44: 45: 46: 47: 48: 49: 50: 51: 52: 53: 54: 55: 56: 57: 58: 59: 60: 61: 62: 63: 64: 65: 66: 67: 68: 69: 70: 71: 72: 73: 74: 75: 76: 77: 78: 79: 80: 81: 82: 83: 84: 85: 86: 87: 88: 89: 90: 91: 92: 93: 94: 95: 96: 97: 98: 99: 100: 101: 102: 103: 104: 105: 106: 107: 108: 109: 110: 111: 112: 113: 114: 115: 116: 117: 118: 119: 120: 121: 122: 123: 124: 125: 126: 127: 128: 129: 130: 131: 132: 133: 134: 135: 136: 137: 138: 139: 140: 141: 142: 143: 144: 145: 146: 147: 148: 149: 150: 151: 152: 153: 154: 155: 156: 157: 158: 159: 160: 161: 162: 163: 164: 165: 166: 167: 168: 169: 170: 171: 172: 173: 174: 175: 176: 177: 178: 179: 180: 181: 182: 183: 184: 185: 186: 187: 188: 189: 190: 191: 192: 193: 194: 195: 196: 197: 198: 199: 200: 201: 202: 203: 204: 205: 206: 207: 208: 209: 210: 211: 212: 213: 214: 215: 216: 217: 218: 219: 220: 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2013: 2014: 2015: 2016: 2017: 2018: 2019: 2020: 2021: 20

```
1 ADDRESSEE: ARNOLD, WHITE & DURKEE
2 STREET: P.O. BOX 4433
3 CITY: HOUSTON
4 STATE: TX
5 COUNTRY: USA
6 ZIP: 77210
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: FLOPPY DISK
10 COMPUTER: IBM PC COMPATIBLE
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: WORDPERFECT 5.1
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/232,453A
15 FILING DATE: APRIL 22, 1994
16 CLASSIFICATION: 514
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 07/748,319
19 FILING DATE: AUGUST 21, 1991
20 CLASSIFICATION: 514
21 ATTORNEY/AGENT INFORMATION:
22 NAME: PARKER, DAVID L.
23 REGISTRATION NUMBER: 32,165
24 REFERENCE/DOCKET NUMBER: USID:251/PAR
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (512) 418-3000
27 TELEFAX: (512) 474-7577
28
29 INFORMATION FOR SEQ ID NO: 4:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 14 amino acids
32 TYPE: amino acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35
36 US-08-232-453A-4
37
38 Query Match 36.4%, Score 4, DB 1, Length 14:
39 Best Local Similarity 100.0%, Pred. No. 2,40-02:
40 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
41
42 QY 1 AKKK 4
43 DB 10 AKKK 13
44
45 RESULT 34
46 US-08-453-862-3
47 Sequence 3, Application US/08453862
48 Patent No. 5738999
49 GENERAL INFORMATION:
50 APPLICANT: Segerson, Thomas P.
51 APPLICANT: Kinzie, J. Mark
52 APPLICANT: Mulvihill, Eileen R.
53 APPLICANT: Saugstad, Julie A.
54 APPLICANT: Westbrook, Gary L.
55 TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
56 NUMBER OF SEQUENCES: 5
57 CORRESPONDENCE ADDRESS:
58 ADDRESSEE: Townsend and Townsend and Crew LLP
59 STREET: Two Embarcadero Center, 8th Floor
60 CITY: San Francisco
61 STATE: CA
62 COUNTRY: USA
63 ZIP: 94111-3834
64
65 COMPUTER READABLE FORM:
66 MEDIUM TYPE: Floppy disk
67 COMPUTER: IBM PC compatible
68 OPERATING SYSTEM: PC-DOS/MS-DOS
69 SOFTWARE: PatentIn Release #1.0, Version #1.25
70 CURRENT APPLICATION DATA:
71 APPLICATION NUMBER: US/08/453,862
72 FILING DATE: 30-MAY-1995
73 CLASSIFICATION: 436
74 PRIOR APPLICATION DATA:
75 APPLICATION NUMBER: US 08/176,401
```

```
1 FILING DATE: 30-MAY-1995
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Parkerson, Steven W.
4 REGISTRATION NUMBER: 32,165
5 REFERENCE/DOCKET NUMBER: USID:251/PAR
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (512) 418-3000
8 TELEFAX: (512) 474-7577
9
10 INFORMATION FOR SEQ ID NO: 4:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 14 amino acids
13 TYPE: amino acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16
17 MOLECULE TYPE: peptide
18
19 US-08-453-862-3
20
21 Query Match 100.0%, Score 4, DB 1, Length 14:
22 Best Local Similarity 100.0%, Pred. No. 2,40-02:
23 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
24
25 QY 1 AKKK 4
26 DB 10 AKKK 11
27
28 RESULT 45
29 US-08-452-734A-4
30 Sequence 3, Application US/08452734A
31 Patent No. 5641042
32 GENERAL INFORMATION:
33 APPLICANT: Segerson, Thomas P.
34 APPLICANT: Kinzie, J. Mark
35 APPLICANT: Mulvihill, Eileen R.
36 APPLICANT: Saugstad, Julie A.
37 APPLICANT: Westbrook, Gary L.
38 TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
39 NUMBER OF SEQUENCES: 5
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: Townsend and Townsend and Crew LLP
42 STREET: Two Embarcadero Center, 8th Floor
43 CITY: San Francisco
44 STATE: CA
45 COUNTRY: USA
46 ZIP: 94111-3834
47
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Floppy disk
50 COMPUTER: IBM PC compatible
51 OPERATING SYSTEM: PC-DOS/MS-DOS
52 SOFTWARE: PatentIn Release #1.0, Version #1.25
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/08/452,734A
55 FILING DATE: 30-MAY-1995
56 CLASSIFICATION: 436
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US 07/748,319
59 FILING DATE: AUGUST 21, 1991
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: (512) 418-3000
62 TELEFAX: (512) 474-7577
63
64 INFORMATION FOR SEQ ID NO: 4:
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 14 amino acids
67 TYPE: amino acid
68 STRANDEDNESS: single
69 TOPOLOGY: linear
70
71 MOLECULE TYPE: peptide
72
73 US-08-452-734A-4
```





```

1 APPLICANT: Sato, Haruya
2 APPLICANT: Yamamoto, Keiji
3 APPLICANT: Suzuki, Kokichi
4 APPLICANT: Ikeda, Masahiro
5 APPLICANT: Sakagami, Masahiro
6 APPLICANT: Taniguchi, Makoto
7 TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
8 FILE REFERENCE: 110-511
9 CURRENT APPLICATION NUMBER: US/08/505,250
10 PRIOR FILING DATE: 1995-11-29
11 PRIOR APPLICATION NUMBER: PCT/JP95/00254
12 PRIOR FILING DATE: 1995-02-27
13 PRIOR APPLICATION NUMBER: JP 198187/94
14 PRIOR FILING DATE: 1994-08-23
15 NUMBER OF SEQ ID NOS: 53
16 SOFTWARE: PatentIn ver. 2.0
17 SEQ ID NO 14
18 LENGTH: 14
19 TYPE: PRT
20 ORGANISM: Artificial Sequence
21 FEATURE:
22 OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
23 OTHER INFORMATION: peptide
24 US-08-505-250-14

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Query Match 36.4% Score 47 IP 4 Length 14:

Best Local Similarity 100.0% Pred. No. 2,400,21 Indexes 0 Gaps 0:

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QY 1 AKKK 4
   IIII
DB 1 AKKK 4

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#### RESULT 40

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US-09-025-596-17
1 Sequence 17, Application US/9025546
2 Patent No. 6340463

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GENERAL INFORMATION:

APPLICANT: Mitchell, William M.

APPLICANT: Stratton, Charles W.

TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE

TITLE OF INVENTION: SEQUENCES

FILE REFERENCE: VDB98-01

CURRENT APPLICATION NUMBER: US/09/025,596

CURRENT FILING DATE: 1998-02-18

EARLIER APPLICATION NUMBER: 08/911,593

EARLIER FILING DATE: 1997-08-14

EARLIER APPLICATION NUMBER: 60/023,521

EARLIER FILING DATE: 1996-08-14

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17

LENGTH: 14

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

US-09-025-596-17

#### Query Match

Best Local Similarity 36.4% Score 47 IP 4 Length 14:

Matches 4: Conservative 0; Mismatches 0; Indexes 0; Gaps 0:

```

QY 4 KEQK 7
   IIII
DB 7 KEQK 10

```

#### RESULT 41

US-09-171-425-8

Sequence 8, Application US/09171425A

Patent No. 6465438

GENERAL INFORMATION:

APPLICANT: Schorr, Joachim

```

1 APPLICANT: Baker, David E.
2 APPLICANT: Smith, Barbara J.
3 TITLE OF INVENTION: METHOD FOR VACCINATION FOR PARVOVIRAL INFECTIONS
4 FILE REFERENCE: 08/000,000
5 CURRENT APPLICATION NUMBER: US/01/14,25A
6 PRIOR FILING DATE: 1998-01-14
7 EARLIER APPLICATION NUMBER: PCT/US97/00000
8 EARLIER FILING DATE: 1997-04-14
9 NUMBER OF SEQ ID NOS: 11
10 SOFTWARE: FASTSEQ for Windows Version 4.0
11 SEQ ID NO 1
12 LENGTH: 14
13 TYPE: PRT
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: Description of Artificial Sequence: oligonucleotides
17 US-09-171-425-8

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Query Match 36.4% Score 47 IP 4 Length 14:  
Best Local Similarity 100.0% Pred. No. 2,400,21  
Matches 4: Conservative 0; Mismatches 0; Indexes 0; Gaps 0:

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QY 1 AKKK 1
   III
DB 8 AKKK 1

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#### RESULT 42

US-09-171-425-8

Sequence 1, Application US/011425A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: METHOD FOR VACCINATION FOR PARVOVIRAL INFECTIONS

FILE REFERENCE: 08/000,000

CURRENT APPLICATION NUMBER: US/01/14,25A

CURRENT FILING DATE: 1998-02-18

EARLIER APPLICATION NUMBER: 60/023,521

EARLIER FILING DATE: 1996-08-14

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: oligonucleotides

OTHER INFORMATION: peptide

US-09-171-425-8

Sequence 1, Application US/011425A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: METHOD FOR VACCINATION FOR PARVOVIRAL INFECTIONS

FILE REFERENCE: 08/000,000

CURRENT APPLICATION NUMBER: US/01/14,25A

CURRENT FILING DATE: 1998-02-18

EARLIER APPLICATION NUMBER: 60/023,521

EARLIER FILING DATE: 1996-08-14

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: oligonucleotides

OTHER INFORMATION: peptide

US-09-171-425-8

Sequence 1, Application US/011425A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: METHOD FOR VACCINATION FOR PARVOVIRAL INFECTIONS

FILE REFERENCE: 08/000,000

CURRENT APPLICATION NUMBER: US/01/14,25A

CURRENT FILING DATE: 1998-02-18

EARLIER APPLICATION NUMBER: 60/023,521

EARLIER FILING DATE: 1996-08-14

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: oligonucleotides

OTHER INFORMATION: peptide

US-09-171-425-8

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; Sequence 3, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RRI-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3-6
; OTHER INFORMATION: /note= "Xaa is any amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note "Xaa is Ser, Thr or Tyr"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8-11
; OTHER INFORMATION: /note= "Xaa is any amino acid"
US-08-178-570-3

Query Match 36.48; Score 4; DB 1; Length 15;
Best local Similarity 100.08; Pred. No. 2,666,21;
Matches 4; Conservative 6; Mismatches 0; Gaps 0;

QY 1 AKKK 4
DB 12 AKKK 15

RESULT 44
US-08-178-570-76
; Sequence 76, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON

```

```

; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RRI-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3-6
; OTHER INFORMATION: /note= "Xaa is any amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note "Xaa is Ser, Thr or Tyr"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8-11
; OTHER INFORMATION: /note= "Xaa is any amino acid"
US-08-178-570-4

Query Match 36.48; Score 4; DB 1; Length 15;
Best local Similarity 100.08; Pred. No. 2,666,21;
Matches 4; Conservative 6; Mismatches 0; Gaps 0;

QY 1 AKKK 4
DB 12 AKKK 15

RESULT 44
US-08-178-570-76
; Sequence 76, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON

```

Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 12 AKKK 15

## RESULT 46

US-08-369-643-76  
; Sequence 76, Application US/08369643A  
; Patent No. 6004757  
; GENERAL INFORMATION:  
; APPLICANT: Cantley, Lewis C.  
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
; FILE REFERENCE: CNS-001CP  
; CURRENT APPLICATION NUMBER: US/08/369,643A  
; EARLIER FILING DATE: 1995-01-06  
; EARLIER APPLICATION NUMBER: US 08/178,576  
; EARLIER FILING DATE: 1994-01-07  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
; OTHER INFORMATION: Synthesized as a substrate for src tyrosine  
; OTHER INFORMATION: Kinases  
US-08-369-643-76

Query Match 36.4%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 11 AKKK 14

## RESULT 47

US-08-461-384B-10  
; Sequence 10, Application US/08461384B  
; Patent No. 6025473  
; GENERAL INFORMATION:  
; APPLICANT: Cole, Susan P.C.  
; APPLICANT: Deeley, Roger G.  
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS  
; STREET: Queen's University at Kingston  
; CITY: Kingston  
; STATE: Ontario  
; COUNTRY: CANADA  
; ZIP: K7L 3N6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,384B  
; FILING DATE: 05-JUN-95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/966,923  
; FILING DATE: 27-OCT-1992  
; APPLICATION NUMBER: 08/029,340  
; FILING DATE: 8-MAR-1993  
; APPLICATION NUMBER: 08/141,893  
; FILING DATE: 26-OCT-1993

1 APPLICATION NUMBER: US/08/461,384B  
2 FILING DATE: 05-JUN-1995  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Steele, Robert M.  
5 REGISTRATION NUMBER: 37,650  
6 REFERENCE/INFORMATION: 08/029,340  
7 TELECOMMUNICATIONS: 08/141,893  
8 FILING DATE: 27-OCT-1992  
9 TELEFAX: (613) 546-1442  
10 INFORMATION FOR SEQUENCE NUMBER:  
11 SEQUENCE CHARACTERISTICS:  
12 LENGTH: 15 amino acids  
13 TYPE: amino acid  
14 MATURE TYPE: 08/141,893  
15 US-08-461,384B-10

## Query Match 36.4%; Score 4; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 11 AKKK 14

## RESULT 48

US-08-407-207A-7  
; Sequence 7, Application US/08407207A  
; Patent No. 6004757  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Susan P.  
; TITLE OF INVENTION: ARTICLES OF A MULTIDRUG RESISTANCE PROTEIN  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS  
; STREET: Queen's University at Kingston  
; CITY: Kingston  
; STATE: Ontario  
; COUNTRY: CANADA  
; ZIP: K7L 3N6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/407,207A  
; FILING DATE: 20-MAR-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/006,023  
; FILING DATE: 27-OCT-1992  
; APPLICATION NUMBER: 08/029,340  
; FILING DATE: 05-JUN-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steele, Robert M.  
; REGISTRATION NUMBER: 37,650  
; REFERENCE/INFORMATION: 08/141,893  
; TELEFAX: (613) 546-1442  
; INFORMATION FOR SEQUENCE NUMBER:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; MATURE TYPE: 08/141,893  
US-08-407-207A-7

Query Match 36.4%; Score 4; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OKOR 9  
 1111  
 Db 8 OKOR 11

## RESULT 49

PCT-US95-00147-3  
 ; Sequence 3, Application PC/TUS9500147  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 60 STATE STREET, suite 510  
 ; CITY: BOSTON  
 ; STATE: MASSACHUSETTS  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/00147  
 ; FILING DATE:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/178,570  
 ; FILING DATE: JANUARY 7, 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DeConi, Giulio A., Jr.  
 ; REGISTRATION NUMBER: 31,503  
 ; REFERENCE/DOCKET NUMBER: BBI-00407PC  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 227-5941  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 3-6  
 ; OTHER INFORMATION: /note= "Xaa is any amino acid"  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 7  
 ; OTHER INFORMATION: /note= "Xaa is Ser, Thr or Lys"  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 8-11  
 ; OTHER INFORMATION: /note= "Xaa is any amino acid"  
 ; PCT-US95-00147-3

Query Match 36.4%; Score 4; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKKK 4  
 1111  
 Db 12 AKKK 15

## RESULT 50

PCT-US95-00147-76

; Sequence 76, Application PC/TUS9500147  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 60 STATE STREET, suite 510  
 ; CITY: BOSTON  
 ; STATE: MASSACHUSETTS  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/00147  
 ; FILING DATE:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/178,570  
 ; FILING DATE: JANUARY 7, 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DeConi, Giulio A., Jr.  
 ; REGISTRATION NUMBER: 31,503  
 ; REFERENCE/DOCKET NUMBER: BBI-00407PC  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 227-5941  
 ; INFORMATION FOR SEQ ID NO: 76:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
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 ; LOCATION: 3-6  
 ; OTHER INFORMATION: /note= "Xaa is any amino acid"  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 7  
 ; OTHER INFORMATION: /note= "Xaa is Ser, Thr or Lys"  
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Query Match 36.4%; Score 4; DB 3; Length 15;  
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 Db 12 AKKK 15

Search completed. Sequence was 200, 11, 26, 12  
 Job time: 1.41 sec

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 17:21:47 ; search time 26 seconds

(without alignments)  
64.015 Million cell: updates/sec

**Title:** US-09-787-443-20

perfect score:

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Searched: 566894 seqs, 151307093 residues

Word size : 0

Total number of hits satisfying chosen parameters. (bits)

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Maximum DK	seq length: 15

post-processing: Listing first 500 summaries

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426	3	27.3	10	10	US-09-805-431-46	Sequence 46, Appl	499	15	09	02	02	044R-379
427	3	27.3	10	10	US-09-995-847-2	Sequence 2, Appl	500	15	09	02	02	044R-379
428	3	27.3	10	10	US-09-773-102A-2	Sequence 2, Appl	501	15	09	02	02	044R-379
429	3	27.3	10	11	US-09-814-604-7	Sequence 7, Appl	502	15	09	02	02	044R-379
430	3	27.3	10	11	US-09-955-845-8	Sequence 8, Appl	503	15	09	02	02	044R-379
431	3	27.3	10	11	US-09-882-774-12	Sequence 12, Appl	504	15	09	02	02	044R-379
432	3	27.3	10	11	US-09-876-235-2	Sequence 2, Appl	505	15	09	02	02	044R-379
433	3	27.3	10	11	US-09-578-917A-48	Sequence 48, Appl	506	15	09	02	02	044R-379
434	3	27.3	10	11	US-09-799-250-343	Sequence 343, Appl	507	15	09	02	02	044R-379
435	3	27.3	10	11	US-09-799-250-343	Sequence 343, Appl	508	15	09	02	02	044R-379
436	3	27.3	10	11	US-09-882-291-15	Sequence 15, Appl	509	15	09	02	02	044R-379
437	3	27.3	10	11	US-09-882-291-15	Sequence 15, Appl	510	15	09	02	02	044R-379
438	3	27.3	10	11	US-09-882-291-15	Sequence 15, Appl	511	15	09	02	02	044R-379
439	3	27.3	10	11	US-09-882-291-15	Sequence 15, Appl	512	15	09	02	02	044R-379
440	3	27.3	10	11	US-09-775-052-45	Sequence 45, Appl	513	15	09	02	02	044R-379
441	3	27.3	10	11	US-09-775-052-45	Sequence 45, Appl	514	15	09	02	02	044R-379
442	3	27.3	10	11	US-09-880-748-1100	Sequence 1100, Appl	515	15	09	02	02	044R-379
443	3	27.3	10	11	US-09-876-904A-22	Sequence 22, Appl	516	15	09	02	02	044R-379
444	3	27.3	10	11	US-09-876-904A-152	Sequence 152, Appl	517	15	09	02	02	044R-379
445	3	27.3	10	11	US-09-876-904A-245	Sequence 245, Appl	518	15	09	02	02	044R-379
446	3	27.3	10	11	US-09-876-904A-257	Sequence 257, Appl	519	15	09	02	02	044R-379
447	3	27.3	10	11	US-09-876-904A-274	Sequence 274, Appl	520	15	09	02	02	044R-379
448	3	27.3	10	11	US-09-876-904A-540	Sequence 540, Appl	521	15	09	02	02	044R-379
449	3	27.3	10	11	US-09-876-904A-546	Sequence 546, Appl	522	15	09	02	02	044R-379
450	3	27.3	10	11	US-09-876-904A-572	Sequence 572, Appl	523	15	09	02	02	044R-379
451	3	27.3	10	11	US-09-876-904A-578	Sequence 578, Appl	524	15	09	02	02	044R-379
452	3	27.3	10	11	US-09-922-226-41	Sequence 41, Appl	525	15	09	02	02	044R-379
453	3	27.3	10	11	US-09-572-404B-447	Sequence 447, Appl	526	15	09	02	02	044R-379

ALTERNATES

RESULT 1

US-09-815-034-5

Sequence 5, ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED EXCEPT WHERE SHOWN OTHERWISE

GENERAL INSTRUCTIONS

APPROPRIATE REVIEWERS

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## 272

1	SEQUENCE NUMBER	20000000000000000000
2	GENERAL INFORMATION	
3	APPLICANT NAME	APPLICANT
4	APPLICANT ADDRESS	APPLICANT ADDRESS
5	APPLICANT CITY	APPLICANT CITY
6	APPLICANT STATE	APPLICANT STATE
7	APPLICANT ZIP CODE	APPLICANT ZIP CODE
8	APPLICANT TAX ID NUMBER	APPLICANT TAX ID NUMBER
9	TITLE OF INVENTION	TITLE OF INVENTION
10	FILE REFERENCE	FILE REFERENCE
11	CURRENT APPLICATION NUMBER	CURRENT APPLICATION NUMBER
12	CURRENT FILING DATE	CURRENT FILING DATE
13	PRIOR APPLICATION NUMBER	PRIOR APPLICATION NUMBER
14	PRIOR FILING DATE	PRIOR FILING DATE
15	PRIOR APPLICATION NUMBER	PRIOR APPLICATION NUMBER
16	PRIOR FILING DATE	PRIOR FILING DATE
17	PRIOR APPLICATION NUMBER	PRIOR APPLICATION NUMBER
18	PRIOR FILING DATE	PRIOR FILING DATE
19	NUMBER OF SEQ. IN SET	NUMBER OF SEQ. IN SET
20	SOFTWARE DATED IN VERSION	SOFTWARE DATED IN VERSION

SEQ ID NO 5

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: preferred peptide for pdz binding domain

US-09-813-653-5

Query Match

Best Local Similarity 100.0%; Score 4; DB 9; Length 8;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5

Db 2 KKKE 5

RESULT 2

US-09-813-448-2

Sequence 2, Application US/09813448

Patent No. US20020142346A1

GENERAL INFORMATION:

APPLICANT: Nestor, John

TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds

FILE REFERENCE: CNS-006

CURRENT APPLICATION NUMBER: US/09/813,448

CURRENT FILING DATE: 2001-03-20

PRIOR APPLICATION NUMBER: US 60/190,946

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: US 60/190,996

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: US 60/191,299

PRIOR FILING DATE: 2000-03-21

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: preferred amino acids for PDZ binding domain

US-09-813-448-2

Query Match

Best Local Similarity 100.0%; Score 4; DB 10; Length 8;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5

Db 2 KKKE 5

RESULT 3

US-09-876-904A-352

Sequence 352, Application US/99876904A

Publication No. US2003007294A1

GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMODIUM (LIPID GENES TM) AND THERAPEUTIC

FILE REFERENCE: TB-2002-00

CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 352

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Human ATR-1, 10 basic residues/sequence zipper

US-09-876-904A-352

Query Match

Best Local Similarity 100.0%; Score 4; DB 11; Length 8;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5

Db 2 KKKE 5

RESULT 4

US-09-876-904A-352

Sequence 344, Application US/99876904A

Publication No. US2003007294A1

GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMODIUM (LIPID GENES TM) AND THERAPEUTIC

FILE REFERENCE: TB-2002-00

CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 344

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: from 10 to 100% (related to TRER/ATP)

US-09-876-904A-352

Query Match

Best Local Similarity 100.0%; Score 4; DB 11; Length 8;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5

Db 2 KKKE 5

RESULT 5

US-09-876-904A-352

Sequence 344, Application US/99876904A

Publication No. US2003007294A1

GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMODIUM (LIPID GENES TM) AND THERAPEUTIC

FILE REFERENCE: TB-2002-00

CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 344

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: from 10 to 100% (related to TRER/ATP)

US-09-876-904A-352

Query Match

Best Local Similarity 100.0%; Score 4; DB 11; Length 8;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
IIII  
Db 5 KKKE 8

## RESULT 6

US-10-014-322A-62  
; Sequence 62, Application US/10014322A  
; Publication No. US20030167129A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, Jr., John  
; APPLICANT: Wilson, Carol  
; APPLICANT: Tan Hehir, Christina  
; APPLICANT: Kates, Steven  
; APPLICANT: Krstenansky, John  
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds  
; FILE REFERENCE: CNS-008  
; CURRENT APPLICATION NUMBER: US/10/014.322A  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: US 60/243,587  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 09/813,651  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 09/813,653  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 09/813,448  
; PRIOR FILING DATE: 2001-03-20  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 62  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Preferred peptide for p37 binding domain  
US-10-014-322A-62

Query Match 36.4%, Score 4, DB 12, Length 8;  
Best Local Similarity 100.0%, Pred. No. 5e-05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 2 KKKE 5  
IIII  
Db 2 KKKE 5

## RESULT 7

US-10-024-935-19  
; Sequence 19, Application US/10024935  
; Publication No. US20020142966A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth Walter Bair  
; APPLICANT: YingNan Fan Chen  
; APPLICANT: Timothy Michael Ramsey  
; APPLICANT: Michael Lloyd Sabio  
; APPLICANT: Sushill Kumar Sharma  
; TITLE OF INVENTION: Inhibitors of the F2F1/tyrosin  
; FILE REFERENCE: 4-31664P1/Procy  
; CURRENT APPLICATION NUMBER: US/10/024,935  
; CURRENT FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-10-024-935-19

Query Match 36.4%, Score 4, DB 14, Length 8;

Best Local Similarity 100.0%, Pred. No. 5e-05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AKKK 4  
IIII  
Db 2 AKKK 5

## RESULT 8

US-10-040-572-4  
; Sequence 8, Application US/10040572  
; Publication No. US2002057180A1  
; GENERAL INFORMATION:  
; APPLICANT: SKY Robotics  
; APPLICANT: Badmash, David  
; APPLICANT: Fiedler, Matthew  
; TITLE OF INVENTION: Artificial ANTI-AP-PTIC COMPOSITIONS  
; FILE REFERENCE: 411,231  
; CURRENT APPLICATION NUMBER: US/10/040,572  
; CURRENT FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
US-10-040-572-4

Query Match 66.4%, Score 4, DB 14, Length 8;  
Best Local Similarity 100.0%, Pred. No. 5e-05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AKKK 4  
IIII  
Db 4 AKKK 7

## RESULT 9

US-09-879-936-24  
; Sequence 24, Application US/09093624  
; Patent No. US2001040040A1  
; GENERAL INFORMATION:  
; APPLICANT: VBI Pharmaceuticals  
; APPLICANT: Mak, A. J. S.  
; APPLICANT: Gates, Robert J.  
; TITLE OF INVENTION: Islet Receptor Agonist Muscarinic Antagonists  
; FILE REFERENCE: 1997-21,048  
; CURRENT APPLICATION NUMBER: US/09/879,936  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/566,478  
; PRIOR FILING DATE: 1997-06-24  
; PRIOR APPLICATION NUMBER: 09/566,479  
; PRIOR FILING DATE: 1997-06-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: PEP-11E  
; LOCATION: (1) (2)  
; OTHER INFORMATION: Postcodes 25, 30, 38, 40, 41  
; NAME/KEY: PEP-11E  
; LOCATION: (9)  
; OTHER INFORMATION: Islet receptor agonist phosphoramidate acid  
US-09-879-936-24

Query Match 66.4%, Score 4, DB 9, Length 9;

Best Local Similarity 100.0%, Pred. No. 5e-05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AKKK 4



? CURRENT APPLICATION NUMBER: US/10/304.443  
 ? CURRENT FILING DATE: 2002-11-26  
 ? PRIOR APPLICATION NUMBER: US/09/698.936A  
 ? PRIOR FILING DATE: 2001-02-20  
 ? NUMBER OF SEQ ID NOS: 121  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO 102  
 ? LENGTH: 9  
 ? TYPE: PRI  
 ? ORGANISM: Human peptide sequence  
 US-10-304-443-102

Query Match 36.4% Score 4; DB 12; Length 9  
 Best Local Similarity 100.0%; Pred. No. 50/65;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KORN 10  
 Db 2 KURN 5

## RESULT 15

US-10-011-321-4  
 ? Sequence 4, Application US/10011321  
 ? Publication No. US20020102268A1

GENERAL INFORMATION:

? APPLICANT: KISS, Terry  
 ? TITLE OF INVENTION: APOPTOSIS MARKER ANTIBODIES AND METHODS OF USE  
 ? FILE REFERENCE: 16026.9033  
 ? CURRENT APPLICATION NUMBER: US/10/011.42;  
 ? CURRENT FILING DATE: 2001-12-03  
 ? PRIOR APPLICATION NUMBER: 09/445,615  
 ? PRIOR FILING DATE: 1999-12-08  
 ? PRIOR APPLICATION NUMBER: 60/101,920  
 ? PRIOR FILING DATE: 1998-09-24  
 ? NUMBER OF SEQ ID NOS: 5  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO: 4  
 ? LENGTH: 9  
 ? TYPE: PRI  
 ? ORGANISM: Homo sapiens

US-10-011-321-4

Query Match 36.4% Score 4; DB 12; Length 9  
 Best Local Similarity 100.0%; Pred. No. 50/65;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 Db 5 AKKK 9

## RESULT 16

US-10-211-207-13  
 ? Sequence 13, Application US/10211207  
 ? Publication No. US20030004113A1

GENERAL INFORMATION:

? APPLICANT: Collins, Mary  
 ? APPLICANT: Madtenas, Joaquin  
 ? APPLICANT: Carreno, Beatriz  
 ? APPLICANT: Kuchroo, Vijay  
 ? TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE  
 ? TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CD134 AND  
 ? FILE REFERENCE: P02A  
 ? FILE REFERENCE: GNN-027  
 ? CURRENT APPLICATION NUMBER: US/10/211.207  
 ? CURRENT FILING DATE: 2002-08-02  
 ? PRIOR APPLICATION NUMBER: US/10/077.106  
 ? PRIOR FILING DATE: 2002-02-15  
 ? NUMBER OF SEQ ID NOS: 25  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO 13  
 ? LENGTH: 9

? TYPE: PRI  
 ? ORGANISM: Homo sapiens  
 US-10-211-207-13

Query Match 36.4% Score 4; DB 12; Length 9  
 Best Local Similarity 100.0%; Pred. No. 50/65;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKK 1  
 Db 5 AKKK 5

## RESULT 17

US-10-211-207-13  
 ? Sequence 13, Application US/10211207

GENERAL INFORMATION:

? APPLICANT: Collins, Mary  
 ? APPLICANT: Madtenas, Joaquin  
 ? APPLICANT: Carreno, Beatriz  
 ? APPLICANT: Kuchroo, Vijay  
 ? TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE  
 ? TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CD134 AND  
 ? FILE REFERENCE: P02A  
 ? FILE REFERENCE: GNN-027  
 ? CURRENT APPLICATION NUMBER: US/10/211.207  
 ? CURRENT FILING DATE: 2002-08-02  
 ? PRIOR APPLICATION NUMBER: US/10/077.106  
 ? PRIOR FILING DATE: 2002-02-15  
 ? NUMBER OF SEQ ID NOS: 25  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO: 13  
 ? LENGTH: 9  
 ? TYPE: PRI  
 ? ORGANISM: Homo sapiens

US-10-211-207-13

Query Match 36.4% Score 4; DB 12; Length 9  
 Best Local Similarity 100.0%; Pred. No. 50/65;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKK 1  
 Db 5 AKKK 5

## RESULT 18

US-10-211-207-13  
 ? Sequence 13, Application US/10211207

GENERAL INFORMATION:

? APPLICANT: Collins, Mary  
 ? APPLICANT: Madtenas, Joaquin  
 ? APPLICANT: Carreno, Beatriz  
 ? APPLICANT: Kuchroo, Vijay  
 ? TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE  
 ? TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CD134 AND  
 ? FILE REFERENCE: P02A  
 ? FILE REFERENCE: GNN-027  
 ? CURRENT APPLICATION NUMBER: US/10/211.207  
 ? CURRENT FILING DATE: 2002-08-02  
 ? PRIOR APPLICATION NUMBER: US/10/077.106  
 ? PRIOR FILING DATE: 2002-02-15  
 ? NUMBER OF SEQ ID NOS: 25  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO: 13  
 ? LENGTH: 9  
 ? TYPE: PRI  
 ? ORGANISM: Homo sapiens  
 ? OTHER INFORMATION: FASTSEQ for Windows Version 4.0  
 ? OTHER INFORMATION: FASTSEQ for Windows Version 4.0  
 US-10-211-207-13

US-10-211-207-13

Query Match 36.4% Score 4; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 5,30-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 7 AKKK 10

## RESULT 19

US-09-876-904A-90  
Sequence 90, Application US/09876904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMA-DNA (LIPID-GENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/GENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPIDOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/2210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 90  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Xenopus  
US-09-876-904A-90

## Query Match

Best Local Similarity 36.4%; Score 4; DB 11; Length 10;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 4 AKKK 7

## RESULT 20

US-09-572-404B-1694  
Sequence 1694, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProPatent version 1.0  
SEQ ID NO 1694  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: Sequence located in LAMA2 OR LAMM at 1-16,1625 and may interact  
OTHER INFORMATION: Sequence 1694 in this patent  
US-09-572-404B-1694

## Query Match

Best Local Similarity 36.4%; Score 4; DB 11; Length 10;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
DB 1 KKKE 4

## RESULT 21

US-09-572-404B-1694  
Sequence 1694, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProPatent version 1.0  
SEQ ID NO 1694  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: Sequence located in LAMA2 OR LAMM at 1-16,1625 and may interact  
OTHER INFORMATION: Sequence 1694 in this patent  
US-09-572-404B-1694

Query Match  
Best Local Similarity 36.4%; Score 4; DB 11; Length 10;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
DB 1 KKKE 4

## RESULT 22

US-09-572-404B-1694  
Sequence 1694, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProPatent version 1.0  
SEQ ID NO 1694  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: Sequence located in CYPX1 at 73-82 and may interact with SGLT  
OTHER INFORMATION: Sequence 1694 in this patent  
US-09-572-404B-1694

Query Match  
Best Local Similarity 36.4%; Score 4; DB 11; Length 10;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
DB 1 KKKE 4

## RESULT 23

US-09-572-404B-1694  
Sequence 1694, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProPatent version 1.0  
SEQ ID NO 1694  
LENGTH: 10

1 TYPE: PRI  
2 ORGANISM: Arabidopsis Thaliana  
3 OTHER INFORMATION: Sequence located in AG at 255-264 and may interact with  
US-09-572-270A-97

Query Match 36.4% Score 4: DB 12: Length 10:  
Best Local Similarity 100.0% Pred. No. 5,40-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKEQ 6  
Db 1 KKEQ 4

RESULT 24  
US-09-572-270A-99  
1 Sequence 99, Application US/09572270A  
2 Publication No. US20030148368A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Proteom Ltd  
5 TITLE OF INVENTION: Inter-complementary peptide listing  
6 FILE REFERENCE:  
7 CURRENT APPLICATION NUMBER: US/09/572.270A  
8 CURRENT FILING DATE: 2000-05-17  
9 NUMBER OF SEQ ID NOS: 1144  
10 SOFTWARE: Protpatent version 1.0  
11 SEQ ID NO 99  
12 LENGTH: 10  
13 TYPE: PRI  
14 ORGANISM: Arabidopsis Thaliana  
15 OTHER INFORMATION: Sequence located in AG at 255-264 and may interact with  
US-09-572-270A-99

Query Match 36.4% Score 4: DB 12: Length 10:  
Best Local Similarity 100.0% Pred. No. 5,40-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKEQ 6  
Db 1 KKEQ 4

RESULT 25  
US-09-572-270A-318  
1 Sequence 318, Application US/09572270A  
2 Publication No. US20030148368A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Proteom Ltd  
5 TITLE OF INVENTION: Inter-complementary peptide listing  
6 FILE REFERENCE:  
7 CURRENT APPLICATION NUMBER: US/09/572.270A  
8 CURRENT FILING DATE: 2000-05-17  
9 NUMBER OF SEQ ID NOS: 1144  
10 SOFTWARE: Protpatent version 1.0  
11 SEQ ID NO 318  
12 LENGTH: 10  
13 TYPE: PRI  
14 ORGANISM: Arabidopsis Thaliana  
15 OTHER INFORMATION: Sequence located in PG2 at 1245-1258 and may interact with  
US-09-572-270A-318

Query Match 36.4% Score 4: DB 12: Length 10:  
Best Local Similarity 100.0% Pred. No. 5,40-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4  
Db 1 AKKK 4

RESULT 26  
US-09-572-270A-320  
1 Sequence 320, Application US/09572270A

1 Publication No. US20030148368A1  
2 GENERAL INFORMATION:  
3 APPLICANT: Proteom Ltd  
4 TITLE OF INVENTION: Inter-complementary peptide listing  
5 FILE REFERENCE:  
6 CURRENT APPLICATION NUMBER: US/09/572.270A  
7 CURRENT FILING DATE: 2000-05-17  
8 NUMBER OF SEQ ID NOS: 1144  
9 SOFTWARE: Protpatent version 1.0  
10 SEQ ID NO 320  
11 LENGTH: 10  
12 TYPE: PRI  
13 ORGANISM: Arabidopsis Thaliana  
14 OTHER INFORMATION: Sequence located in PG2 at 1245-1258 and may interact with  
US-09-572-270A-320

Query Match 36.4% Score 4: DB 12: Length 10:  
Best Local Similarity 100.0% Pred. No. 5,40-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKEQ 6  
Db 1 KKEQ 4

RESULT 27  
US-09-572-270A-320  
1 Sequence 320, Application US/09572270A  
2 Publication No. US20030148368A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Proteom Ltd  
5 TITLE OF INVENTION: Inter-complementary peptide listing  
6 FILE REFERENCE:  
7 CURRENT APPLICATION NUMBER: US/09/572.270A  
8 CURRENT FILING DATE: 2000-05-17  
9 NUMBER OF SEQ ID NOS: 1144  
10 SOFTWARE: Protpatent version 1.0  
11 SEQ ID NO 320  
12 LENGTH: 10  
13 TYPE: PRI  
14 ORGANISM: Arabidopsis Thaliana  
15 OTHER INFORMATION: Sequence located in PG2 at 1245-1258 and may interact with  
US-09-572-270A-320

Query Match 36.4% Score 4: DB 12: Length 10:  
Best Local Similarity 100.0% Pred. No. 5,40-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKEQ 6  
Db 1 KKEQ 4

RESULT 28  
US-09-572-270A-444  
1 Sequence 444, Application US/09572270A  
2 Publication No. US20030148368A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Proteom Ltd  
5 TITLE OF INVENTION: Inter-complementary peptide listing  
6 FILE REFERENCE:  
7 CURRENT APPLICATION NUMBER: US/09/572.270A  
8 CURRENT FILING DATE: 2000-05-17  
9 NUMBER OF SEQ ID NOS: 1144  
10 SOFTWARE: Protpatent version 1.0  
11 SEQ ID NO 444  
12 LENGTH: 10  
13 TYPE: PRI  
14 ORGANISM: Arabidopsis Thaliana  
15 OTHER INFORMATION: Sequence located in PG2 at 1245-1258 and may interact with  
US-09-572-270A-444

Query Match 36.4% Score 4: DB 12: Length 10:  
Best Local Similarity 100.0% Pred. No. 5,40-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKEQ 6  
Db 1 KKEQ 4

RESULT 29  
US-09-572-270A-444  
1 Sequence 444, Application US/09572270A  
2 Publication No. US20030148368A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Proteom Ltd  
5 TITLE OF INVENTION: Inter-complementary peptide listing  
6 FILE REFERENCE:  
7 CURRENT APPLICATION NUMBER: US/09/572.270A  
8 CURRENT FILING DATE: 2000-05-17  
9 NUMBER OF SEQ ID NOS: 1144  
10 SOFTWARE: Protpatent version 1.0  
11 SEQ ID NO 444  
12 LENGTH: 10  
13 TYPE: PRI  
14 ORGANISM: Arabidopsis Thaliana  
15 OTHER INFORMATION: Sequence located in PG2 at 1245-1258 and may interact with  
US-09-572-270A-444

; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of  
 ; FILE OF INVENTION: Cancer  
 ; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062.109A  
 ; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 10/005.480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 444  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-062-109A-444

Query Match 36.4% Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5,76-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KORN 10  
 DB 6 KORN 9

## RESULT 29

; Sequence 273, Application US/09/876,904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PSOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 273  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila sp.  
 ; FEATURE:  
 ; OTHER INFORMATION: Recombination: repair protein 1  
 US-09-876-904A-273

Query Match 36.4% Score 4; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5,76-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 5  
 DB 6 KKE 9

## RESULT 30

; Sequence 354, Application US/09/876,904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PSOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 354  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: (The cysteine region that binds DNA)  
 US-09-876-904A-354

Query Match 36.4% Score 4; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5,76-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 5  
 DB 6 KKE 9

## RESULT 31

; Sequence 354, Application US/09/876,904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PSOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 354  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Recombination: repair protein 1  
 US-10-062-109A-444

Query Match 36.4% Score 4; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5,76-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 5  
 DB 6 KKE 9

## RESULT 32

; Sequence 354, Application US/09/876,904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PSOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 354  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens



US-10-304-443-91

Query Match 36.48: Score 4: DB 12: Length 11  
Best Local Similarity 100.0%; Pred. No. 5,76+02;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
DB 3 KORN 6

RESULT 37

US-10-020-269-34

Sequence 34: Application US/10020269  
Publication No. US20030175310A1  
GENERAL INFORMATION:  
APPLICANT: Mitchell, William M.  
APPLICANT: Stratton, Charles W.  
TITLE OF INVENTION: IDENTIFICATION OF ANTI-GENIC PEPTIDE  
TITLE OF INVENTION: SEQUENCES  
FILE REFERENCE: VDB98-01  
CURRENT APPLICATION NUMBER: US/10/020-269  
CURRENT FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/020-106  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/020-921  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-14  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 34  
LENGTH: 11  
TYPE: PRI  
ORGANISM: Chlamydia pneumoniae

US-10-020-269-34

Query Match 36.48: Score 4: DB 12: Length 11  
Best Local Similarity 100.0%; Pred. No. 5,76+02;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4  
DB 3 AKKK 6

RESULT 34

US-09-985-157-11  
Sequence 11: Application US/09985157  
Patent No. US20020145797A1  
GENERAL INFORMATION:  
APPLICANT: SHOKAT, Kevan M.  
TITLE OF INVENTION: Engineered Protein Kinases Which Can Utilize Modified Nucleotides  
TITLE OF INVENTION: Triphosphate Substrates  
FILE REFERENCE: 51518-5002-05  
CURRENT APPLICATION NUMBER: US/09/985,157  
CURRENT FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: US 09/367,065  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: PCT/US98/02522  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: US 60/046,727  
PRIOR FILING DATE: 1997-05-16  
PRIOR APPLICATION NUMBER: US 08/797,552  
PRIOR FILING DATE: 1997-02-07  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 12  
TYPE: PRI  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Optimized Abl substrate

US-09-985-157-11

Query Match 36.48: Score 4: DB 10: Length 12  
Best Local Similarity 100.0%; Pred. No. 4,10+02;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4  
DB 9 AKKK 7

RESULT 35

US-09-982-291-54  
Sequence 54: Application US/09982291  
Publication No. US20030175310A1  
GENERAL INFORMATION:  
APPLICANT: Mitchell, William M.  
APPLICANT: Stratton, Charles W.  
TITLE OF INVENTION: IDENTIFICATION OF ANTI-GENIC PEPTIDE  
TITLE OF INVENTION: SEQUENCES  
FILE REFERENCE: VDB98-01  
CURRENT APPLICATION NUMBER: US/09/982,291  
CURRENT FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/020-106  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/020-921  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-14  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 12  
TYPE: PRI  
ORGANISM: Chlamydia pneumoniae

US-09-982-291-54  
Query Match 36.48: Score 4: DB 12: Length 12  
Best Local Similarity 100.0%; Pred. No. 4,10+02;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4  
DB 9 AKKK 7

RESULT 36

US-09-982-291-54  
Sequence 54: Application US/09982291  
Publication No. US20030175310A1  
GENERAL INFORMATION:  
APPLICANT: Mitchell, William M.  
APPLICANT: Stratton, Charles W.  
TITLE OF INVENTION: IDENTIFICATION OF ANTI-GENIC PEPTIDE  
TITLE OF INVENTION: SEQUENCES  
FILE REFERENCE: VDB98-01  
CURRENT APPLICATION NUMBER: US/09/982,291  
CURRENT FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/020-106  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/020-921  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-14  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 12  
TYPE: PRI  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Optimized Abl substrate

US-09-982-291-54  
Query Match 36.48: Score 4: DB 12: Length 12  
Best Local Similarity 100.0%; Pred. No. 4,10+02;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4  
DB 9 AKKK 7

RESULT 37

US-09-954-385-126  
? Sequence 126, Application US/09954385  
? Publication No. US20030100467A1  
? GENERAL INFORMATION:  
? APPLICANT: Aehle, Wolfgang  
? APPLICANT: Baldwin, Toby L.  
? APPLICANT: Van Gastel, Franciscus J.G.  
? APPLICANT: Janssen, Giselle G.  
? APPLICANT: Murray, Christopher J.  
? APPLICANT: Wang, Huaming  
? APPLICANT: Winetzk, Deborah S.  
? TITLE OF INVENTION: Binding Phenol oxidizing Enzyme-partic  
? TITLE OF INVENTION: Complexes  
? FILE REFERENCE: GC690  
? CURRENT APPLICATION NUMBER: US/09/954-385  
? CURRENT FILING DATE: 2001-09-12  
? NUMBER OF SEQ ID NOS: 433  
? SOFTWARE: FASTSEQ for Windows Version 4.0  
? SEQ ID NO 126  
? LENGTH: 12  
? TYPE: PRT  
? ORGANISM: Artificial Sequence  
? FEATURE:  
? OTHER INFORMATION: binding peptide  
US-09-954-385-126

Query Match 36.4% Score 43 14 12 Length 12  
Best Local Similarity 100.0% Pref No. 6, Ident 12  
Matches 4: Conservative 0; Mismatches 0; Gaps 0  
QY 6 OKOR 9  
DB 8 OKOR 11

US-10-293-086-75  
? Sequence 75, Application US/1029386  
? Publication No. US2003013410A1  
? GENERAL INFORMATION:  
? APPLICANT: Cujec, Thomas P.  
? TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors  
? FILE REFERENCE: 50036/048002  
? CURRENT APPLICATION NUMBER: US/10/293-086  
? CURRENT FILING DATE: 2003-03-25  
? PRIOR APPLICATION NUMBER: US 60/187,990  
? PRIOR FILING DATE: 2001-11-13  
? NUMBER OF SEQ ID NOS: 144  
? SOFTWARE: FASTSEQ for Windows Version 4.0  
? SEQ ID NO 75  
? LENGTH: 12  
? TYPE: PRT  
? ORGANISM: Artificial Sequence  
? FEATURE:  
? OTHER INFORMATION: Phenylalanine derivative  
US-10-293-086-75

Query Match 36.4% Score 43 14 12 Length 12  
Best Local Similarity 100.0% Pref No. 6, Ident 12  
Matches 4: Conservative 0; Mismatches 0; Gaps 0  
QY 1 AKKK 4  
DB 9 AKKK 12

US-10-293-086-95  
? Sequence 95, Application US/10294086  
? Publication No. US2003013410A1  
? GENERAL INFORMATION:  
? APPLICANT: Cujec, Thomas P.

? TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors  
? TITLE OF INVENTION: Inhibitors for their use  
? FILE REFERENCE: 50036/048002  
? CURRENT APPLICATION NUMBER: US/10/293-086-95  
? CURRENT FILING DATE: 2003-03-25  
? PRIOR APPLICATION NUMBER: US 60/187,990  
? PRIOR FILING DATE: 2001-11-13  
? NUMBER OF SEQ ID NOS: 144  
? SOFTWARE: FASTSEQ for Windows Version 4.0  
? SEQ ID NO 95  
? LENGTH: 12  
? TYPE: PRT  
? ORGANISM: Artificial Sequence  
? FEATURE:  
? OTHER INFORMATION: binding peptide  
US-10-293-086-95

Query Match 36.4% Score 43 14 12 Length 12  
Best Local Similarity 100.0% Pref No. 6, Ident 12  
Matches 4: Conservative 0; Mismatches 0; Gaps 0  
QY 6 OKOR 9  
DB 8 OKOR 11

US-10-293-086-75  
? Sequence 75, Application US/1029386  
? Publication No. US2003013410A1  
? GENERAL INFORMATION:  
? APPLICANT: Cujec, Thomas P.  
? TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors  
? FILE REFERENCE: 50036/048002  
? CURRENT APPLICATION NUMBER: US/10/293-086  
? CURRENT FILING DATE: 2003-03-25  
? PRIOR APPLICATION NUMBER: US 60/187,990  
? PRIOR FILING DATE: 2001-11-13  
? NUMBER OF SEQ ID NOS: 144  
? SOFTWARE: FASTSEQ for Windows Version 4.0  
? SEQ ID NO 144  
? LENGTH: 12  
? TYPE: PRT  
? ORGANISM: Artificial Sequence  
? FEATURE:  
? OTHER INFORMATION: Phenylalanine derivative  
US-10-293-086-75

Query Match 36.4% Score 43 14 12 Length 12  
Best Local Similarity 100.0% Pref No. 6, Ident 12  
Matches 4: Conservative 0; Mismatches 0; Gaps 0  
QY 1 AKKK 4  
DB 9 AKKK 12

US-10-293-086-95  
? Sequence 95, Application US/10294086  
? Publication No. US2003013410A1  
? GENERAL INFORMATION:  
? APPLICANT: Cujec, Thomas P.

1 PRIOR FILING DATE: 2000-05-26  
2 NUMBER OF SEQ ID NOS: 36  
3 SOFTWARE: PatentIn version 3.1  
4 SEQ ID NO 35  
5 LENGTH: 12  
6 TYPE: PRT  
7 ORGANISM: Artificial Sequence  
8 FEATURE:  
9 OTHER INFORMATION: peptide  
US-10-355-975-35

Query Match 36.4% Score 4: DB 12: Length 12:  
Best Local Similarity 100.0%: Pred. No. 6,100-2:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 AKKK 4  
Db 9 AKKK 12

RESULT 42  
US-10-119-528-100  
1 Sequence 100, Application US/10119528  
2 Publication No. US2003017522A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Mann, M.  
5 APPLICANT: Mortensen, P.  
6 TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING PHARMACOLOGICAL  
7 FILE REFERENCE: MDSP-P01-004  
8 CURRENT APPLICATION NUMBER: US/10119528  
9 CURRENT FILING DATE: 2002-04-09  
10 PRIOR APPLICATION NUMBER: 60/282,551  
11 PRIOR FILING DATE: 2001-04-09  
12 PRIOR APPLICATION NUMBER: 60/285,362  
13 PRIOR FILING DATE: 2001-04-20  
14 NUMBER OF SEQ ID NOS: 112  
15 SOFTWARE: PatentIn version 3.1  
16 SEQ ID NO 100  
17 LENGTH: 12  
18 TYPE: PRT  
19 ORGANISM: Arabidopsis thaliana  
US-10-119-528-100

Query Match 36.4% Score 4: DB 12: Length 12:  
Best Local Similarity 100.0%: Pred. No. 6,100-2:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 4 KEOK 7  
Db 8 KEOK 11

RESULT 43  
US-10-032-827A-7  
1 Sequence 7, Application US/10032827A  
2 Publication No. US2003004979A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Schwartz, John J.  
5 APPLICANT: Jacobson, Joseph  
6 APPLICANT: Dasgupta, Ruchita  
7 TITLE OF INVENTION: Engineered Stimulus Responsive Switches  
8 FILE REFERENCE: EN2-004  
9 CURRENT APPLICATION NUMBER: US/10-032-827A  
10 CURRENT FILING DATE: 2001-10-23  
11 PRIOR APPLICATION NUMBER: US 60/242,546  
12 PRIOR FILING DATE: 2000-10-23  
13 NUMBER OF SEQ ID NOS: 20  
14 SOFTWARE: PatentIn version 3.0  
15 SEQ ID NO 7  
16 LENGTH: 12  
17 TYPE: PRT  
18 ORGANISM: Artificial Sequence  
19 FEATURE:

1 OTHER INFORMATION: Sequences 1-7 are Allotypes of Katush  
US-10-032-827A-7  
2 Query Match 36.4% Score 4: DB 15: Length 12:  
3 Best Local Similarity 100.0%: Pred. No. 6,100-2:  
4 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 AKKK 4  
Db 9 AKKK 12

RESULT 44  
US-10-044-107-1  
1 Sequence 10, Application 10,100-1:  
2 Publication No. US2003017522A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Mann, M.  
5 APPLICANT: Mortensen, P.  
6 TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING PHARMACOLOGICAL  
7 FILE REFERENCE: MDSP-P01-004  
8 CURRENT APPLICATION NUMBER: US/10119528  
9 CURRENT FILING DATE: 2002-04-09  
10 PRIOR APPLICATION NUMBER: 60/282,551  
11 PRIOR FILING DATE: 2001-04-09  
12 PRIOR APPLICATION NUMBER: 60/285,362  
13 PRIOR FILING DATE: 2001-04-20  
14 NUMBER OF SEQ ID NOS: 112  
15 SOFTWARE: PatentIn version 3.1  
16 SEQ ID NO 13  
17 LENGTH: 12  
18 TYPE: PRT  
19 ORGANISM: Arabidopsis thaliana  
US-10-044-107-1

Query Match 36.4% Score 4: DB 15: Length 12:  
Best Local Similarity 100.0%: Pred. No. 6,100-2:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 AKKK 4  
Db 9 AKKK 12

RESULT 45  
US-10-267-449-3  
1 Sequence 3, Application 3,100-1:  
2 Publication No. US2003017522A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Mann, M.  
5 APPLICANT: Mortensen, P.  
6 TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING PHARMACOLOGICAL  
7 FILE REFERENCE: MDSP-P01-004  
8 CURRENT APPLICATION NUMBER: US/10-267-449-3  
9 CURRENT FILING DATE: 2001-10-23  
10 PRIOR APPLICATION NUMBER: US 60/242,546  
11 PRIOR FILING DATE: 2000-10-23  
12 NUMBER OF SEQ ID NOS: 20  
13 SOFTWARE: PatentIn version 3.0  
14 SEQ ID NO 3  
15 LENGTH: 12  
16 TYPE: PRT  
17 ORGANISM: Artificial Sequence  
18 FEATURE:

Query Match 36.4% Score 4: DB 15: Length 12:  
Best Local Similarity 100.0%: Pred. No. 6,100-2:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4  
 DB 6 AKKK 9

## RESULT 46

US-09-746-170-19  
 ; Sequence 19, Application US/09746170  
 ; Patent No. US20020127543A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kain, Jonathan  
 ; APPLICANT: Walker, Stephen  
 ; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules  
 ; FILE REFERENCE: 22620/1280  
 ; CURRENT APPLICATION NUMBER: US/09/746,170  
 ; CURRENT FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/71,804  
 ; PRIOR FILING DATE: 1999-12-22  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 19  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Hepatitis C virus  
 US-09-746-170-19

Query Match 36.4%; Score 4; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OKQR 9  
 DB 5 OKQR 8

## RESULT 47

US-09-876-904A-88  
 ; Sequence 88, Application US/09876904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/USOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002-00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 88  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic xenopus  
 ; OTHER INFORMATION: nucleoplasmic  
 US-09-876-904A-88

Query Match 36.4%; Score 4; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 DB 7 AKKK 10

## RESULT 48

US-09-876-904A-89  
 ; Sequence 89, Application US/09876904A

Publication No. US20030072794A1

GENERAL INFORMATION:  
 APPLICANT: BOULIKAS, TENI  
 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/USOGENIC PEPTIDE  
 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 FILE REFERENCE: TB-2002-00  
 CURRENT APPLICATION NUMBER: US/09/876,904A  
 CURRENT FILING DATE: 2001-06-08  
 PRIOR APPLICATION NUMBER: US 60/210,925  
 PRIOR FILING DATE: 2000-06-09  
 NUMBER OF SEQ ID NOS: 629  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 89  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Xenopus  
 OTHER INFORMATION: nucleoplasmic  
 US-09-876-904A-89

Query Match 36.4%; Score 4; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 DB 1 AKKK 1

## RESULT 49

US-09-876-904A-912  
 ; Sequence 912, Application US/09876904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/USOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002-00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 912  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Unknown Organism  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: XPC gene product  
 US-09-876-904A-912

Query Match 36.4%; Score 4; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 DB 1 AKKK 4

## RESULT 50

US-10-291-25-132  
 ; Sequence 132, Application US/1-291,25-  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Iowa Research Foundation  
 ; APPLICANT: Davidson, Beverly L.  
 ; APPLICANT: XIA, GUOLIN  
 ; APPLICANT: LAW, LAM K.

: TITLE OF INVENTION: RECEPTOR-TARGETED ADENOVIRAL VECTORS
: FILE REFERENCE: 875.051US1
: CURRENT APPLICATION NUMBER: US/10/291,250
: CURRENT FILING DATE: 2002-11-07
: PRIOR APPLICATION NUMBER: US 60/339,282
: PRIOR FILING DATE: 2001-12-11
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 32
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: A protein motif.
US-10-291-250-32

Query Match 36.4% Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 6,40-02;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 AKKK 4
Db 4 AKKK 7

Search completed: September 30, 2003, 17:25:43
Job time : 28 secs









375	3	27.3	9	15	AAR56376	Peptide inhibitor	438	1	1	1	1	AA543138	Human, non-pat. exp. 1
376	3	27.3	9	15	AAR56377	Peptide inhibitor	439	1	1	1	1	AA543139	Human, non-pat. exp. 1
377	3	27.3	9	15	AAR49225	H1A-A1-MAGE-5 anti-	440	1	1	1	1	AA543140	Human, non-pat. exp. 1
378	3	27.3	9	15	AAR51616	Minotape monopep-	441	1	1	1	1	AA543141	Human, non-pat. exp. 1
379	3	27.3	9	15	AAR58533	Peptide chain (cyclo)	442	1	1	1	1	AA543142	Human, non-pat. exp. 1
380	3	27.3	9	15	AAR59128	Peptide treatment (	443	1	1	1	1	AA543143	Human, non-pat. exp. 1
381	3	27.3	9	15	AAR73007	Antigen treatment (	444	1	1	1	1	AA543144	Human, non-pat. exp. 1
382	3	27.3	9	16	AAR84879	H2K(D) ELISA immu-	445	1	1	1	1	AA543145	Human, non-pat. exp. 1
383	3	27.3	9	16	AAR62822	MAGE-5 derived tur-	446	1	1	1	1	AA543146	Human, non-pat. exp. 1
384	3	27.3	9	16	AAR79836	Tumour rejection a-	447	1	1	1	1	AA543147	Human, non-pat. exp. 1
385	3	27.3	9	16	AAR80896	MAGE-2 peptide (re-	448	1	1	1	1	AA543148	Human, non-pat. exp. 1
386	3	27.3	9	16	AAR79447	96-Lanema anti-tum-	449	1	1	1	1	AA543149	Human, non-pat. exp. 1
387	3	27.3	9	16	AAR65136	MAGE-3 immunogen-	450	1	1	1	1	AA543150	Human, non-pat. exp. 1
388	3	27.3	9	16	AAR65991	Renal cell carcinoma	451	1	1	1	1	AA543151	Human, non-pat. exp. 1
389	3	27.3	9	16	AAR79669	Protein kinase A p-	452	1	1	1	1	AA543152	Human, non-pat. exp. 1
390	3	27.3	9	16	AAR79674	Cyclohexyl (cyclo-2)	453	1	1	1	1	AA543153	Human, non-pat. exp. 1
391	3	27.3	9	16	AAR79675	Cyclohexyl (cyclo-2)	454	1	1	1	1	AA543154	Human, non-pat. exp. 1
392	3	27.3	9	16	AAR84576	Cyclohexyl (cyclo-2)	455	1	1	1	1	AA543155	Human, non-pat. exp. 1
393	3	27.3	9	16	AAR49633	Bleomycin (cyclo-2)	456	1	1	1	1	AA543156	Human, non-pat. exp. 1
394	3	27.3	9	17	AAR49587	Bleomycin (cyclo-2)	457	1	1	1	1	AA543157	Human, non-pat. exp. 1
395	3	27.3	9	17	AAR49587	Bleomycin (cyclo-2)	458	1	1	1	1	AA543158	Human, non-pat. exp. 1
396	3	27.3	9	17	AAR49587	Bleomycin (cyclo-2)	459	1	1	1	1	AA543159	Human, non-pat. exp. 1
397	3	27.3	9	17	AAR49587	Bleomycin (cyclo-2)	460	1	1	1	1	AA543160	Human, non-pat. exp. 1
398	3	27.3	9	17	AAR49266	Human lymphocyte de-	461	1	1	1	1	AA543161	Human, non-pat. exp. 1
399	3	27.3	9	17	AAR56403	Human lymphocyte de-	462	1	1	1	1	AA543162	Human, non-pat. exp. 1
400	3	27.3	9	17	AAR498739	Antibody Fab H2	463	1	1	1	1	AA543163	Human, non-pat. exp. 1
401	3	27.3	9	17	AAR497527	Peptide 27 (11-25)	464	1	1	1	1	AA543164	Human, non-pat. exp. 1
402	3	27.3	9	17	AAR497527	Antibody peptide	465	1	1	1	1	AA543165	Human, non-pat. exp. 1
403	3	27.3	9	17	AAR497527	Antibody peptide	466	1	1	1	1	AA543166	Human, non-pat. exp. 1
404	3	27.3	9	17	AAR497527	Antibody peptide	467	1	1	1	1	AA543167	Human, non-pat. exp. 1
405	3	27.3	9	17	AAR497527	Antibody peptide	468	1	1	1	1	AA543168	Human, non-pat. exp. 1
406	3	27.3	9	17	AAR497527	Antibody peptide	469	1	1	1	1	AA543169	Human, non-pat. exp. 1
407	3	27.3	9	17	AAR497527	Antibody peptide	470	1	1	1	1	AA543170	Human, non-pat. exp. 1
408	3	27.3	9	17	AAR497527	Antibody peptide	471	1	1	1	1	AA543171	Human, non-pat. exp. 1
409	3	27.3	9	17	AAR497527	Antibody peptide	472	1	1	1	1	AA543172	Human, non-pat. exp. 1
410	3	27.3	9	17	AAR497527	Antibody peptide	473	1	1	1	1	AA543173	Human, non-pat. exp. 1
411	3	27.3	9	17	AAR497527	Antibody peptide	474	1	1	1	1	AA543174	Human, non-pat. exp. 1
412	3	27.3	9	17	AAR497527	Antibody peptide	475	1	1	1	1	AA543175	Human, non-pat. exp. 1
413	3	27.3	9	17	AAR497527	Antibody peptide	476	1	1	1	1	AA543176	Human, non-pat. exp. 1
414	3	27.3	9	17	AAR497527	Antibody peptide	477	1	1	1	1	AA543177	Human, non-pat. exp. 1
415	3	27.3	9	17	AAR497527	Antibody peptide	478	1	1	1	1	AA543178	Human, non-pat. exp. 1
416	3	27.3	9	17	AAR497527	Antibody peptide	479	1	1	1	1	AA543179	Human, non-pat. exp. 1
417	3	27.3	9	17	AAR497527	Antibody peptide	480	1	1	1	1	AA543180	Human, non-pat. exp. 1
418	3	27.3	9	17	AAR497527	Antibody peptide	481	1	1	1	1	AA543181	Human, non-pat. exp. 1
419	3	27.3	9	17	AAR497527	Antibody peptide	482	1	1	1	1	AA543182	Human, non-pat. exp. 1
420	3	27.3	9	17	AAR497527	Antibody peptide	483	1	1	1	1	AA543183	Human, non-pat. exp. 1
421	3	27.3	9	17	AAR497527	Antibody peptide	484	1	1	1	1	AA543184	Human, non-pat. exp. 1
422	3	27.3	9	17	AAR497527	Antibody peptide	485	1	1	1	1	AA543185	Human, non-pat. exp. 1
423	3	27.3	9	17	AAR497527	Antibody peptide	486	1	1	1	1	AA543186	Human, non-pat. exp. 1
424	3	27.3	9	17	AAR497527	Antibody peptide	487	1	1	1	1	AA543187	Human, non-pat. exp. 1
425	3	27.3	9	17	AAR497527	Antibody peptide	488	1	1	1	1	AA543188	Human, non-pat. exp. 1
426	3	27.3	9	17	AAR497527	Antibody peptide	489	1	1	1	1	AA543189	Human, non-pat. exp. 1
427	3	27.3	9	17	AAR497527	Antibody peptide	490	1	1	1	1	AA543190	Human, non-pat. exp. 1
428	3	27.3	9	17	AAR497527	Antibody peptide	491	1	1	1	1	AA543191	Human, non-pat. exp. 1
429	3	27.3	9	17	AAR497527	Antibody peptide	492	1	1	1	1	AA543192	Human, non-pat. exp. 1
430	3	27.3	9	17	AAR497527	Antibody peptide	493	1	1	1	1	AA543193	Human, non-pat. exp. 1
431	3	27.3	9	17	AAR497527	Antibody peptide	494	1	1	1	1	AA543194	Human, non-pat. exp. 1
432	3	27.3	9	17	AAR497527	Antibody peptide	495	1	1	1	1	AA543195	Human, non-pat. exp. 1
433	3	27.3	9	17	AAR497527	Antibody peptide	496	1	1	1	1	AA543196	Human, non-pat. exp. 1
434	3	27.3	9	17	AAR497527	Antibody peptide	497	1	1	1	1	AA543197	Human, non-pat. exp. 1
435	3	27.3	9	17	AAR497527	Antibody peptide	498	1	1	1	1	AA543198	Human, non-pat. exp. 1
436	3	27.3	9	17	AAR497527	Antibody peptide	499	1	1	1	1	AA543199	Human, non-pat. exp. 1
437	3	27.3	9	17	AAR497527	Antibody peptide	500	1	1	1	1	AA543200	Human, non-pat. exp. 1
438	3	27.3	9	17	AAR497527	Antibody peptide	501	1	1	1	1	AA543201	Human, non-pat. exp. 1
439	3	27.3	9	17	AAR497527	Antibody peptide	502	1	1	1	1	AA543202	Human, non-pat. exp. 1
440	3	27.3	9	17	AAR497527	Antibody peptide	503	1	1	1	1	AA543203	Human, non-pat. exp. 1
441	3	27.3	9	17	AAR497527	Antibody peptide	504	1	1	1	1	AA543204	Human, non-pat. exp. 1
442	3	27.3	9	17	AAR497527	Antibody peptide	505	1	1	1	1	AA543205	Human, non-pat. exp. 1
443	3	27.3	9	17	AAR497527	Antibody peptide	506	1	1	1	1	AA543206	Human, non-pat. exp. 1
444	3	27.3	9	17	AAR497527	Antibody peptide	507	1	1	1	1	AA543207	Human, non-pat. exp. 1
445	3	27.3	9	17	AAR497527	Antibody peptide	508	1	1	1	1	AA543208	Human, non-pat. exp. 1
446	3	27.3	9	17	AAR497527	Antibody peptide	509	1	1	1	1	AA543209	Human, non-pat. exp. 1
447	3	27.3	9	20	AAV45506	Immunogenic peptide	510	1	1	1	1	AAV45506	Human, non-pat. exp. 1

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AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	AAV45506	

XX OS Synthetic.  
 XX PN WO200018801-A2.  
 XX PD 06-APR-2000.  
 XX PF 23-SEP-1999; 99WO-DK00500.  
 XX PR 29-SEP-1998; 98DK-0001232.  
 XX PR 29-APR-1999; 99DK-0000592.  
 XX (RONN/) RONN L C B.  
 PA (BOCK/) BOCK E.  
 PA (HOLM/) HOLM A.  
 PA (OLSE/) OLSEN M.  
 PA (OSTE/) OSTERGARD S.  
 PA (JENS/) JENSEN P H.  
 PA (POUL/) POULSEN F H.  
 PA (SORO/) SOROKA V.  
 PA (KALE/) KALETS I.  
 PA (BERE/) BEREZIN V.  
 XX  
 PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
 XX  
 XX WPI: 2000-293111/25.  
 XX  
 PT Compositions that bind neural cell adhesion molecules useful for  
 PT treating disorders of the nervous system and muscles e.g. Alzheimer's  
 PT and Parkinson's diseases.  
 XX  
 XX Example 4: Page 25; 119pp; English.  
 XX  
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
 CC NCAM is found in three forms, two of which are transmembrane forms, while  
 CC the third is attached via a lipid anchor to the cell membrane. All three  
 CC NCAM forms have an extracellular structure consisting five immunoglobulin  
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the  
 CC N-terminal. The present sequence represents a peptide which binds to the  
 CC NCAM Ig1 domain. The peptide can be used in a compound which binds to the  
 CC outgrowth from NCAM presenting cells, and is also capable of promoting  
 CC the proliferation of NCAM presenting cells. The compound may be used in  
 CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
 CC The compound may in particular be used to treat diseases of the central  
 CC and peripheral nervous systems such as post operative nerve damage,  
 CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
 CC dementias, sclerosis, nerve degeneration associated with diabetes  
 CC mellitus, disorders affecting the circadian clock or neuro-muscular  
 CC transmission and schizophrenia. Conditions affecting the muscles may also  
 CC be treated with the compound, such as conditions associated with impaired  
 CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
 CC (e.g. diabetes mellitus types 1 and 11), kidney (e.g. nephrosis), heart,  
 CC liver and bowel may also be treated using the compound. The compound is  
 CC used in a prosthetic nerve guide, and also to stimulate the ability to  
 CC learn, and to stimulate the memory of a subject.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 11; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKSRKGNSSLM 11  
 | | | | | | | | | |  
 DB 1 AKSRKGNSSLM 11

RESULT 2  
 ABG69349

ID ABG69349 Standard; Fragmented 11 AA;  
 AC ABG69349;  
 XX 21 OCT-2002 (first entry)  
 XX Human neural cell adhesion molecule (NCAM) peptide #21.  
 XX  
 KW Human neural cell adhesion molecule; NCAM; heart muscle cell survival;  
 KW acute myocardial infarction; central nervous system disorder; stroke;  
 KW peripheral nervous system disorder; postoperative nerve damage;  
 KW traumatic nerve damage; spinal cord injury; nerve fiber; schizophrenia;  
 KW post-ischaemic disease; multifactorial dementia; multiple sclerosis;  
 KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW atrophic muscle disorder; and regeneration; nephrosis;  
 XX  
 XS Bemo sapiens.  
 XX WC200247719-A2.  
 XX 29 JUN 2002.  
 XX 12-DEC 2001; 2001W-1830-02.  
 XX 12-DEC 2001; 2001W-0001-00.  
 XX (ENKA-) ENKA PHARM AS.  
 XX Bock E, Berezin V, Kallouh I;  
 XX WPI: 2002-584374/2.  
 XX  
 PT Use of a compound comprising a peptide of neural cell adhesion  
 PT molecule, in the preparation of treatment for preventing death of  
 PT cells presenting NCAM and treating central nervous  
 PT system diseases.  
 XX  
 PS Disclosure: Page 16; 57pp; English.  
 XX  
 CC The invention relates to use of a compound (1) comprising a peptide  
 CC which comprises at least 5 contiguous amino acid residues of a sequence  
 CC of the neural cell adhesion molecule (NCAM), its fragment, variant or its  
 CC mimic, for the preparation of a medicament for preventing death of cells  
 CC presenting the NCAM or an NCAM ligand. (1) is useful in the preparation  
 CC of a medicament for preventing death of cells presenting the NCAM or an  
 CC NCAM ligand. The medicament is for the stimulation of the survival of  
 CC heart muscle cells, such as survival after acute myocardial infarction.  
 CC The medicament is for the treatment of diseases or conditions of the  
 CC central and peripheral nervous system, such as postoperative nerve  
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,  
 CC impaired myelination of nerve fibres, post-ischaemic damage, and  
 CC resulting from a stroke, multifactorial dementia, multiple sclerosis, nerve  
 CC degeneration associated with diabetes mellitus, neuro-muscular  
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease  
 CC and Huntington's disease. The medicament is for the treatment of diseases  
 CC or conditions of the muscles, including conditions with impaired function  
 CC of neuromuscular connections, such as genetic or traumatic atrophic  
 CC muscle disorders, and for the treatment of diseases or conditions of  
 CC various organs, such as degenerative conditions of the gonads, pancreas  
 CC (e.g. diabetes mellitus types 1 and 11) and kidney (e.g. nephrosis).  
 CC ABG69349 AbG69349 represents human NCAM peptides of the invention.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 11; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKSRKGNSSLM 11  
 | | | | | | | | | |  
 DB 1 AKSRKGNSSLM 11





The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (AB125347 to AB25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. App1191 to AB125472 represent peptide sequences used in the exemplification of the present invention.

Sequence 8 AA:

Query Match 36.4% Score 47 (48.22) Length 40

Best Local Similarity 100.0% Prod. No. 9 60096

Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 GNSS 9

1:11

DB 3 GNSS 6

#### RESULT 8

ABP14271

ID ABP14271 standard; Peptide: 8 AA.

AC AC

XX ABP14271;

DT 15-JUL-2002 (first entry)

XX HIV A03 super motif env peptide #11.

DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

XX W020012481D-A1.

PN 12-APR 2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412864.

XX (EPIM-) EPIMMUNE INC.

XX Scott A. Sidney J. Southernwood S. Livingston Bb. George J. Bb. Baker SM. Cellis E. Kubo RT. Gray BM.

XX WPI: 2001-354887/37.

PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1) peptide groups, useful for vaccinating against HIV 1.

PS Claim 32: Page 161: 448pp; English.

XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (AB125347 to

AB125347). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. App1191 to AB125472 represent peptide sequences used in the exemplification of the present invention.

Sequence 8 AA:

Query Match 36.4% Score 47 (48.22) Length 40

Best Local Similarity 100.0% Prod. No. 9 60096

Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 GNSS 9

1:11

DB 3 GNSS 6

#### RESULT 9

ABP14271

ID ABP14271 standard; Peptide: 8 AA.

AC AC

XX ABP14271;

DT 15-JUL-2002 (first entry)

XX HIV A03 super motif env peptide #11.

DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

XX W020012481D-A1.

PN 12-APR 2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412864.

XX (EPIM-) EPIMMUNE INC.

XX Scott A. Sidney J. Southernwood S. Livingston Bb. George J. Bb. Baker SM. Cellis E. Kubo RT. Gray BM.

XX WPI: 2001-354887/37.

PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1) peptide groups, useful for vaccinating against HIV 1.

PS Claim 32: Page 161: 448pp; English.

XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (AB125347 to

AB125347). (1) has virucide activity and can be used in vaccines. (1)

may be used for immunising subjects against HIV-1 infections. The use of

group-based vaccines has several advantages over traditional vaccines.

CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1531 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

SO Sequence 8 AA;

Query Match 36.45; Score 4; Len 22; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 9, 40,055;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9

DB 4 GNSS 7

RESULT 19  
 ABP19802

ID ABP19802 standard; Peptide: 8 AA.

XX ABP19832;

DT 15-JUL 2002 (first entry)

DE HIV A03 motif env peptide #6.

XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;  
 KW vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; viricide

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMMUNE INC.

PI Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Gray RM;

DR WPI: 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV 1

XX Claim 32: Page 276; 448pp; English.

CC The present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25417 to  
 CC ABP25337). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.

CC directed to immune escape due to mutations. The groups for inclusion in an  
 CC group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1531 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

SO Sequence 8 AA;

Query Match 36.45; Score 4; Len 22; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 9, 40,055;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9

DB 4 GNSS 7

RESULT 11  
 ABP22240

ID ABP22240 standard; Peptide: 8 AA.

XX ABP22240;

XX 15-JUL 2002 (first entry)

DE HIV A11 motif env peptide #5.

XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;  
 KW vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; viricide.

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMMUNE INC.

PI Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Gray RM;

DR WPI: 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV 1

XX Claim 32: Page 276; 448pp; English.

CC The present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25417 to  
 CC ABP25337). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.



CC treating proliferative disorders, e.g. cancers and leukaemias. The  
 CC peptides are also for identifying substances which interfere with  
 CC protein-protein interactions involving cyclins (i.e. cyclin A, E or D),  
 CC especially CDK/cyclin interactions, and which are capable of inhibiting  
 CC CDK2 and/or CDK4 activity. P21 peptides other than p21(149-159)  
 CC competitively inhibit the binding of peptide p21(149-159) to cyclin and  
 CC may be used to identify substances that bind to, or inhibit peptide-  
 CC cyclin interactions. Substances for screening in the assays include  
 CC antibody products specific for p21 or cyclin binding regions,  
 CC combinatorial libraries and single compound collections. The present  
 CC sequence is a peptide derived from the C-terminus of p21.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 DB 1111  
 2 AKSR 5

#### RESULT 14

ID AAR49852 standard; peptide; 9 AA.

XX AAR49852;

XX 25-MAR-2003 (updated)  
 DT 20-AUG-1994 (first entry)

XX Sequence of antigenic peptide based on non consensual sequences of  
 DE HIV-1 env protein.

XX Human immunodeficiency virus; HIV 1; env; AIDS.

XX Synthetic.

XX DE4228787-A1.

XX 03-MAR-1994.

XX 29-AUG-1992; 92DE-4228787.

XX 29-AUG-1992; 92DE-4228787.

XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.

XX Dietrich U, Grez M, Ruebsamen-waismann H, Van Briesen H;

XX WPI; 1994-075444/10.

XX New HIV-1 viral isolates - useful in the produ of a new HIV-1  
 PT vaccine

XX Claim 2; Page 4; 8pp; German.

XX HIV-1 D747, HIV-1 D757 and HIV-1 D760 are new viral isolates  
 CC deposited under ECACC V92082718, V92082719 and V92082720  
 CC respectively. The new isolates were isolated from patients in India  
 CC who did not yet show typical AIDS symptoms. Vaccines may be produced  
 CC using peptides which corresp. to regions of the env protein that  
 CC differ from the HIV-1 AA consensus sequences that are already  
 CC published. Such peptides are given in AAR49851-54.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KNS 8  
 DB 1111  
 6 KNS 4

#### RESULT 15

ID AAW77371 standard; protein; 9 AA.

XX AAW77371;

XX 14-DEC-1993 (first entry)

XX mIL-10 (VSV) Protein N terminus

XX Gossackie virus (VSV) vector; immune suppressor; other reported  
 KW viral heart disease vector; heart transplant; inflammatory disease.

XX Biopartovectone S1

XX Kus apt

XX Synthesis

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

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XX Key 11-SEP-1998

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XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998

XX Key 11-SEP-1998





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XX PD 12-APR-2001.
XX PF
XX PR 05-OCT-2000: 2000WO-US27766.
XX PR 05 OCT-1999; 99US-0412861.
XX PA (EPIMV) EPIMUNE INC.
XX PI Settle A. Sidney J. Southwood S. Livingston St. Chestnut St.
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV 1
XX PS Claim 32; Page 118; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (A0125447 to
XX CC A025977). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group based vaccine approach is the ability
XX CC to combine selected groups (C1 and H1), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be mediated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. A011501 to A025472
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 9 AA:
36.4%; Score 4; Dp 22; Length 9;
Query Match Best Local Similarity 100.0%; Pred. No. 9; No. 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 6 GNSS 9
Db 4 GNSS 7
1111
RESULT 19
ABP12151
XX ID ABP12151 standard; Peptide: 9 AA.
XX AC ABP12151;
XX XX
XX DT 15 JUL-2002 (first entry)
XX DE HIV A02 super motif env peptide #208
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; rev;
XX KW vif; tat; cytoxic T lymphocyte; CTL immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX XX
XX PD 12-APR-2001.
XX PR

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XX PF 05-OCT-2001: 2001WO-US27766.
XX PR 05 OCT-2000: 2000WO-US27766.
XX PA (EPIMV) EPIMUNE INC.
XX PI Settle A. Sidney J. Southwood S. Livingston St. Chestnut St.
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV 1
XX PS Claim 32; Page 118; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (A0125447 to
XX CC A025977). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group based vaccine approach is the ability
XX CC to combine selected groups (C1 and H1), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be mediated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. A011501 to A025472
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 9 AA.
36.4%; Score 4; Dp 22; Length 9;
Query Match Best Local Similarity 100.0%; Pred. No. 9; No. 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 6 GNSS 9
Db 4 GNSS 7
1111
RESULT 20
ABP12151
XX ID ABP12151 standard; Peptide: 9 AA.
XX AC ABP12151;
XX XX
XX DT 15 JUL-2002 (first entry)
XX DE HIV A 02 super motif env peptide #208
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; rev;
XX KW vif; tat; cytoxic T lymphocyte; CTL immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX XX
XX PD 12-APR-2001.
XX PR 05 OCT-2000: 2000WO-US27766.
XX PR 05 OCT-1999; 99US-0412861.

```

XX (EPIM-) EPIMUNE INC.  
XX  
XX  
PI Settle A, Sidney J, Southwood S, Livingstone RB, Chesnut K,  
PI Baker DM, Celis E, Kubo RT, Gray HM;  
XX WPI: 2001-354887/37.  
XX  
XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV 1  
XX  
XX Claim 32; Page 276; 448pp; English.  
XX  
XX The present invention describes a composition (1) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (AB12543 to  
CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
CC may be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for use herein in  
CC an group-based vaccine may be selected from conserved regions of viral  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. App1156; to ABP254.2  
CC represent peptide sequences used in the exemplification of the present  
CC invention.  
XX  
XX SQ Sequence 9 AA;  
Query Match 36.4%; SCORE 4; DR 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 60-05;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
QY 6 GNSS 9  
DB 1111  
4 GNSS 7  
RESULT 21  
ABP19810  
XX ABP19810 standard; Peptide: 9 AA.  
XX  
XX AC ABP19810;  
XX  
XX DT 15-JUL-2002 (first entry)  
XX  
XX DE HIV A03 motif env peptide #14.  
XX  
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; rev;  
KW vif; vif; tat; cytotoxic T lymphocyte; (The immune response of target  
KW antigen; vaccine; HIV infection; immunisation; virulence;  
XX  
XX OS Human immunodeficiency virus type 1.  
XX  
XX PN WO200124810-A1.  
XX  
XX PD 12-APR-2001.  
XX  
XX PF 05-OCT-2000; 2000WO-US27766.  
XX  
XX PR 05-OCT-1999; 99US-0412863.  
XX  
XX PA (EPIM-) EPIMUNE INC.  
XX

11 Settle A, Sidney J, Southwood S, Livingstone RB, Chesnut K,  
12 Baker DM, Celis E, Kubo RT, Gray HM;  
13 WPI: 2001-354887/37.  
14 Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
15 peptide groups, useful for vaccinating against HIV 1.  
16  
17 Claim 32; Page 276; 448pp; English.  
18  
19 The present invention describes a composition (1) comprising a prepared  
20 human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
21 sequence selected from 51 defined amino acid sequences (AB12543 to  
22 ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
23 may be used for immunising subjects against HIV-1 infections. The use of  
24 group-based vaccines has several advantages over traditional vaccines,  
25 particularly when compared to the use of whole antigens in vaccine  
26 compositions. There is evidence that the immune response to whole  
27 antigens is directed largely toward variable regions of the antigen,  
28 allowing for immune escape due to mutations. The groups for use herein in  
29 an group-based vaccine may be selected from conserved regions of viral  
30 tumour-associated antigens, which therefore reduces the likelihood of  
31 escape mutants. Furthermore, immunosuppressive groups that may be present  
32 in whole antigens can be avoided with the use of group-based vaccines.  
33 An additional advantage of an group-based vaccine approach is the ability  
34 to combine selected groups (CTL and HTL), and further, to modify the  
35 composition of the groups, achieving, for example, enhanced  
36 immunogenicity. Accordingly, the immune response can be modulated, as  
37 appropriate, for the target disease. Similar engineering of the response  
38 is not possible with traditional approaches. App1156; to ABP254.2  
39 represent peptide sequences used in the exemplification of the present  
40 invention.  
41  
42 SQ Sequence 9 AA;  
Query Match 36.4%; SCORE 4; DR 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 60-05;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
QY 6 GNSS 9  
DB 1111  
4 GNSS 7  
RESULT 22  
ABP19810  
11 ABP19810 standard; Peptide: 9 AA.  
12  
13 AC ABP19810;  
14  
15 DT 15-JUL-2002 (first entry)  
16  
17 DE HIV A03 motif env peptide #14.  
18  
19 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; rev;  
20 KW vif; vif; tat; cytotoxic T lymphocyte; (The immune response of target  
21 KW antigen; vaccine; HIV infection; immunisation; virulence;  
22  
23 XX  
24 XX OS Human immunodeficiency virus type 1.  
25  
26 XX  
27 XX PN WO200124810-A1.  
28  
29 XX  
30 XX PD 12-APR-2001.  
31  
32 XX  
33 XX PF 05-OCT-2000; 2000WO-US27766.  
34  
35 XX  
36 XX PR 05-OCT-1999; 99US-0412863.  
37  
38 XX  
39 XX PA (EPIM-) EPIMUNE INC.  
40  
41 XX

DR WPI: 2001-541537/60.  
 XX Immunostimulant peptide, used as an anti-carcinoma vaccine, comprises a  
 PT an epitope of the non-VNTR, non-leader region of a mucin  
 XX  
 XX  
 PS Disclosure: Page 36; 84pp; English.  
 XX  
 CC The patent discloses peptide or polypeptides capable of eliciting  
 CC an immune response, comprising an amino acid sequence corresponding  
 CC to an epitope of the non-central portion of varying numbers of an  
 CC amino acid motif (VNTR), non-leader region of a mucin, the peptides  
 CC of the invention, fusion proteins comprising the peptide and conjugate  
 CC compounds with carbohydrate polymers are used to induce a cell mediated  
 CC immune response against mucin in the prevention or treatment of  
 CC carcinoma, preferably adenocarcinoma, most preferably breast cancer.  
 CC They are also used to pulse dendritic cell for in vivo transfer and  
 CC use as a vaccine. They are also used in gene therapy. The present  
 CC sequence is human mucin-1 (MUC-1) peptide which is an epitope for  
 CC cytotoxic T-lymphocytes (CTL).  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 36.4%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 100%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 7 NSSL 10  
 DB 1 NSSL 4  
 RESULT 23  
 AAB68480  
 ID AAB68480 standard; peptide: 9 AA.  
 AC AAB68480;  
 DT 23-JUL-2001 (first entry)  
 XX Peptide encoded by a unique region in exon 1 of dog motilin receptor.  
 XX  
 XX Motilin receptor; gastrointestinal disease; gastric motility disorder;  
 KW gastroparesis; irritable bowel syndrome; diarrhoea.  
 XX  
 XX Canis sp.  
 XX W0200132710-A1.  
 XX  
 XX 10-MAY-2001.  
 XX  
 XX 25-OCT-2000; 2000W0-US29426.  
 XX  
 XX 29-OCT-1999; 99US-0162264.  
 XX (MERI ) MERCK & CO INC.  
 XX  
 XX Tan C, McKee K;  
 XX WPI: 2001-343479/36.  
 XX  
 XX Novel polypeptides related to dog and rabbit motilin receptor  
 PT polypeptide, comprising unique regions from dog and motilin receptor  
 PT amino acid sequence, useful for identifying compounds for treating  
 PT diarrhoea in humans.  
 XX  
 XX Claim 3; Page 20; 42pp; English.  
 PS  
 CC AAB68480-84 represent peptides encoded by the unique region of exon 1  
 CC of a dog motilin receptor gene. The specification describes an unique  
 CC sequence present in exon 1 of the motilin receptor, which is not present  
 CC in human or Sphaeroides nephelus 75E7 motilin receptor sequences. The  
 CC unique nucleic acid sequence is useful for measuring the ability of a  
 CC compound to affect motilin receptor activity. Motilin receptor

CC Polypeptides and polypeptides are used to identify therapeutic  
 CC compounds which are useful for treating gastrointestinal diseases and  
 CC disorders such as gastric motility disorders, gastroparesis, diarrhoea,  
 CC bowel syndrome, and Irritable.  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 36.4%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 100%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 NSSL 9  
 DB 3 NSSL 6  
 RESULT 24  
 AAE41377  
 ID AAE41377 standard; peptide: 9 AA.  
 AC AAE41377;  
 DT 24-FEB-2003 (first entry)  
 XX Human MUC1 mutant peptide  
 DE Human MUC1 mutant peptide  
 XX  
 XX Human T-lymphocyte carcinoma viral infected cell gene therapy mutant;  
 KW mutant; mucin-1;  
 XX  
 XX Homo Sapiens;  
 OS Synthetic  
 XX  
 XX Key Location / modifications  
 FT Miss-difference / site Wild Type Pro substituted with Leu  
 XX W020027242-A2  
 XX 16-SEP-2002  
 XX 11-MAR-2003; 2002W0-EP 2006;  
 XX 03-MAR-2003; 2003US 2004500;  
 XX 14-MAY-2003; 2003US 2004500;  
 XX 14-MAY-2003; 2003US 2004500;  
 XX (A11-3) CA11157-GEN A;  
 XX  
 XX Wrote P, Walder P, Feller M, Mortens M, Feller M;  
 XX WPI: 2002 759846/42  
 XX  
 XX Provisional identification of epitope peptides for and action of on  
 PT T-lymphocytes and for treating cancer, comprises selected epitope  
 PT regions in nucleotide sequences and identifying CDR T cell epitopes in  
 PT the protein  
 XX  
 XX Disclosure: Page 10; 32pp; English  
 XX  
 XX The present invention relates to a method for providing, identifying and/or  
 CC synthesizing peptides which induce cytotoxic T-lymphocytes and to the  
 CC uses of the identified peptides for vaccination. The method is useful  
 CC for providing, identifying and/or synthesizing peptides that are useful  
 CC in manufacturing a pharmaceutical composition for the induction of  
 CC cytotoxic T-lymphocytes, and for the prevention, treatment or diagnosis  
 CC of cancer, viral, infectious. The invention is also used to design  
 CC therapy. The present sequence is human MUC1 mutant peptide used to  
 CC illustrate the method of the invention.  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 36.4%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 100%;





CC as an immunogen to produce anti-McCycDm antibodies, these antibodies  
 CC may be used to detect the protein of the invention or to analyze its  
 CC function.

SQ Sequence 9 AA:

Query Match 36.4%; Score 4; FR 24; Length 9  
 Best Local Similarity 100.0%; Prod. No. 9; 100%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 KGS 8

fill

DB 4 KGS 7

RESULT 24

AAU75716  
 ID AAU75716 standard; Peptide: 9 AA.

XX AAU75716;

DT 23-APR-2002 (first entry)

XX McCycDm antigenic peptide #15.

XX D-cyclin; McCycDm; plant growth regulator; herbicide; transgenic plant;  
 XX plant regeneration; cell fate; plant development; plant morphology;  
 XX plant biochemistry; plant physiology; cyclic type kinase; kinase peptide;  
 XX Cd2-related kinase; barrel medic; immunogen; antigen; antibody.

XX Medicago truncatula.

XX KEY Location/Qualifiers

FT Misc-difference 1 /label= X  
 FT /note= "D, DV, VDV, WVDV, FVVV or absent."

FT Misc-difference 9 /label= X

FT /note= "R, R6, R6K, REKK, REKKQ1,  
 REKKQTR or absent."

PN W0200196579-A1.

PD 20 DEC-2001.

XX 15 JUN 2001; 2001WO-EP06771.

XX 16-JUN 2000; 2000EP-0870133.

PR 11-JUL-2000; 2000US-217603P.

XX (CROP ) CROPDDESIGN NV.

XX Miskolczi P, Pettko-szantner A, Horvath G, Indels D, Fodor A;  
 PI Gyorgyey J;

XX WPI: 2002-090211/12.

XX Polynucleotide encoding new plant type D-cyclin and the polypeptide  
 PT useful for modifying cell fate, plant development, plant morphology,  
 PT plant biochemistry and plant physiology

XX Example 10; Page 75; 151pp; English.

XX This invention relates to the protein and nucleic acid sequences of a  
 CC new plant type D-cyclin McCycDm which may be used as a plant growth  
 CC regulator or as a herbicide. The nucleotide sequences of the invention  
 CC are useful for production of transgenic plants, plant cells or tissues,  
 CC and for effecting the expression of the McCycDm protein where the  
 CC nucleic acid is operably linked to one or more control sequences. The  
 CC invention also comprises a method for regenerating a plant from the  
 CC plant cell. The nucleic acid sequence of the invention is useful for  
 CC modifying cell fate, plant development, plant morphology, plant  
 CC biochemistry or plant physiology. The McCycDm protein is useful for

XX This invention relates to the protein and nucleic acid sequences of a  
 CC new plant type D-cyclin McCycDm which may be used as a plant growth  
 CC regulator or as a herbicide. The nucleotide sequences of the invention  
 CC are useful for production of transgenic plants, plant cells or tissues,  
 CC and for effecting the expression of the McCycDm protein where the  
 CC nucleic acid is operably linked to one or more control sequences. The  
 CC invention also comprises a method for regenerating a plant from the  
 CC plant cell. The nucleic acid sequence of the invention is useful for  
 CC modifying cell fate, plant development, plant morphology, plant  
 CC biochemistry or plant physiology. The McCycDm protein is useful for

XX Sequence 9 AA:

Query Match 36.4%; Score 4; FR 24; Length 9  
 Best Local Similarity 100.0%; Prod. No. 9; 100%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 KGS 8

fill

DB 4 KGS 7

RESULT 24

AAU75716  
 ID AAU75716 standard; Peptide: 9 AA.

XX AAU75716;

DT 23-APR-2002 (first entry)

XX McCycDm antigenic peptide #15.

XX D-cyclin; McCycDm; plant growth regulator; herbicide; transgenic plant;  
 XX plant regeneration; cell fate; plant development; plant morphology;  
 XX plant biochemistry; plant physiology; cyclic type kinase; kinase peptide;  
 XX Cd2-related kinase; barrel medic; immunogen; antigen; antibody.

XX Medicago truncatula.

XX KEY Location/Qualifiers

FT Misc-difference 1 /label= X  
 FT /note= "D, DV, VDV, WVDV, FVVV or absent."

FT Misc-difference 9 /label= X

FT /note= "R, R6, R6K, REKK, REKKQ1,  
 REKKQTR or absent."

PN W0200196579-A1.

PD 20 DEC-2001.

XX 15 JUN 2001; 2001WO-EP06771.

XX 16-JUN 2000; 2000EP-0870133.

PR 11-JUL-2000; 2000US-217603P.

XX (CROP ) CROPDDESIGN NV.

XX Miskolczi P, Pettko-szantner A, Horvath G, Indels D, Fodor A;  
 PI Gyorgyey J;

XX WPI: 2002-090211/12.

XX Polynucleotide encoding new plant type D-cyclin and the polypeptide  
 PT useful for modifying cell fate, plant development, plant morphology,  
 PT plant biochemistry and plant physiology

XX Example 10; Page 75; 151pp; English.

XX This invention relates to the protein and nucleic acid sequences of a

CC new plant type D-cyclin McCycM which may be used as a plant growth  
CC regulator or as a herbicide. The nucleotide sequences of the invention  
CC are useful for production of transgenic plants, plant cells or tissues,  
CC and for effecting the expression of the McCycM protein where the  
CC nucleic acid is operably linked to one or more control sequences. The  
CC invention also comprises a method for regenerating a plant from the  
CC plant cell. The nucleic acid sequence of the invention is useful for  
CC modifying cell fate, plant development, plant morphology, plant  
CC biochemistry or plant physiology. The McCycM protein is useful for  
CC identifying and obtaining proteins interacting with it, comprising a  
CC screening assay preferably a two-hybrid screening assay. The protein is  
CC also useful for modulating the interaction between and/or the activity  
CC of complexes comprising type D-cyclin and Cdc2-type or Cdc2-related  
CC kinases and/or other D-cyclin interacting protein partners. The protein  
CC is also useful for identifying compound or mixture of compounds which  
CC specifically binds to the protein. This sequence represents the  
CC McCycM antigenic peptide #71 of the invention. This peptide may be used  
CC as an immunogen to produce anti-McCycM antibodies, these antibodies  
CC may be used to detect the protein of the invention or to alter its  
CC function.

XX Sequence 9 AA:

Query Match 36.4%; Score 47; E-Value 1.0e-10; Length 71  
Best Local Similarity 100.0%; Pred. No. 9; Identity 0; Mismatches 0; Gaps 0  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 KGNS 8  
DQ 2 KGNS 5

RESULT 31

ABB74310

ID ABB74310 standard; Peptide; 9 AA.

XX AC ABB74310;

XX DT 18-APR-2002 (first entry)

XX DE Simple nuclear localisation signal peptide SEQ ID NO: 74.

XX KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogenic;

XX liposome; micelle; karyophilic; cytosolic; cytoplasmic; solid tumour;  
XX peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
XX breast carcinoma; prostate carcinoma.

XX OS Synthetic.

XX PN W020619836-A2.

XX PD 13-DEC-2001.

XX PF 08-JUN-2001; 2001WO-US18657.

XX PR 09 JUN 2000; 2000US-210925P.

XX PA (H051/) ROULIKAS T.

XX PI Roulikas T;

XX DR WPI: 2002-164295/21.

XX PT Encapsulation of plasmid DNA (Liposomes) and therapeutic agents with  
XX nuclear localization signal/fusogenic peptide encapsulates into targeted  
XX liposome complexes -

PS Claim 14; Page 56; 107pp; English.

XX The present invention describes a method for producing micelles with  
XX entrapped therapeutic agents. The method comprises: (i) combining  
XX negatively charged agent with a cationic lipid in a ratio where 40-90 %  
XX of the negatively charged atoms are neutralised by positive charges on.

CC cytoplasmic domains, and in some cases, nuclear localization signal (NLS).  
CC obtained and (2) combining the micelle complex of (4) with a fusogenic  
CC karyophilic peptide or lipids in a 1:1 or 2:1 ratio, thereby producing  
CC micelles with entrapped therapeutic agents. Also described is a method  
CC for delivering a therapeutic agent *in vivo*, comprising the administration  
CC of the micelles of ABB74310. Abbreviations represent specifically defined  
CC or generic localisation signals (NLS) peptides for use in the method as the  
CC fusogenic karyophilic peptides. The micelles produced can have a fusogenic  
CC and attractive properties for both the lipid polynucleotide complex  
CC produced are useful for identifying the protein of the invention and  
CC diseases. The method is also useful for the production of the plant or  
CC directed transgenic plants for producing peptides, lipid polynucleotide  
CC complexes, signal or a delivery of polynucleotides, the described  
CC sequences display a directed activity in eukaryotic and prokaryotic  
CC including but not limited to those, carcinoma or prostate carcinoma  
CC ABB74310 to ABB74310, and thus, for the identification of the protein  
CC described.

XX Sequence 9 AA:

Query Match 36.4%; Score 47; E-Value 1.0e-10; Length 71  
Best Local Similarity 100.0%; Pred. No. 9; Identity 0; Mismatches 0; Gaps 0  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 KSGK 6

XX DT 18-APR-2002 (first entry)

XX DE Simple nuclear localisation signal peptide SEQ ID NO: 74.

XX KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogenic;

XX liposome; micelle; karyophilic; cytosolic; cytoplasmic; solid tumour;  
XX peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
XX breast carcinoma; prostate carcinoma.

XX OS Synthetic.

XX PN W020619836-A2.

XX PD 13-DEC-2001.

XX PF 08-JUN-2001; 2001WO-US18657.

XX PR 09 JUN 2000; 2000US-210925P.

XX PA (H051/) ROULIKAS T.

XX PI Roulikas T;

XX DR WPI: 2002-164295/21.

XX PT Encapsulation of plasmid DNA (Liposomes) and therapeutic agents with

XX nuclear localization signal/fusogenic peptide encapsulates into targeted

XX liposome complexes -

PS Claim 14; Page 56; 107pp; English.

XX The present invention describes a method for producing micelles with

XX entrapped therapeutic agents. The method comprises: (i) combining

XX negatively charged agent with a cationic lipid in a ratio where 40-90 %

XX of the negatively charged atoms are neutralised by positive charges on.



CC monitoring the effect of an agent on the activity of a protease, including  
 CC drug screening applications to identify agents that modulate the activity  
 CC of a particular protease and studying the effect of a factor on  
 CC expression of the protease-encoding gene, detecting protease activity of  
 CC interest in a cell is useful for determining the particular state of the  
 CC cell associated with the particular protease, e.g., certain active  
 CC caspases indicate that a cell is undergoing an apoptotic event. Protease  
 CC detection applications can be used in diagnostic applications, including  
 CC diagnosis of bacterial and/or viral pathogenic infection. The present  
 CC sequence is that of a nuclear localisation signal (NLS) containing  
 CC peptide disclosed in illustrations of the invention.

SQ Sequence 9 AA:

Query Match 36.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; gaps 0;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 KSKK 5  
 IIII  
 DB 3 KSKK 6

RESULT 33

ABJ19497  
 ID ABJ19497 standard; Peptide: 9 AA.

AC ABJ19497;

XX 27-MAR-2003 (first entry)

XX CODEHCP generated degenerate primer pep:line #14.

XX Panel: degenerate primer pair; screening: virus family:  
 XX high throughput screening; ULIS DNA packaging protein; VHA.

XX Unidentified.

XX W0200299129-A2.

PN 12-DEC-2002.

XX 07-JUN-2002: 2002W0-CR02640.

XX 07-JUN-2001: 2001GB-0013908.

XX (UNLO ) UNIV COLLEGE LONDON.

XX Griffiths DJ, Kellam P, Weiss RA;

XX WPI: 2003-148676/14.

XX Designing a panel of degenerate primer pairs, useful for screening new  
 PT members of multiple known virus families in a biological sample,  
 PT comprises deducing the sequences of the primers using computer based  
 PT calculations.

XX Disclosure: Page 26; 31pp; English.

XX The invention relates to a novel method for designing a panel of  
 CC degenerate primer pairs for screening for new members of multiple known  
 CC virus families in a biological sample. The method can be used in high  
 CC throughput screening to detect viruses. This sequence represents a  
 CC peptide derived from a degenerate per primer of the invention.

SQ Sequence 9 AA:

Query Match 36.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; gaps 0;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 6 GNSS 9  
 IIII

ID 2 GNSS 9

ABJ19497

XX ABJ19497 standard; Peptide: 9 AA.

XX ABJ19497;

XX 27-MAR-2003 (first entry)

XX CODEHCP generated degenerate primer pep:line #14.

XX Panel: degenerate primer pair; screening: virus family:  
 XX high throughput screening; ULIS DNA packaging protein; VHA.

XX Unidentified.

XX W0200299129-A2.

PN 12-DEC-2002.

XX 07-JUN-2002: 2002W0-CR02640.

XX 07-JUN-2001: 2001GB-0013908.

XX (UNLO ) UNIV COLLEGE LONDON.

XX Griffiths DJ, Kellam P, Weiss RA;

XX WPI: 2003-148676/14.

XX Designing a panel of degenerate primer pairs, useful for screening new  
 PT members of multiple known virus families in a biological sample,  
 PT comprises deducing the sequences of the primers using computer based  
 PT calculations.

XX Disclosure: Page 26; 31pp; English.

XX The invention relates to a novel method for designing a panel of  
 CC degenerate primer pairs for screening for new members of multiple known  
 CC virus families in a biological sample. The method can be used in high  
 CC throughput screening to detect viruses. This sequence represents a  
 CC peptide derived from a degenerate per primer of the invention.

SQ Sequence 9 AA:

Query Match 36.4%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9; gaps 0;

Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GNSS 9

IIII

ID 2 GNSS 9

ABJ19497

XX ABJ19497 standard; Peptide: 9 AA.

XX ABJ19497;

XX 27-MAR-2003 (first entry)

XX CODEHCP generated degenerate primer pep:line #14.

XX Panel: degenerate primer pair; screening: virus family:  
 XX high throughput screening; ULIS DNA packaging protein; VHA.

XX Unidentified.

XX W0200299129-A2.

PN 12-DEC-2002.

XX 07-JUN-2002: 2002W0-CR02640.

XX 07-JUN-2001: 2001GB-0013908.

XX (UNLO ) UNIV COLLEGE LONDON.

XX Griffiths DJ, Kellam P, Weiss RA;

XX WPI: 2003-148676/14.

XX Designing a panel of degenerate primer pairs, useful for screening new  
 PT members of multiple known virus families in a biological sample,  
 PT comprises deducing the sequences of the primers using computer based  
 PT calculations.

```

FT Misc-difference 2 /note= "AC-D2Nal"
FT FT /label= OTHER
FT FT /note= "D4Clphe"
FT Modified-site 3
FT FT /note= "D-form, omega-amino
FT gp. linked to side chain carboxy gp. of
FT Glu10 via peptide bond"
FT Modified-site 6
FT FT /note= "Lys(Nicotinyl)
FT D-form residue"
FT Modified-site 8
FT FT /note= "Lys(N-epsilon-Isopropyl)"
FT Modified-site 10
FT FT /note= "D-form reiside, side chain carboxy gp.
FT linked to omega-amino gp. of LysG3 via
FT peptide bond, the C-terminal carboxy
FT is in amide form"
XX
XX W09524424-A1.
XX
XX 14-SEP-1995.
XX
XX 27-FEB-1995; 95WO-US02410.
XX
XX 09-MAR-1994; 94US-0208544.
XX
XX (ABSO ) ABBOTT LAB.
XX
XX Haviv F, Sauer DR;
XX
XX WPI; 1995-328233/42.
XX
XX New cyclic peptide LHRH antagonists used for treating conditions
XX mediated by sex hormones, e.g. prostate cancer, endometriosis and
XX uterine fibroids
XX
XX Claim 4; Page 43; 50pp; English.
XX
XX The cyclic peptide luteinising hormone releasing hormone (LHRH)
XX antagonists AAR8990-R89073 inhibit the release of LHRH in mamma's,
XX useful in the treatment of conditions which are mediated by sex
XX hormones, e.g. prostate cancer, endometriosis, uterine fibroids
XX and precocious puberty.
XX
XX Sequence 10 AA;
XX
XX Query Match 36.48; Score 4; DH 16; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 7.5e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 KSRK 5
XX Db 3 KSRK 6
XX
XX RESULT 36
XX ABP11602
XX ID ABP11602 standard; Peptide: 10 AA.
XX
XX AC ABP11602;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV A01 super motif env peptide #85.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
XX vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; viricide.
XX
XX Human immunodeficiency virus type 1.
XX
XX W0200124810-A1.

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XX 12-APR-2001
XX
XX 05-OCT-2000; 2000US-242404.
XX
XX 05-OCT-1999; 99US-312444
XX (PTM-) EIMMUN; IN
XX
XX Sette A, Sidney J, Southwood S, Thompson RO, Chesnut R,
XX Baker DM, Chishti K, Kottke T, Jolly BM.
XX
XX WPI; 2001 354837/41
XX
XX Vaccine composition for immunising human immunodeficiency virus 1 (HIV-1)
XX peptide groups, used in a vaccine for at least HIV 1
XX
XX Claim 32; Para 16, 33-41; Def. 1-5b.
XX
XX The present invention describes a composition (i) comprising a protein or
XX human immunodeficiency virus (HIV-1) group comprising an amino acid
XX sequence selected from 5 amino acid amino acid sequences (AA2647 to
XX AB92547), (ii) a group of adjuvants and can be used in vaccines. (i)
XX may be used for immunisation against HIV-1 infections. The use of
XX group-based vaccine has several advantages over traditional vaccines,
XX particularly with respect to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (vif and gag), and further, to modify the
XX composition of the groups, deconvolving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modified, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP11531 to ABP11512
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 10 AA.
XX
XX Query Match 36.48; Score 4; DH 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 7.5e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GNSS 9
XX Db 111
XX 4 GNSS 7
XX
XX RESULT 47
XX ASB12104
XX ID ABP12104 standard; Peptide: 10 AA.
XX
XX AC ABP12104;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV A02 super motif env peptide #44
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
XX vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; viricide.
XX
XX Human immunodeficiency virus type 1
XX
XX W0200124810-A1.
XX
XX 12-APR-2001.

```

PF 05-OCT-2000: 2000WO-US27766.  
 XX PR 05-OCT-1999: 99US-0412863.  
 XX PA (EPIM-) EPIMUNE INC.  
 XX PI Sette A, Sidney J, Southwood S, Livingston BB, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey BM;  
 XX DR WPI: 2001-354887/37.  
 XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX PT peptide groups, useful for vaccinating against HIV-1.  
 XX PS Claim 32: Page 121: 448pp; English.  
 XX CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397); (ii) has virucide activity and can be used in vaccines; (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTI), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11591 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX SQ Sequence 10 AA;  
 XX SQ Query Match 36.4%; Score 4; IB 22, Length 107  
 XX SQ Best local Similarity 100.0%; Pred. No. 7.5e-02;  
 XX SQ Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 XX QY 6 GNSS 9  
 XX DB IIII  
 XX DB 4 GNSS 7  
 XX RESULT 38  
 XX ABP12786  
 XX ID ABP12786 standard; Peptide: 10 AA.  
 XX AC ABP12786;  
 XX DT 15-JUL-2002 (first entry)  
 XX XX HIV A02 super motif gag peptide #257.  
 XX DE HIV; HIV-1; human immunodeficiency virus; env; gag; gag; gag; gag;  
 XX KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitopes;  
 XX KW antigen; vaccine; HIV infection; immunisation; virucide;  
 XX XX Human immunodeficiency virus type 1.  
 XX OS W0200124810-A1.  
 XX XX W0200124810-A1.  
 XX FN 12-APR-2001.  
 XX PD 05-OCT-2000; 2000WO-US27766.  
 XX PF 05-OCT-1999; 99US-0412863.  
 XX XX 05-OCT-1999; 99US-0412863.  
 XX PR

XX (EPIM-) EPIMUNE INC.  
 XX PA Sette A, Sidney J, Southwood S, Livingston BB, Chesnut R;  
 XX PI Baker DM, Celis E, Kubo RT, Grey BM;  
 XX WPI: 2001-354887/37.  
 XX XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX PT peptide groups, useful for vaccinating against HIV-1.  
 XX PT Claim 32: Page 121: 448pp; English.  
 XX XX The present invention describes a composition (i) comprising a prepared  
 XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 XX sequence selected from 51 defined amino acid sequences (ABP25347 to  
 XX ABP25397); (ii) has virucide activity and can be used in vaccines; (i)  
 XX may be used for immunising subjects against HIV-1 infections. The use of  
 XX group-based vaccines has several advantages over traditional vaccines,  
 XX particularly when compared to the use of whole antigens in vaccine  
 XX compositions. There is evidence that the immune response to whole  
 XX antigens is directed largely toward variable regions of the antigen,  
 XX allowing for immune escape due to mutations. The groups for inclusion in  
 XX an group-based vaccine may be selected from conserved regions of viral or  
 XX tumour-associated antigens, which therefore reduces the likelihood of  
 XX escape mutants. Furthermore, immunosuppressive groups that may be present  
 XX in whole antigens can be avoided with the use of group-based vaccines.  
 XX An additional advantage of an group-based vaccine approach is the ability  
 XX to combine selected groups (CTL and HTI), and further, to modify the  
 XX composition of the groups, achieving, for example, enhanced  
 XX immunogenicity. Accordingly, the immune response can be modulated, as  
 XX appropriate, for the target disease. Similar engineering of the response  
 XX is not possible with traditional approaches. ABP11591 to ABP25412  
 XX represent peptide sequences used in the exemplification of the present  
 XX invention.  
 XX SQ Sequence 10 AA;  
 XX SQ Query Match 36.4%; Score 4; IB 22, Length 107  
 XX SQ Best local Similarity 100.0%; Pred. No. 7.5e-02;  
 XX SQ Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 XX QY 6 GNSS 9  
 XX DB IIII  
 XX DB 4 GNSS 7  
 XX RESULT 38  
 XX ABP25412  
 XX ID ABP25412 standard; Peptide: 10 AA.  
 XX AC ABP25412;  
 XX DT 15-JUL-2002 (first entry)  
 XX XX HIV A02 super motif gag peptide #257.  
 XX DE HIV; HIV-1; human immunodeficiency virus; env; gag; gag; gag; gag;  
 XX KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitopes;  
 XX KW antigen; vaccine; HIV infection; immunisation; virucide;  
 XX XX Human immunodeficiency virus type 1.  
 XX OS W0200124810-A1.  
 XX XX W0200124810-A1.  
 XX FN 12-APR-2001.  
 XX PD 05-OCT-2000; 2000WO-US27766.  
 XX PF 05-OCT-1999; 99US-0412863.  
 XX XX 05-OCT-1999; 99US-0412863.  
 XX PR (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston RB, Chesnut R,  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 DR WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccination against HIV;  
 XX Claim 32; Page 185; 448pp; English.  
 XX The present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV 1) group comprising a prepared  
 CC sequence selected from 51 defined amino acid sequences (ABP2547 to  
 CC ABP2549). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV 1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (C1 and B1), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1561 to ABP2547  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 XX SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; DP 22; Length 17;  
 Best local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Labels 0; Gaps 0;  
 QY 6 GNS5 9  
 DB 4 GNS5 7  
 I I I I  
 RESULT 4C  
 ABP17602  
 ID ABP17602 standard; Peptide; 10 AA.  
 XX  
 AC ABP17602;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV B58 super motif env peptide #1.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif; vpr;  
 KW vpr; vif; tat; cytoxic T lymphocyte; C1; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virus;  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W0200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000W0-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIIM-) EPIIMUNE INC.  
 XX  
 XX Sette A, Sidney J, Southwood S, Livingston RB, Chesnut R,  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)

PI WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccination against HIV;  
 XX Claim 32; Page 185; 448pp; English.  
 XX The present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV 1) group comprising a prepared  
 CC sequence selected from 51 defined amino acid sequences (ABP2547 to  
 CC ABP2549). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV 1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (C1 and B1), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1561 to ABP2547  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 XX SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; DP 22; Length 17;  
 Best local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Labels 0; Gaps 0;  
 QY 6 GNS5 9  
 DB 4 GNS5 7  
 I I I I  
 RESULT 4C  
 ABP17602  
 ID ABP17602 standard; Peptide; 10 AA.  
 XX  
 AC ABP17602;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV B58 super motif env peptide #1.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif; vpr;  
 KW vpr; vif; tat; cytoxic T lymphocyte; C1; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virus;  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W0200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000W0-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIIM-) EPIIMUNE INC.  
 XX  
 XX Sette A, Sidney J, Southwood S, Livingston RB, Chesnut R,  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)

PT peptide groups, useful for vaccinating against HIV 1;  
 PS Claim 32: Page 233; 448pp; English.  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (AR25437 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of virus or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modified, as  
 CC appropriate, for the target disease. Similar requirements of the response  
 CC is not possible with traditional approaches. Accordingly, ABP25437 to ABP25397  
 CC represent peptide sequences used in the experimentation of the present  
 CC invention.  
 XX Sequence 10 AA:  
 SQ  
 Query Match 36.4%; Score 4; 10 zzz; Length 1;  
 Best Local Similarity 100.0%; Pred. No. 7,6002;  
 Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 6 GNSS 9  
 Db IIII  
 Db 5 GNSS 8  
 RESULT 42  
 ABP19695  
 ID ABP19695 standard; Peptide: 10 AA.  
 XX  
 AC ABP19695;  
 DT 15 JUL 2002 (first entry)  
 XX  
 DE HIV A01 motif env peptide #5.  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX W0200124810-A1.  
 PN  
 XX  
 XX 12 APR 2001.  
 XX  
 XX 05-0001-2000; 2000WO-US27766.  
 XX  
 PR 05-0001-1499; 99US-0412863.  
 XX  
 XX (EPIM ) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livineston SB, Carson J, et  
 PI Baker DM, Cellis E, Kubo RT, Grey HE.  
 XX  
 XX WPI: 2001-354887/37.  
 XX  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccinating against HIV 1.  
 PT  
 PS Claim 32: Page 273; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (AR25437 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of virus or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modified, as  
 CC appropriate, for the target disease. Similar requirements of the response  
 CC is not possible with traditional approaches. Accordingly, ABP25437 to ABP25397  
 CC represent peptide sequences used in the experimentation of the present  
 CC invention.  
 XX Sequence 10 AA:  
 SQ  
 Query Match 36.4%; Score 4; 10 zzz; Length 1;  
 Best Local Similarity 100.0%; Pred. No. 7,6002;  
 Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 6 GNSS 9  
 Db IIII  
 Db 5 GNSS 8  
 RESULT 42  
 ABP19695  
 ID ABP19695 standard; Peptide: 10 AA.  
 XX  
 AC ABP19695;  
 DT 15 JUL 2002 (first entry)  
 XX  
 DE HIV A01 motif env peptide #5.  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX W0200124810-A1.  
 PN  
 XX  
 XX 12 APR 2001.  
 XX  
 XX 05-0001-2000; 2000WO-US27766.  
 XX  
 PR 05-0001-1499; 99US-0412863.  
 XX  
 XX (EPIM ) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livineston SB, Carson J, et  
 PI Baker DM, Cellis E, Kubo RT, Grey HE.  
 XX  
 XX WPI: 2001-354887/37.  
 XX  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccinating against HIV 1.  
 PT  
 PS Claim 32: Page 273; 448pp; English.

CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 10 AA;

Query Match 36.4%; Score 4; E: 2.2; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 7 56-02;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9  
 Db 1111  
 1 GNSS 4

RESULT 44

ABP19814

ID ABP19814 standard; Peptide: 10 AA.

XX AC ABP15814;

DT 15-JUL-2002 (first entry)

XX DE HIV A03 motif env peptide #18.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; pol; vpr;  
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMUNE INC.

XX P1 Settle A, Sidney J, Southwood S, Livingston B, Clouston B;

XX P1 Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WP1: 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1;

XX PS Claim 32; Page 276; 448pp; English.

XX CC The present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of

XX group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 10 AA;

Query Match 36.4%; Score 4; E: 2.2; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 7 56-02;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9

Db 1111

4 GNSS 7

RESULT 44

ABP19814

ID ABP19814 standard; Peptide: 10 AA.

XX AC ABP15814;

DT 15-JUL-2002 (first entry)

XX DE HIV A03 motif env peptide #18.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; pol; vpr;  
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMUNE INC.

XX P1 Settle A, Sidney J, Southwood S, Livingston B, Clouston B;

XX P1 Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WP1: 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1;

XX PS Claim 32; Page 276; 448pp; English.

XX CC The present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen.  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP2542  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; PB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GNSS 9  
 Db 3 GNSS 6  
 RESULT 46  
 ABP19819  
 ID ABP19819 standard; Peptide: 10 AA.  
 XX  
 AC ABP19819;  
 DT 15-JUL-2002 (first entry)  
 DE HIV A03 motif env peptide #23.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vpr; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; viricide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W0200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX  
 DR WPT; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV 1.  
 XX  
 PS Claim 32; Page 276; 448pp; English.  
 XX  
 CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP2542  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; PB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GNSS 9  
 Db 3 GNSS 6  
 RESULT 47  
 ABP25398  
 ID ABP25398 standard; Peptide: 10 AA.  
 XX  
 AC ABP25398;  
 DT 16-JUL-2002 (first entry)  
 DE HIV A03 motif env peptide #24.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vpr; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; viricide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W2012481 A1.  
 XX  
 PD 12-APR-2001  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX  
 DR WPT; 2001-354887/37  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1  
 XX  
 PS Claim 32; Page 283; 448pp; English  
 XX  
 CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

XX Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9  
Db 2 GNSS 5

RESULT 48

ABP22288

ID ABP22288 standard; Peptide: 10 AA.

XX AC ABP22288;

XX D1 15-JUL-2002 (first entry)

XX DE HIV All motif env peptide #11.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; asq; nef; vif;  
XX vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
XX antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN W0200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA {EPTM-} EPTMUNE INC.

XX PI Settle A, Sidney J, Southwood S, Livingston RD, Chesnut R;  
XX Baker DM, Cells E, Kubo RT, Grey HM;

XX DR WP1: 2001-354867/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
XX peptide groups, useful for vaccinating against HIV-1.

XX PS Claim 32; Page 326; 448pp; English.

XX The present invention describes a composition (i) comprising a prepared  
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
XX sequence selected from 51 defined amino acid sequences (Abp25347 to  
XX Abp25397); (ii) has virucide activity and can be used in vaccines; (i)  
XX may be used for immunising subjects against HIV-1 infections. The use of  
XX group-based vaccines has several advantages over traditional vaccines,  
XX particularly when compared to the use of whole antigens in vaccine  
XX compositions. There is evidence that the immune response to whole  
XX antigens is directed largely toward variable regions of the antigen,  
XX allowing for immune escape due to mutations. The groups for inclusion in  
XX an group-based vaccine may be selected from conserved regions of viral or  
XX tumour-associated antigens, which therefore reduces the likelihood of  
XX escape mutants. Furthermore, immunosuppressive groups that may be present  
XX in whole antigens can be avoided with the use of group-based vaccines.  
XX An additional advantage of an group-based vaccine approach is the ability  
XX to combine selected groups (CTL and HTL), and further, to modify the  
XX composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

XX Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9

Db 2 GNSS 5

RESULT 49

ABP22289

ID ABP22289 standard; Peptide: 10 AA.

XX AC ABP22289;

XX D1 15-JUL-2002 (first entry)

XX DE HIV All motif env peptide #12

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; asq; nef; vif;  
XX vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
XX antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1

XX PN W0200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA {EPTM-} EPTMUNE INC.

XX PI Settle A, Sidney J, Southwood S, Livingston RD, Chesnut R;  
XX Baker DM, Cells E, Kubo RT, Grey HM;

XX DR WP1: 2001-354867/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
XX peptide groups, useful for vaccinating against HIV-1.

XX PS Claim 32; Page 326; 448pp; English.

XX The present invention describes a composition (i) comprising a prepared  
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
XX sequence selected from 51 defined amino acid sequences (Abp25347 to  
XX Abp25397); (ii) has virucide activity and can be used in vaccines; (i)  
XX may be used for immunising subjects against HIV-1 infections. The use of  
XX group-based vaccines has several advantages over traditional vaccines,  
XX particularly when compared to the use of whole antigens in vaccine  
XX compositions. There is evidence that the immune response to whole  
XX antigens is directed largely toward variable regions of the antigen,  
XX allowing for immune escape due to mutations. The groups for inclusion in  
XX an group-based vaccine may be selected from conserved regions of viral or  
XX tumour-associated antigens, which therefore reduces the likelihood of  
XX escape mutants. Furthermore, immunosuppressive groups that may be present  
XX in whole antigens can be avoided with the use of group-based vaccines.  
XX An additional advantage of an group-based vaccine approach is the ability  
XX to combine selected groups (CTL and HTL), and further, to modify the  
XX composition of the groups, achieving, for example, enhanced  
XX immunogenicity. Accordingly, the immune response can be modulated, as  
XX appropriate, for the target disease. Similar engineering of the response  
XX is not possible with traditional approaches. ABP11501 to ABP25412





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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:14 : Search time 11.655 seconds  
(with local alignment)  
93.34 / 8.1106 cell updates/sec

Title: US-09-787-443-21  
Perfect score: 11 AKSRKGNSSLM 11  
Sequence:

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2664

Minimum DB seq length: 8  
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : PIR\_76:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	27.3	8	2	S59622
2	3	27.3	9	1	YF82
3	3	27.3	9	2	A6097
4	3	27.3	9	2	S35538
5	3	27.3	9	2	A44873
6	3	27.3	9	2	PT6670
7	3	27.3	10	2	S51912
8	3	27.3	10	2	P00037
9	3	27.3	10	2	PT0309
10	3	27.3	11	2	S66606
11	3	27.3	11	2	H54346
12	3	27.3	11	2	G61497
13	3	27.3	12	2	C49215
14	3	27.3	12	2	S26549
15	3	27.3	12	2	S65409
16	3	27.3	12	2	A44874
17	3	27.3	12	2	S29854
18	3	27.3	12	2	S47460
19	3	27.3	12	2	PH1463
20	3	27.3	12	2	PH1466
21	3	27.3	12	2	PT0216
22	3	27.3	13	2	A53608
23	3	27.3	13	2	S36887
24	3	27.3	13	2	S09395
25	3	27.3	14	2	A49018
26	3	27.3	14	2	B34135
27	3	27.3	14	2	A47421
28	3	27.3	14	2	PH1608
29	3	27.3	15	2	S16888

1	3	27.3	15	2	PH1608
2	3	27.3	15	2	S16888
3	3	27.3	15	2	PH1608
4	3	27.3	15	2	S16888
5	3	27.3	15	2	PH1608
6	3	27.3	15	2	S16888
7	3	27.3	15	2	PH1608
8	3	27.3	15	2	S16888
9	3	27.3	15	2	PH1608
10	3	27.3	15	2	S16888
11	3	27.3	15	2	PH1608
12	3	27.3	15	2	S16888
13	3	27.3	15	2	PH1608
14	3	27.3	15	2	S16888
15	3	27.3	15	2	PH1608
16	3	27.3	15	2	S16888
17	3	27.3	15	2	PH1608
18	3	27.3	15	2	S16888
19	3	27.3	15	2	PH1608
20	3	27.3	15	2	S16888
21	3	27.3	15	2	PH1608
22	3	27.3	15	2	S16888
23	3	27.3	15	2	PH1608
24	3	27.3	15	2	S16888
25	3	27.3	15	2	PH1608
26	3	27.3	15	2	S16888
27	3	27.3	15	2	PH1608
28	3	27.3	15	2	S16888
29	3	27.3	15	2	PH1608

103	2	18.2	10	1	SPERNK	neurokinin A, cell	176	1	2	11266	cytochrome c oxidase
104	2	18.2	10	2	A43405	6-phosphogluco-2	177	1	2	11266	neurokinin A, cell
105	2	18.2	10	2	A60624	active casin, 13	178	1	2	644871	neurokinin A, cell
106	2	18.2	10	2	A60410	beta-neoendoplasmic	179	1	2	120766	6-phosphogluco-2
107	2	18.2	10	2	A31571	hyper-neoendoplasmic	180	1	2	120766	neurokinin A, cell
108	2	18.2	10	2	JN0024	neurokinin A, cell	181	1	2	120766	neurokinin A, cell
109	2	18.2	10	2	PQ0177	neurokinin A, cell	182	1	2	120766	neurokinin A, cell
110	2	18.2	10	2	A60647	neurokinin A, cell	183	1	2	120766	neurokinin A, cell
111	2	18.2	10	2	C45474	thrombospondin 2	184	1	2	120766	neurokinin A, cell
112	2	18.2	10	2	B33710	thrombospondin 2	185	1	2	120766	neurokinin A, cell
113	2	18.2	10	2	G60787	sperm-activating p	186	1	2	120766	neurokinin A, cell
114	2	18.2	10	2	G60787	sperm-activating p	187	1	2	120766	neurokinin A, cell
115	2	18.2	10	2	E60787	sperm-activating p	188	1	2	120766	neurokinin A, cell
116	2	18.2	10	2	E6527	sperm-activating p	189	1	2	120766	neurokinin A, cell
117	2	18.2	10	2	E39572	sperm-activating p	190	1	2	120766	neurokinin A, cell
118	2	18.2	10	2	D60589	sperm-activating p	191	1	2	120766	neurokinin A, cell
119	2	18.2	10	2	G60588	sperm-activating p	192	1	2	120766	neurokinin A, cell
120	2	18.2	10	2	A60588	sperm-activating p	193	1	2	120766	neurokinin A, cell
121	2	18.2	10	2	A49581	stathmin, 11-12	194	1	2	120766	neurokinin A, cell
122	2	18.2	10	2	A49581	stathmin, 11-12	195	1	2	120766	neurokinin A, cell
123	2	18.2	10	2	B49581	stathmin, 11-12	196	1	2	120766	neurokinin A, cell
124	2	18.2	10	2	A24867	stathmin, 11-12	197	1	2	120766	neurokinin A, cell
125	2	18.2	10	2	S23107	stathmin, 11-12	198	1	2	120766	neurokinin A, cell
126	2	18.2	10	2	S23186	stathmin, 11-12	199	1	2	120766	neurokinin A, cell
127	2	18.2	10	2	S07202	stathmin, 11-12	200	1	2	120766	neurokinin A, cell
128	2	18.2	10	2	B61035	stathmin, 11-12	201	1	2	120766	neurokinin A, cell
129	2	18.2	10	2	G61035	stathmin, 11-12	202	1	2	120766	neurokinin A, cell
130	2	18.2	10	2	D37176	stathmin, 11-12	203	1	2	120766	neurokinin A, cell
131	2	18.2	10	2	D37197	stathmin, 11-12	204	1	2	120766	neurokinin A, cell
132	2	18.2	10	2	S09387	stathmin, 11-12	205	1	2	120766	neurokinin A, cell
133	2	18.2	10	2	B39517	stathmin, 11-12	206	1	2	120766	neurokinin A, cell
134	2	18.2	10	2	139702	stathmin, 11-12	207	1	2	120766	neurokinin A, cell
135	2	18.2	10	2	S70721	stathmin, 11-12	208	1	2	120766	neurokinin A, cell
136	2	18.2	10	2	C39151	stathmin, 11-12	209	1	2	120766	neurokinin A, cell
137	2	18.2	10	2	PC4442	stathmin, 11-12	210	1	2	120766	neurokinin A, cell
138	2	18.2	10	2	S48182	stathmin, 11-12	211	1	2	120766	neurokinin A, cell
139	2	18.2	10	2	140032	stathmin, 11-12	212	1	2	120766	neurokinin A, cell
140	2	18.2	10	2	JP0072	stathmin, 11-12	213	1	2	120766	neurokinin A, cell
141	2	18.2	10	2	F41899	stathmin, 11-12	214	1	2	120766	neurokinin A, cell
142	2	18.2	10	2	A40753	stathmin, 11-12	215	1	2	120766	neurokinin A, cell
143	2	18.2	10	2	PA0050	stathmin, 11-12	216	1	2	120766	neurokinin A, cell
144	2	18.2	10	2	A27617	stathmin, 11-12	217	1	2	120766	neurokinin A, cell
145	2	18.2	10	2	S19296	stathmin, 11-12	218	1	2	120766	neurokinin A, cell
146	2	18.2	10	2	PG1065	stathmin, 11-12	219	1	2	120766	neurokinin A, cell
147	2	18.2	10	2	F61512	stathmin, 11-12	220	1	2	120766	neurokinin A, cell
148	2	18.2	10	2	S65728	stathmin, 11-12	221	1	2	120766	neurokinin A, cell
149	2	18.2	10	2	A42089	stathmin, 11-12	222	1	2	120766	neurokinin A, cell
150	2	18.2	10	2	C39111	stathmin, 11-12	223	1	2	120766	neurokinin A, cell
151	2	18.2	10	2	A24546	stathmin, 11-12	224	1	2	120766	neurokinin A, cell
152	2	18.2	10	2	S43625	stathmin, 11-12	225	1	2	120766	neurokinin A, cell
153	2	18.2	10	2	A30823	stathmin, 11-12	226	1	2	120766	neurokinin A, cell
154	2	18.2	10	2	A90917	stathmin, 11-12	227	1	2	120766	neurokinin A, cell
155	2	18.2	10	2	PT0243	stathmin, 11-12	228	1	2	120766	neurokinin A, cell
156	2	18.2	10	2	PT0322	stathmin, 11-12	229	1	2	120766	neurokinin A, cell
157	2	18.2	10	2	S23371	stathmin, 11-12	230	1	2	120766	neurokinin A, cell
158	2	18.2	10	2	S10765	stathmin, 11-12	231	1	2	120766	neurokinin A, cell
159	2	18.2	10	2	S71944	stathmin, 11-12	232	1	2	120766	neurokinin A, cell
160	2	18.2	10	2	C41946	stathmin, 11-12	233	1	2	120766	neurokinin A, cell
161	2	18.2	10	2	B38887	stathmin, 11-12	234	1	2	120766	neurokinin A, cell
162	2	18.2	10	2	AX0060	stathmin, 11-12	235	1	2	120766	neurokinin A, cell
163	2	18.2	10	2	A55645	stathmin, 11-12	236	1	2	120766	neurokinin A, cell
164	2	18.2	10	2	PH0900	stathmin, 11-12	237	1	2	120766	neurokinin A, cell
165	2	18.2	10	2	PH0927	stathmin, 11-12	238	1	2	120766	neurokinin A, cell
166	2	18.2	10	2	PH0944	stathmin, 11-12	239	1	2	120766	neurokinin A, cell
167	2	18.2	10	2	PH0834	stathmin, 11-12	240	1	2	120766	neurokinin A, cell
168	2	18.2	10	2	PH0946	stathmin, 11-12	241	1	2	120766	neurokinin A, cell
169	2	18.2	10	2	PH0925	stathmin, 11-12	242	1	2	120766	neurokinin A, cell
170	2	18.2	10	2	PH0926	stathmin, 11-12	243	1	2	120766	neurokinin A, cell
171	2	18.2	10	2	PH0916	stathmin, 11-12	244	1	2	120766	neurokinin A, cell
172	2	18.2	10	2	PH0895	stathmin, 11-12	245	1	2	120766	neurokinin A, cell
173	2	18.2	10	2	PH0948	stathmin, 11-12	246	1	2	120766	neurokinin A, cell
174	2	18.2	10	2	T13838	stathmin, 11-12	247	1	2	120766	neurokinin A, cell
175	2	18.2	10	2	T14019	stathmin, 11-12	248	1	2	120766	neurokinin A, cell







C:Accession: S51912  
 R:Jin, H.; Leser, G.P.; Lamb, R.A.  
 EMBO J. 13, 5504-5515, 1994  
 A:Title: The influenza virus hemagglutinin cytoplasmic tail is not essential for virus  
 A:Reference number: S51912; MUID:95045445; PMID:7957116  
 A:Accession: S51912  
 A>Status: not compared with conceptual translation  
 A:Molecule type: genomic RNA  
 A:Residues: 1-10 <JIN>  
 A:Experimental source: isolate A/Udorn/72  
 C:Keywords: hemagglutinin; homotrimer

Query Match 27.3%; Score 3; DP 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2,400,000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 5 KGN 7  
 III  
 Db 1 KGN 3

## RESULT 8

PU0037

alpha-peptide/alcaline lyase fused protein 1 - Pseudomonas sp. (truncated)  
 C:Species: Pseudomonas sp.  
 C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 12 Sep 1992  
 C:Accession: PU0037  
 R:Fujiyama, K.; Maki, H.; Kinoshita, S.; Yoshida, T.  
 submitted to JIPID, October 1994  
 A:Description: High gene expression in E. coli of recombinant alkaline lyase as a fused  
 A:Reference number: PU0037

A:Accession: PU0037  
 A:Molecule type: protein  
 A:Residues: 1-10 <FUJ>  
 C:Genetics:  
 A:Gene: lacZ'/ali

Query Match 27.3%; Score 3; DP 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2,400,000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 7 NSS 9  
 III  
 Db 4 NSS 6

## RESULT 9

PT0309

Ig heavy chain CRO3 region (clone 6-94) - human (truncated)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep 1993 #text\_change 16 Aug 1994  
 C:Accession: PT0309  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shaver, S.; Caton, A.J.; Kovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A:Reference number: PT0222; MUID:91108337; PMID:1899132  
 A:Accession: PT0309  
 A:Molecule type: DNA  
 A:Residues: 1-10 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotrimer; immunoglobulin

Query Match 27.3%; Score 3; DP 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2,400,000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNS 8  
 III  
 Db 4 GNS 6

## RESULT 10

S66606

cytoplasmic 2'-oxaldehyde-5-phosphate-1-thioester - Chlamydomonas reinhardtii (truncated)  
 C:Species: Chlamydomonas reinhardtii  
 C:Date: 15-Feb-1997 #sequence\_revision 15-Mar 1997 #text\_change 17 Mar 1997  
 A:Accession: S66606  
 R:Schubert, S.; Tshisuoka, K.; Pol-Zimmer, G.; Linquist, P.  
 Eur. J. Biochem. 242, 865-871, 1996  
 A:Title: Cytoplasmic 2'-oxaldehyde-5-phosphate-1-thioester - Chlamydomonas reinhardtii  
 A:Reference number: S66606  
 A:Accession: S66606  
 A:Molecule type: protein  
 A:Residues: 1-11 <SCH>  
 A:Experimental source: strain 1000

Query Match 27.3%; Score 3; DP 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2,400,000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKS 4  
 III  
 Db 1 AKS 3

## RESULT 11

S61447

pyruvate decarboxylase (EC 4.1.1.1) - Escherichia coli (strain ATCC 8739) (truncated)  
 C:Species: Escherichia coli (strain ATCC 8739)  
 C:Date: 05-Jun-1990 #sequence\_revision 07-Sep 1996 #text\_change 05 May 2000  
 C:Accession: P54446  
 R:Blatt, C.; Malt, A.; Malt, B.W.  
 Biochemistry 29, 1000-1004, 1990  
 A:Title: Pyruvate decarboxylase (EC 4.1.1.1) type I, pyruvate decarboxylase  
 A:Reference number: P54446  
 A:Accession: P54446  
 A>Status: protein  
 A:Molecule type: protein  
 A:Residues: 1-11 <BLA>

C:Keywords: pyruvate decarboxylase; pyruvate decarboxylase  
 Query Match 27.3%; Score 3; DP 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2,400,000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 KGN 7  
 III  
 Db 4 KGN 6

## RESULT 12

G61447

seed protein WS-2 - winged bean (truncated)  
 C:Species: Psophocarpus tetragonolobus (winged bean)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct 1994 #text\_change 07 Oct 1994  
 C:Accession: G61447  
 R:Gilliland, R.  
 J. Protein Chem. 10, 135-140, 1991  
 A:Title: Microsequences and genes of winged bean seed proteins obtained from two  
 A:Reference number: G61447  
 A:Accession: G61447  
 A>Status: protein  
 A:Molecule type: protein  
 A:Residues: 1-11 <GIL>  
 C:Keywords: albumin; protein; seed

Query Match 27.3%; Score 3; DP 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2,400,000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKS 4  
 III  
 Db 1 AKS 3





R: Lechner, P.J.  
 Submitted to the EMBL Data Library, August 1994  
 A: Description: Human HLA-A\*0201 restricted recognition of influenza A is determined by T  
 A: Reference number: S47355  
 A: Accession: S47360  
 A: Status: preliminary  
 A: Molecule type: mRNA  
 A: Residues: 1-12 <LEH>  
 A: Cross references: EMBL:235684; NID:Q527452; EDB:2AA4476; L184962; E  
 C: Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 12;

Best local Similarity 100.0%; Pred. No. 2.6+0.0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SSL 1;

DB 10 SSL 12

#### RESULT 19

PH1463

T-cell receptor beta chain (clone A24/10.1) - mouse (Tramont)

C: Species: Mus musculus (house mouse)

C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995

C: Accession: PH1463

R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K

J. Exp. Med. 177, 811-820, 1993

A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility

A: Reference number: PH1430; MUID:94171821; EMBL:844471

A: Accession: PH1463

A: Molecule type: mRNA

A: Residues: 1-12 <CAS>

A: Experimental source: cytolytic T-lymphocyte

A: Superfamily: immunoglobulin homology

C: Keywords: receptor; T-cell

Query Match

Best local Similarity 100.0%; Pred. No. 2.6+0.0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SSL 10

DB 4 SSL 5

#### RESULT 20

PH1466

T-cell receptor beta chain (clone A3/74.1) - mouse (Tramont)

C: Species: Mus musculus (house mouse)

C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995

C: Accession: PH1466

R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K

J. Exp. Med. 177, 811-820, 1993

A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility

A: Reference number: PH1430; MUID:94171821; EMBL:844471

A: Accession: PH1466

A: Molecule type: mRNA

A: Residues: 1-12 <CAS>

A: Experimental source: cytolytic T-lymphocyte

A: Superfamily: immunoglobulin homology

C: Keywords: receptor; T-cell

Query Match

Best local Similarity 100.0%; Pred. No. 2.6+0.0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SSL 10

DB 3 SSL 5

#### RESULT 21

PH1464  
 T-cell receptor beta chain (clone A3/74.1) - mouse (Tramont)  
 C: Species: Mus musculus (house mouse)  
 C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995  
 C: Accession: PH1464  
 R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K  
 J. Exp. Med. 177, 811-820, 1993  
 A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility  
 A: Reference number: PH1430; MUID:94171821; EMBL:844471  
 A: Accession: PH1464  
 A: Molecule type: mRNA  
 A: Residues: 1-12 <CAS>  
 A: Experimental source: cytolytic T-lymphocyte  
 A: Superfamily: immunoglobulin homology  
 C: Keywords: receptor; T-cell

Query Match

Best local Similarity 100.0%; Pred. No. 2.6+0.0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SSL 10

DB 3 SSL 5

PH1465  
 T-cell receptor beta chain (clone A24/10.1) - mouse (Tramont)  
 C: Species: Mus musculus (house mouse)  
 C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995  
 C: Accession: PH1465  
 R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K  
 J. Exp. Med. 177, 811-820, 1993  
 A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility  
 A: Reference number: PH1430; MUID:94171821; EMBL:844471  
 A: Accession: PH1465  
 A: Molecule type: mRNA  
 A: Residues: 1-12 <CAS>  
 A: Experimental source: cytolytic T-lymphocyte  
 A: Superfamily: immunoglobulin homology  
 C: Keywords: receptor; T-cell

Query Match

Best local Similarity 100.0%; Pred. No. 2.6+0.0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SSL 10

DB 3 SSL 5

PH1466  
 T-cell receptor beta chain (clone A3/74.1) - mouse (Tramont)  
 C: Species: Mus musculus (house mouse)  
 C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995  
 C: Accession: PH1466  
 R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K  
 J. Exp. Med. 177, 811-820, 1993  
 A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility  
 A: Reference number: PH1430; MUID:94171821; EMBL:844471  
 A: Accession: PH1466  
 A: Molecule type: mRNA  
 A: Residues: 1-12 <CAS>  
 A: Experimental source: cytolytic T-lymphocyte  
 A: Superfamily: immunoglobulin homology  
 C: Keywords: receptor; T-cell

Query Match

Best local Similarity 100.0%; Pred. No. 2.6+0.0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SSL 10

DB 3 SSL 5

PH1467  
 T-cell receptor beta chain (clone A3/74.1) - mouse (Tramont)  
 C: Species: Mus musculus (house mouse)  
 C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995  
 C: Accession: PH1467  
 R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K  
 J. Exp. Med. 177, 811-820, 1993  
 A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility  
 A: Reference number: PH1430; MUID:94171821; EMBL:844471  
 A: Accession: PH1467  
 A: Molecule type: mRNA  
 A: Residues: 1-12 <CAS>  
 A: Experimental source: cytolytic T-lymphocyte  
 A: Superfamily: immunoglobulin homology  
 C: Keywords: receptor; T-cell

Query Match

Best local Similarity 100.0%; Pred. No. 2.6+0.0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SSL 10

DB 3 SSL 5

## RESULT 24

S09395  
 hypothetical protein - fruit fly (Drosophila melanogaster) (fragment)  
 C:Species: Drosophila melanogaster  
 C>Date: 19-Mar-1997 #sequence\_revision 24 Jul-1997 #text\_change 24 Jul-1997  
 C:Accession: S09395  
 R:Gisselmann, G.; Sewing, S.; Madsen, B.W.; Mailart, A.; Audat-Petit, D.; Mueller-Helber, EBO J. 8, 2359-2364, 1989  
 A>Title: The interference of truncated with normal potassium channel subunits leads to a  
 A:Reference number: S09395; MUID:90005442; PMID:251689  
 A:Accession: S09395  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-13 <GIS>

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2, 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 NSS 9  
 DB 11 NSS 13

## RESULT 25

A49018  
 myosin heavy chain, fast skeletal muscle type X - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 01-May-1994 #sequence\_revision 03 May-1994 #text\_change 10-A-q-1994  
 C:Accession: A49018; S32161  
 R:Denardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Veileca, M.; Buckingham, M.; Schaffitzel, J. Cell Biol. 123, 823-835, 1993  
 A>Title: Type 2X-myosin heavy chain is coded by a muscle fiber type specific and develop  
 A:Reference number: A49018; MUID:94043465; PMID:822714  
 A:Accession: A49018  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <DEN>  
 A:Cross-references: GB:X72591; NID:Q288645; PID:CAA51189.1; PID:Q288646  
 R:Denardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Veileca, M.; Merlier, J.; Buckingham, submitted to the EMBL Data Library, March 1993  
 A:Description: Type 2X myosin heavy chain is coded by a muscle fiber type-specific and c  
 A:Reference number: S32161  
 A:Accession: S32161  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <DEN2>  
 A:Cross-references: EMBL:X72591; NID:Q288645; PID:CAA51189.1; PID:Q288646  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: skeletal muscle

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2, 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KSR 4  
 DB 2 KSR 4

## RESULT 26

B34135  
 DNA-binding protein q - Crithidia fasciculata mitochondrion (fragment)  
 C:Species: mitochondrion Crithidia fasciculata  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 07-Dec-1999  
 C:Accession: B34135  
 R:Tittawella, I.  
 FEBS Lett. 260, 57-61, 1990  
 A>Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasc  
 A:Reference number: A34135  
 A:Accession: B34135

A:Molecule type: protein  
 A:Residues: 1-14 <LIV>  
 A:Genetics:  
 A:Genome: mitochondrial  
 A:Genetic code: S036  
 C:Keywords: mitochondrion

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2, 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NSS 5  
 DB 10 NSS 14

## RESULT 27

A42421  
 leukotriene B-4 synthase (human) (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 19-May-1994 #sequence\_revision 03 May-1994 #text\_change 17-Mar-1994  
 C:Accession: A42421  
 R:Yokoyama, C.; Smith, W.L.; Smith, W.L.; Kusama, T.; Kobayashi, Y.; Saito, F.; Tanabe, T. Biol. Chem. 269, 16124-16128, 1994  
 A>Title: Enzymatic activation of leukotriene B-4 by a mouse enzyme cloned from pig  
 A:Reference number: A42421; MUID:9452600; PMID:8594367  
 A:Accession: A42421  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <YOK>  
 C:Keywords: oxidized arase

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2, 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKS 4  
 DB 3 AKS 5

## RESULT 28

PH1658  
 12 B chain V-D-J region, mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jun-1994 #sequence\_revision 02 Jun-1994 #text\_change 17-Mar-1994  
 C:Accession: PH1658; PH1659  
 R:Levinson, L.A.; Cammer-Morse, L.; Lockart, P. J. Exp. Med. 178, 457-469, 1993  
 A>Title: Molecular characterization of transgene-induced myeloid leukaemia in P-100  
 A:Reference number: PH1658; MUID:940139; PMID:8415407  
 A:Accession: PH1658  
 A:Molecule type: DNA  
 A:Residues: 1-14 <LEV>  
 A:Experimental situation: bone marrow pro-B lymphocyte, wild type clone 400  
 A:Accession: PH1659  
 A:Molecule type: DNA  
 A:Residues: 1-14 <LEV>  
 A:Experimental situation: bone marrow pro-B lymphocyte, wild type clone 423  
 C:Keywords: lymphocyte

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2, 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NSS 9  
 DB 6 NSS 9

## RESULT 29

S16866  
 ribosomal protein S12 - Mycobacterium bovis (fragment)

C:Species: Mycobacterium bovis  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 31-Jan-1997  
 C:Accession: S36888  
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
 FEBS Lett. 331, 9-14, 1993  
 A:Title: Isolation and amino acid sequence of the 6S ribosomal protein S19 from Mycobacterium bovis  
 A:Reference number: S36887; MUID:94009653; PMID:8495418  
 A:Accession: S36888  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <OHA>  
 C:Superfamily: Escherichia coli ribosomal protein S12  
 C:Keywords: protein biosynthesis; ribosome

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 RKG 6  
 III  
 DB 8 RKG 10

RESULT 30  
 S21411  
 modulation protein noda - Rhizobium loti (fragment)  
 C:Species: Rhizobium loti  
 C:Date: 22-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 08-Oct-1999  
 C:Accession: S21411  
 R:Scott, D.H.; Young, C.A.; Collins-Emerson, J.M.; Torzadeh, E.A.; Rockwell, P.S.; Low, L.  
 submitted to the EMBL Data Library, April 1992  
 A:Description: Mutational and structural analysis of Rhizobium loti modulation genes.  
 A:Reference number: S21410  
 A:Accession: S21411  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-15 <SCO>  
 A:Cross-references: EMBL:X65620; NID:q46240; PILE:FAA15674; PILE:q290061; PILE:q160622  
 C:Genetics:  
 C:Gene: noda

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 RKG 6  
 III  
 DB 10 RKG 12

RESULT 31  
 PA0102  
 fructose-bisphosphate aldolase (EC 4.1.2.13) III - humans (Fusarium sporotrichioides)  
 C:Species: Fusarium sporotrichioides  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0102  
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Gene, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
 A:Reference number: PA0051  
 A:Accession: PA0102  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: aldohyde-lyase; carbon-carbon lyase

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SRK 5  
 III  
 DB 7 SRK 9

RESULT 32  
 FA0055  
 fructose-bisphosphate aldolase (EC 4.1.2.13) III - humans (Fusarium sporotrichioides)  
 C:Species: Fusarium sporotrichioides  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0055  
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Gene, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
 A:Reference number: FA0054  
 A:Accession: FA0055  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: aldohyde-lyase; carbon-carbon lyase

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 RKG 6  
 III  
 DB 8 RKG 10

RESULT 33  
 FA0054  
 fructose-bisphosphate aldolase (EC 4.1.2.13) III - humans (Fusarium sporotrichioides)  
 C:Species: Fusarium sporotrichioides  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0054  
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Gene, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, October 1994  
 A:Description: Mutational and structural analysis of Rhizobium loti modulation genes.  
 A:Reference number: FA0053  
 A:Accession: FA0054  
 A:Molecule type: DNA  
 A:Residues: 1-15 <SCO>  
 A:Cross-references: EMBL:X65620; NID:q46240; PILE:FAA15674; PILE:q290061; PILE:q160622  
 C:Genetics:  
 C:Gene: noda

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 RKG 6  
 III  
 DB 10 RKG 12

RESULT 34  
 FA0053  
 fructose-bisphosphate aldolase (EC 4.1.2.13) III - humans (Fusarium sporotrichioides)  
 C:Species: Fusarium sporotrichioides  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0053  
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Gene, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
 A:Reference number: FA0052  
 A:Accession: FA0053  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: aldohyde-lyase; carbon-carbon lyase

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 RKG 6  
 III  
 DB 10 RKG 12

RESULT 35

PC4131  
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)  
C:Species: Pseudomonas aeruginosa  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: PC4131  
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.  
Gene 167, 87-91, 1995  
A:Title: Sequencing and characterization of the downstream region of the genes encoding  
y for biosynthesis of heme d1.  
A:Reference number: JC4552; MUID:96144254; PMID:8566817  
A:Accession: PC4131  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-8 <KAW>  
A:Cross-references: DDBJ:D50473; NID:q1217594  
A:Note: this ORF is not annotated in GenBank entry PSN1FC, release 114.0

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SR 4  
DB 5 SR 6

RESULT 36  
S37141  
IPSA protein - Erwinia chrysanthemi  
C:Species: Erwinia chrysanthemi  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S37141  
R:Douillie, A.; Toussaint, A.; Faelen, M.  
submitted to the EMBL Data Library, August 1993  
A:Description: Identification of the integration host factor genes of E. chrysanthemi.  
A:Reference number: S37139  
A:Accession: S37141  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-8 <DOU>  
A:Cross-references: EMBL:X74750; NID:q394669; PIDN:CAA52769.1; PDB:58138

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KS 3  
DB 3 KS 4

RESULT 37  
S63493  
dissimilatory sulfite reductase gamma chain, membrane bound and soluble (result of  
C:Species: Desulfovibrio desulfuricans  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C:Accession: S63493; S63494  
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Krocsek, F.M.E.  
Eur. J. Biochem. 233, 873-879, 1995  
A:Title: Molecular properties of the dissimilatory sulfite reductase from  
A:Reference number: S63489; MUID:96085152; PMID:8542854  
A:Accession: S63493  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <STE>  
A:Accession: S63494  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <ST2>

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Query Match: 18.2%; Score 2; Pos 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2; 40-05;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SR 4  
 II  
 DB 1 SR 2

RESULT 41  
 JS0315  
 Leucokinin V - Madeira cockroach  
 C:Species: Leucophaea maderae (Madeira cockroach)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text change 20-Jun-2000  
 C:Accession: JS0315  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A:Title: Isolation, primary structure, and synthesis of leucokinin V and VII from cockroach  
 A:Reference number: JS0315  
 A:Accession: JS0315  
 A:Molecule type: protein  
 A:Residues: 1-8 <HQL>  
 C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulates contractile and  
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide  
 C:Keywords: amidated carboxyl end (Gly) #status experimental  
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match: 18.2%; Score 2; Pos 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2; 40-05;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SS 9  
 II  
 DB 5 SS 6

RESULT 42  
 JS0316  
 Leucokinin VI - Madeira cockroach  
 C:Species: Leucophaea maderae (Madeira cockroach)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text change 20-Jun-2000  
 C:Accession: JS0316  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A:Title: Isolation, primary structure, and synthesis of leucokinin V and VII from cockroach  
 A:Reference number: JS0315  
 A:Accession: JS0316  
 A:Molecule type: protein  
 A:Residues: 1-8 <HQL>  
 C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulates contractile and  
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match: 18.2%; Score 2; Pos 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2; 40-05;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SS 9  
 II  
 DB 2 SS 3

RESULT 43  
 JS0317  
 Leucokinin VII - Madeira cockroach  
 C:Species: Leucophaea maderae (Madeira cockroach)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text change 20-Jun-2000  
 C:Accession: JS0317  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 31-34, 1987  
 A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII from cockroach  
 A:Reference number: JS0317

C:Accession: I48934  
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, K.; Maeyaki, Y.; Nabeshi, I.; Mann, Genome 5, 349-355, 1994  
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR  
 A:Reference number: I48934; MCID:94319082; PMID:8043449  
 A:Accession: I48934  
 A>Status: preliminary; translated from GR/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <RES>  
 A:Cross-references: EMBL:005691; NID:q457610; PFIN:AABG462.1; PID:q44823  
 Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AK 2  
 Db 7 AK 8

## RESULT 47

PT0595  
 T-cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 40-May-1997  
 C:Accession: PT0595  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
 A:Reference number: PT0509; MUID:91277601; PMID:1711568  
 A:Accession: PT0595  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RES>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SS 9  
 Db 2 SS 3

## RESULT 48

PT0627  
 T-cell receptor beta chain V-D-J region (100-28) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 40-May-1997  
 C:Accession: PT0627  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
 A:Reference number: PT0509; MUID:91277601; PMID:1711568  
 A:Accession: PT0627  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RES>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SS 9  
 Db 2 SS 3

## RESULT 49

I48934  
 T-cell receptor beta chain V-D-J region (100-28) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 40-May-1997  
 C:Accession: I48934  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
 A:Reference number: PT0509; MUID:91277601; PMID:1711568  
 A:Accession: PT0627  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RES>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SS 9  
 Db 2 SS 3

## RESULT 50

PT0522  
 T-cell receptor beta chain V-D-J region (100-41) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 40-May-1997  
 C:Accession: PT0522  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
 A:Reference number: PT0509; MUID:91277601; PMID:1711568  
 A:Accession: PT0522  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RES>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SS 9  
 Db 2 SS 3

Search completed: 09-Sep-2003 11:07:07 AM  
 Job 1386 1 12.40 seconds

GenCore version 5.1.6  
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OM protein - protein search, using sw model;

Run on: September 30, 2003, 10:07:04 : Search time: 6.25 seconds

(without alignments)  
82.767 Million cell updates/sec

**Title:** US-09-787-443-21

perfect score: 11

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scoring table: OLIGO
Gapop 60.0 . Gapext 60.0
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Searched: 127863 seqs, 47026705 residues

Word size : 0

Parameter	Value
Total number of hits satisfying chosen parameters	797

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt\_41:•

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	3	27.3	8	1	RS7_MYCIT	P34564	mycobacteri
2	3	27.3	9	1	THVF_PIG	P31255	sus scrofa
3	3	27.3	11	1	Q2QA_COMTE	PR0464	comamonas
4	3	27.3	13	1	CPL_APLCA	Q10998	aplysia cal
5	3	27.3	13	1	NEUT_CAVPO	P32560	cavia porce
6	3	27.3	15	1	48KD_BACCE	PR0173	bacillus ce
7	2	18.2	8	1	ACT_CARMA	PR0709	carcinus ma
8	2	18.2	8	1	ALL3_CYDPA	PR2154	cydia pomon
9	2	18.2	8	1	CAD1_ENTFO	P34268	enterococu
10	2	18.2	8	1	CLP_THICU	PR0486	thiobacilli
11	2	18.2	8	1	LCK1_LEUMA	P21140	leucophaea
12	2	18.2	8	1	LCK2_LEUMA	P21141	leucophaea
13	2	18.2	8	1	LCK3_LEUMA	P21142	leucophaea
14	2	18.2	8	1	LCK5_LEUMA	P19987	leucophaea
15	2	18.2	8	1	LCK6_LEUMA	P19568	leucophaea
16	2	18.2	8	1	LCK7_LEUMA	P19589	leucophaea
17	2	18.2	8	1	NS3_MYCJU	PR1152	mycobacteri
18	2	18.2	8	1	RS1_FHNGH	P19985	erwinia chr
19	2	18.2	9	1	CONC_CONGE	P15486	corvus georg
20	2	18.2	9	1	FARS_PENMO	PR1320	penaeus mon
21	2	18.2	9	1	FIBB_MACFU	P19145	macaca fusc
22	2	18.2	9	1	LPCA_STAAU	P13984	staphylococ
23	2	18.2	9	1	NEF_HV128	P12481	human immun
24	2	18.2	9	1	PTSP_BOMMO	PR2003	bombyx mori
25	2	18.2	9	1	RT33_BOVIN	PR2526	bos taurus
26	2	18.2	9	1	SAMP_MUSCA	P19095	musculus ca
27	2	18.2	9	1	ULAK_MOUSE	P99031	mus muscu
28	2	18.2	9	1	UPAT_HUMAN	P30093	homo sapien
29	2	18.2	10	1	AH3_PRUSE	P29261	prunus sero
30	2	18.2	10	1	AKHX_LOCMI	PR1626	locusta mig
31	2	18.2	10	1	ANGT_CHICK	PR0108	gallus gall
32	2	18.2	10	1	COXA_ONCMY	PR0128	oncorhynch
33	2	18.2	10	1	COXQ_SHEEP	PR0337	ovis aries

107	2	18.2	13	1	BRK_PARID	P42717	parapolybia	180	2	18.2	15	1	RNS	USSE	P59034	psuedoaria
108	2	18.2	13	1	CD71_LITEW	P42051	litoria cwi	181	2	18.2	15	1	USSE	USSE	P61420	solium fol
109	2	18.2	13	1	DM0_CANFA	P45818	canis famli	182	2	18.2	15	1	USSE	USSE	P61420	solium fol
110	2	18.2	13	1	CHP_PARID	P42718	parapolybia	183	2	18.2	15	1	USSE	USSE	P61420	solium fol
111	2	18.2	13	1	CRBL_VESCR	P17233	vespa anali	184	2	18.2	15	1	USSE	USSE	P61420	solium fol
112	2	18.2	13	1	CRBL_VESCR	P01518	vespa crabr	185	2	18.2	15	1	USSE	USSE	P61420	solium fol
113	2	18.2	13	1	CRBL_VESCR	P17235	vespa lew	186	2	18.2	15	1	USSE	USSE	P61420	solium fol
114	2	18.2	13	1	CRBL_VESCR	P17234	vespa xanth	187	2	18.2	15	1	USSE	USSE	P61420	solium fol
115	2	18.2	13	1	EP65_HUMAN	P54963	homo sapien	188	2	18.2	15	1	USSE	USSE	P61420	solium fol
116	2	18.2	13	1	LPAA_PORGI	P41411	porphyromon	189	2	18.2	15	1	USSE	USSE	P61420	solium fol
117	2	18.2	13	1	NO40_PEA	P55959	pisum sativ	190	2	18.2	15	1	USSE	USSE	P61420	solium fol
118	2	18.2	13	1	NO40_VICSA	P55961	vicia sativ	191	2	18.2	15	1	USSE	USSE	P61420	solium fol
119	2	18.2	13	1	NP1_LYMST	P40176	lymaea sta	192	2	18.2	15	1	USSE	USSE	P61420	solium fol
120	2	18.2	13	1	NP2_LYMST	P40179	lymaea sta	193	2	18.2	15	1	USSE	USSE	P61420	solium fol
121	2	18.2	13	1	NP4_LYMST	P40181	lymaea sta	194	2	18.2	15	1	USSE	USSE	P61420	solium fol
122	2	18.2	13	1	NP5_LYMST	P40182	lymaea sta	195	2	18.2	15	1	USSE	USSE	P61420	solium fol
123	2	18.2	13	1	SA2A_ONCMY	P42238	oncorhynch	196	2	18.2	15	1	USSE	USSE	P61420	solium fol
124	2	18.2	13	1	SA2B_ONCMY	P42239	oncorhynch	197	2	18.2	15	1	USSE	USSE	P61420	solium fol
125	2	18.2	13	1	SODM_CANFA	P54712	canis famli	198	2	18.2	15	1	USSE	USSE	P61420	solium fol
126	2	18.2	13	1	TAL3_TREME	P41476	tremella me	199	2	18.2	15	1	USSE	USSE	P61420	solium fol
127	2	18.2	13	1	TEJA_RANJA	P43407	rana tapom	200	2	18.2	15	1	USSE	USSE	P61420	solium fol
128	2	18.2	13	1	TEMD_RANTE	P56918	rana temp	201	2	18.2	15	1	USSE	USSE	P61420	solium fol
129	2	18.2	13	1	TEMD_RANTE	P56919	rana temp	202	2	18.2	15	1	USSE	USSE	P61420	solium fol
130	2	18.2	13	1	TEMD_RANTE	P56920	rana temp	203	2	18.2	15	1	USSE	USSE	P61420	solium fol
131	2	18.2	13	1	UHAL_HUMAN	P40528	homo sapien	204	2	18.2	15	1	USSE	USSE	P61420	solium fol
132	2	18.2	13	1	YPE2_LACLC	P42021	lactococcus	205	2	18.2	15	1	USSE	USSE	P61420	solium fol
133	2	18.2	14	1	ALYT_ALYOB	P08944	alytes obs	206	2	18.2	15	1	USSE	USSE	P61420	solium fol
134	2	18.2	14	1	ATP6_SPIOG	P40386	spinoacia ci	207	2	18.2	15	1	USSE	USSE	P61420	solium fol
135	2	18.2	14	1	CAL1_CALG1	P20728	calotropis	208	2	18.2	15	1	USSE	USSE	P61420	solium fol
136	2	18.2	14	1	CRBL_VESCR	P17236	vespa orien	209	2	18.2	15	1	USSE	USSE	P61420	solium fol
137	2	18.2	14	1	GLGS_SPIOG	P55235	spinoacia ci	210	2	18.2	15	1	USSE	USSE	P61420	solium fol
138	2	18.2	14	1	GLPK_STRGR	P25815	streptomyce	211	2	18.2	15	1	USSE	USSE	P61420	solium fol
139	2	18.2	14	1	HCYA_MEGCR	P15983	megathura c	212	2	18.2	15	1	USSE	USSE	P61420	solium fol
140	2	18.2	14	1	HY14_PIG	P01155	sus scrofa	213	2	18.2	15	1	USSE	USSE	P61420	solium fol
141	2	18.2	14	1	LPW_ECOLI	P03053	escherichia	214	2	18.2	15	1	USSE	USSE	P61420	solium fol
142	2	18.2	14	1	MAST_VESBA	P21654	vespa basal	215	2	18.2	15	1	USSE	USSE	P61420	solium fol
143	2	18.2	14	1	MAST_VESCR	P21516	vespa crabr	216	2	18.2	15	1	USSE	USSE	P61420	solium fol
144	2	18.2	14	1	MAST_VESIE	P21514	vespa lew	217	2	18.2	15	1	USSE	USSE	P61420	solium fol
145	2	18.2	14	1	MAST_VESMA	P4205	vespa randa	218	2	18.2	15	1	USSE	USSE	P61420	solium fol
146	2	18.2	14	1	MAST_VESKA	P4205	vespa randa	219	2	18.2	15	1	USSE	USSE	P61420	solium fol
147	2	18.2	14	1	PSAG_CUCSA	P42047	cucumis sat	220	2	18.2	15	1	USSE	USSE	P61420	solium fol
148	2	18.2	14	1	RS19_CLOPP	P46228	clover prol	221	2	18.2	15	1	USSE	USSE	P61420	solium fol
149	2	18.2	14	1	RS19_LOWHP	P46228	clover prol	222	2	18.2	15	1	USSE	USSE	P61420	solium fol
150	2	18.2	14	1	SKK3_LEIQU	P45561	leiurus gal	223	2	18.2	15	1	USSE	USSE	P61420	solium fol
151	2	18.2	14	1	TAT_HVLZ8	P12511	human immun	224	2	18.2	15	1	USSE	USSE	P61420	solium fol
152	2	18.2	14	1	TKN1_SCHGR	P42470	schistocerc	225	2	18.2	15	1	USSE	USSE	P61420	solium fol
153	2	18.2	14	1	TKNM_RANNA	P40551	rana rargar	226	2	18.2	15	1	USSE	USSE	P61420	solium fol
154	2	18.2	14	1	UHA2_CANFA	P55506	canis famli	227	2	18.2	15	1	USSE	USSE	P61420	solium fol
155	2	18.2	14	1	UN07_CLOPA	P1152	clostridium	228	2	18.2	15	1	USSE	USSE	P61420	solium fol
156	2	18.2	14	1	UN37_CLOPA	P1158	clostridium	229	2	18.2	15	1	USSE	USSE	P61420	solium fol
157	2	18.2	14	1	UN46_CLOPA	P1162	clostridium	230	2	18.2	15	1	USSE	USSE	P61420	solium fol
158	2	18.2	15	1	ACT_PINPS	P41585	pinus pinas	231	2	18.2	15	1	USSE	USSE	P61420	solium fol
159	2	18.2	15	1	AH2_PROSE	P29260	pinus sero	232	2	18.2	15	1	USSE	USSE	P61420	solium fol
160	2	18.2	15	1	ASPL_LACSN	P42646	lactobacilli	233	2	18.2	15	1	USSE	USSE	P61420	solium fol
161	2	18.2	15	1	ATP2_SPIOG	P40386	spinoacia ci	234	2	18.2	15	1	USSE	USSE	P61420	solium fol
162	2	18.2	15	1	CDN2_LITGI	P56247	litoria gil	235	2	18.2	15	1	USSE	USSE	P61420	solium fol
163	2	18.2	15	1	CDN3_LITGI	P56248	litoria gil	236	2	18.2	15	1	USSE	USSE	P61420	solium fol
164	2	18.2	15	1	CDN4_LITCE	P42073	litoria oae	237	2	18.2	15	1	USSE	USSE	P61420	solium fol
165	2	18.2	15	1	CDN5_LITCE	P42073	litoria oae	238	2	18.2	15	1	USSE	USSE	P61420	solium fol
166	2	18.2	15	1	CDN6_LITCE	P42073	litoria cap	239	2	18.2	15	1	USSE	USSE	P61420	solium fol
167	2	18.2	15	1	CH11_PEA	P21225	pisum sativ	240	2	18.2	15	1	USSE	USSE	P61420	solium fol
168	2	18.2	15	1	CKX_WHEAT	P58763	tritium ae	241	2	18.2	15	1	USSE	USSE	P61420	solium fol
169	2	18.2	15	1	COX1_THUOB	P40978	thymus obo	242	2	18.2	15	1	USSE	USSE	P61420	solium fol
170	2	18.2	15	1	CX3B_GUNGU	P58842	canus querc	243	2	18.2	15	1	USSE	USSE	P61420	solium fol
171	2	18.2	15	1	CYSK_CLOPA	P41340	clostridium	244	2	18.2	15	1	USSE	USSE	P61420	solium fol
172	2	18.2	15	1	DCMM_PSECH	P14917	psuedomonas	245	2	18.2	15	1	USSE	USSE	P61420	solium fol
173	2	18.2	15	1	EFIA_MICCR	P41266	microplitis	246	2	18.2	15	1	USSE	USSE	P61420	solium fol
174	2	18.2	15	1	FIRA_ANAPL	P13801	anas platyr	247	2	18.2	15	1	USSE	USSE	P61420	solium fol
175	2	18.2	15	1	FRF2_LITIN	P42022	litoria fol	248	2	18.2	15	1	USSE	USSE	P61420	solium fol
176	2	18.2	15	1	HS11_PINPS	P11083	pinus pinas	249	2	18.2	15	1	USSE	USSE	P61420	solium fol
177	2	18.2	15	1	IRBP_CRISP	P12665	crispidae	250	2	18.2	15	1	USSE	USSE	P61420	solium fol
178	2	18.2	15	1	MCRA_METTE	P22948	methanococ	251	2	18.2	15	1	USSE	USSE	P61420	solium fol
179	2	18.2	15	1	MM01_RAY	P81553	rattus norv	252	2	18.2	15	1	USSE	USSE	P61420	solium fol







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DR HAMAP: MF_00480: -: 1.
DR InterPro: IPR000235: Ribosomal_S7
DR PROSITE: PS00052: RIBOSOMAL_S7: PARTIAL.
KW Ribosomal protein; RNA-binding; tRNA-binding; tRNA binding.
FT INIT_MET 0 BY SIMILARITY.
FT NON_TER 8
SQ SEQUENCE 8 AA: 850 MW: 63276DC768732417 CRC64:
Query Match 27.3%: Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKG 6
DB 2 RKG 4

RESULT 2
THYF_PIG
ID THYF_PIG STANDARD: PRT; 9 AA.
AC P01255:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;
OX NCBI_TaxID:9823;
RN [1]
RP SEQUENCE.
RX MEDLINE:78026571; PubMed-914862;
RA Pleau J.-M., Dardenne M., Blouquin Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
RL from pig serum. II. Amino acid sequence."
RL J. Biol. Chem. 252:8045-8047(1977).
CC -I- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
DR ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR: A01523; YFPG.
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1
SQ SEQUENCE 9 AA: 876 MW: D500B87866C5B33D CRC64:

Query Match 27.3%: Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKS 3
DB 2 AKS 4

RESULT 3
Q2OA_COMTE
ID Q2OA_COMTE STANDARD: PRT; 1; AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinolone 2-oxido-reductase, alpha chain (Er 1, 5, 9, 17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID:285;
RN [1]
RP SEQUENCE.
RC STRAIN-63;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinolone 2-oxido-reductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation."
RL Eur. J. Biochem. 232:536-544(1995).

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QY 1 AKS 3
DB 1 AKS 4

RESULT 4
PCT_APLA
ID PCT_APLA STANDARD: PRT; 13 AA.
AC Q10909:
DT 01-OCT-1996 (Rel. 41, Created)
DT 01-OCT-1996 (Rel. 41, Last sequence update)
DT 01-OCT-1996 (Rel. 41, Last annotation update)
DE Corporal protein 1 (P1).
OS Aplysia californica (California sea slug).
CC Eukaryota; Metazoa; Mollusca; Gastropoda; Cephalopoda;
CC Apusobranchia; Bellerophonidae; Eutherozoa; Mollusca;
CC Aplysiidae; Aplysiidae; Aplysia;
OX NCBI_TaxID:6509;
RN [1]
RP SEQUENCE.
RX MEDLINE:9706171; PubMed-864266;
RA Phares G.A., Lloyd F.E.;
RT "Partial cDNA, primary structure, and function, localization of
RL corpora protein 1 from Aplysia."
RL Biophys. J. 76:763-765(1999).
CC -I- FUNCTION: MAY FUNCTION AS A PEPTIDE TRANSMITTER.
CC -I- GUSSE SPECIFICITY: PCTA PROBABLY IN THE PERIPHERAL AND PERI-
CC SANGUIN.
SQ SEQUENCE 13 AA: 1344 MW: 9160682967005 CRC64:

Query Match 27.3%: Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 0 RSG 13
DB 0 RSG 13

RESULT 5
MEDT_PAVI
ID MEDT_PAVI STANDARD: PRT; 15 AA.
AC P82571:
DT 01-OCT-1994 (Rel. 33, Created)
DT 01-OCT-1994 (Rel. 33, Last sequence update)
DT 28-FEB-2004 (Rel. 41, Last annotation update)
DE Neurotensin (NT).
OS Rattus norvegicus (Norway rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Hystricomorpha; Caviidae; Cavia;
OX NCBI_TaxID:10141;
RN [1]
RP SEQUENCE.

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RC TISSUE=Small intestine;  
 RX MEDLINE=86248085; PubMed=308775;  
 RA Shaw C., Thim L., Conlon J.M.;  
 RT \* [Ser7]neurotensin: isolation from guinea pig intestine.\*;  
 RL FEBS Lett. 202:187-192(1986).  
 CC -!- FUNCTION: Smooth muscle-contracting peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.  
 DR PIR: A53608; A53608.  
 KW Vasoactive; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 13 AA: 1680 MW: 4C8314644C4115B1 CRC64:

Query Match 27.3% Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSR 4  
 Db 6 KSR 8

## RESULT 6

48KD\_BACCE  
 ID 48KD\_BACCE STANDARD: PRT: 15 AA.  
 AC P80173;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-OCT-1993 (Rel. 27, Last annotation update)  
 DE 48 kDa protein (Fragment).  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=1210-88;  
 RX MEDLINE=93307641; PubMed=8319899;  
 RA Granum P.E., Nissen H.;  
 RT \*Sphingomyelinase is part of the 'enterotoxin complex' produced by  
 RT Bacillus cereus.\*;  
 RL FEMS Microbiol. Lett. 110:97-100(1993).  
 CC -!- FUNCTION: NOT KNOWN, PART OF THE ENTEROTOXIN COMPLEX.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA: 1644 MW: 88442960R4H0FR62 CRC64:

Query Match 27.3% Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10  
 Db 11 SSL 13

## RESULT 7

ACT\_CARMA  
 ID ACT\_CARMA STANDARD: PRT: 8 AA.  
 AC P80709;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Actin (Fragment).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
 RA Baghdassarian D.;  
 RT \*A transaldolase. An enzyme implicated in crab steroidogenesis.\*;  
 RL Endocrine 5:23-32(1996).

CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
 IN VARIOUS TYPES OF CELL MOTILITY AND ARE BIOCHEMICALLY EXPRESSED  
 IN ALL EUKARYOTIC CELLS.  
 CC -!- SUBCELLULAR LOCATION: Cytoskeleton.  
 CC -!- MISCELLANEOUS: ON THE EDGE OF THE DETERMINED PI OF THIS PROTEIN IS  
 6.8. ITS MW IS 46 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.  
 DR InterPro: IPR004911; Actin-like.  
 DR InterPro: IPR004911; Actin-like.  
 DR PRESITE: PS04061; ACTINS 1; PARTIAL.  
 DR PRESITE: PS04121; ACTINS 2; PARTIAL.  
 DR PRESITE: PS11521; ACTINS ACT-LIKE; PARTIAL.  
 KW Structural protein.  
 FT K\_NTER 1 1  
 FT K\_NTER 2 2  
 SQ SEQUENCE 8 AA: 926 MW: 11490ANDAAEA5 CRC64:

Query Match 100% Score 8; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.0e-05;  
 Matches 8; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSL 3  
 Db 7 SSL 6

## RESULT 8

ALLA\_CYDIN  
 ID ALLA\_CYDIN STANDARD: PRT: 4 AA.  
 AC P82154;  
 DT 30-MAY-2000 (Rel. 34, Created)  
 DT 30-MAY-2000 (Rel. 34, Last sequence update)  
 DT 30-MAY-2000 (Rel. 34, Last annotation update)  
 DE Cydostatin A.  
 OS Cydium pomosella (Green sea slug).  
 OC Eukaryota; Metazoa; Actinoptera; Insecta; Lepidoptera;  
 OC Noctuidae; Eupitheciinae; Cydostatininae; Cydostatininae;  
 OX NCBI\_TaxID=4260;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Leaf.  
 EX MEDLINE=9455474; PubMed=9455474;  
 RA Davey M., East P.D., Harpelle A.;  
 RT \*Lepidopteran peptides of the cydostatin superfamily.\*;  
 RL Peptides 14:101-104(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLA CYDIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA: 926 MW: 92674DDA64774.5 CRC64:

Query Match 100% Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.0e-05;  
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSL 4  
 Db 1 SSL 2

## RESULT 9

CA31\_ENTFA  
 ID CA31\_ENTFA STANDARD: PRT: 8 AA.  
 AC L13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone (All).  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Bacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1451;  
 RN [1]

RP SEQUENCE  
 RX MEDLINE=85051889; PubMed=6437872;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that  
 induces plasmid transfer in *Streptococcus faecalis*.";  
 RL FEBS Lett. 178:97-100(1984).  
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC PHEROMONE.  
 KW HEMOLYSIN PLASMID PAD1.  
 SQ SEQUENCE 8 AA: 819 MW: 047DD732C735B9C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SL 10  
 DB 3 SL 4

## RESULT 10

CLP\_THICU STANDARD; PRT: 8 AA.  
 AC P80488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Chemolithotroph-specific protein (Fragment).  
 OS Thiobacillus cuprinus.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Thiomonas.  
 OX NCBI\_TaxID=36860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 5494;  
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED  
 CC CHEMOLITHOTROPHICALLY.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 785 MW: 91487B06DDC2D75D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GN 7  
 DB 7 GN 8

## RESULT 11

ICK1\_LEUMA STANDARD; PRT: 8 AA.  
 AC P21140;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin I (L-1).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two neuropeptides  
 RT from *Leucophaea maderae*: members of a new family of  
 RT Cephalomyotrophins.";  
 RL Comp. Biochem. Physiol. 84C:205-211(1986).

CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTIONS  
 CC OF MUSCLES AND EPITHELIUM (HINDGUT).  
 KW Neuropeptide; Amidation;  
 FT MOD\_RES 8 AA: 804 MW: 004050P437476A CRC64;  
 SQ SEQUENCE 8 AA: 804 MW: 004050P437476A CRC64;

Query Match 14.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NS 6  
 DB 5 NS 7

## RESULT 12

ICK2\_LEUMA STANDARD; PRT: 8 AA.  
 AC P21141;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin I (L-1).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two neuropeptides  
 RT from *Leucophaea maderae*: members of a new family of  
 RT Cephalomyotrophins".  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTIONS  
 CC OF MUSCLES AND EPITHELIUM (HINDGUT).  
 KW Neuropeptide; Amidation;  
 FT MOD\_RES 8 AA: 802 MW: 004050P437601A CRC64;

Query Match 14.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SS 6  
 DB 5 SS 7

## RESULT 13

ICK3\_LEUMA STANDARD; PRT: 8 AA.  
 AC P21142;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin I (L-1).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two additional new peptides  
 RT from *Leucophaea maderae*: members of a new family of  
 RT Cephalomyotrophins".





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QY      9 SL 10
DB      4 SL 5

RESULT 21
LPCA_STA0U
ID LPCA_STA0U      STANDARD:      PRI:      9 AA.
AC P36884:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OG Plasmid pSC56, Plasmid pSC57, Plasmid pUB112, and Plasmid p136m1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=436; PLASMID=pSC57;
RX MEDLINE=92027652; PubMed=1929326;
RA Schwarz S., Cardoso M.;
RT *Nucleotide sequence and phylogeny of a chloramphenicol

QY      9 SL 10
DB      4 SL 5

RESULT 22
LPCA_STA0U
ID LPCA_STA0U      STANDARD:      PRI:      9 AA.
AC P36884:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OG Plasmid pSC56, Plasmid pSC57, Plasmid pUB112, and Plasmid p136m1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=436; PLASMID=pSC57;
RX MEDLINE=92027652; PubMed=1929326;
RA Schwarz S., Cardoso M.;
RT *Nucleotide sequence and phylogeny of a chloramphenicol

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QY      9 SL 10
DB      4 SL 5

RESULT 23
LPCA_STA0U
ID LPCA_STA0U      STANDARD:      PRI:      9 AA.
AC P36884:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OG Plasmid pSC56, Plasmid pSC57, Plasmid pUB112, and Plasmid p136m1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=436; PLASMID=pSC57;
RX MEDLINE=92027652; PubMed=1929326;
RA Schwarz S., Cardoso M.;
RT *Nucleotide sequence and phylogeny of a chloramphenicol

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FT DOMAIN 1 >9 PENTAXIN.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA: 965 MW; D05B5735B386769 CRG64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1 to 05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 KS 3  
 Db 5 KS 6

## RESULT 27

ULAK\_MOUSE STANDARD; PRT; 9 AA.  
 AC P99031;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Unknown protein from 2D-page of liver tissue (Spec. 28 00.41D)  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yee J.-X.,  
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser B.F.,  
 RA Cowthorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P.I. OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.  
 DR SWISS-2DPAGE: P99031; MOUSE.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA: 1106 MW; E1E842C1240B145A CRG64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1 to 05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 RK 5  
 Db 5 RK 6

## RESULT 28

UPA7\_HUMAN STANDARD; PRT; 9 AA.  
 AC P30093;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spec. 1d) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Xavier F., Pasquari C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RL "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P.I. OF THIS UNKNOWN  
 CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.  
 DR SWISS-2DPAGE: P30093; HUMAN.  
 FT NON\_TER 1

FT UNSTORE 5  
 FT NON\_TER 5  
 SQ SEQUENCE 9 AA: 1443 MW; 772727 CRG64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1 to 05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 KS 3  
 Db 5 KS 6

## RESULT 29

AB\_CROUSE STANDARD; PRT; 15 AA.  
 AC P29261;  
 DT 01-DEC-1993 (Rel. 34, Created)  
 DT 01-DEC-1993 (Rel. 34, Last sequence update)  
 DT 01-NOV-1993 (Rel. 33, Last annotation update)  
 DE Amyloid-like protein from liver tissue (Spec. 11 117) (Amyloid-like protein)  
 DE (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Vertebrata; Mammalia; Rodentia; Muridae; Muridae; Mus.  
 OC Spermophyta; Magnoliopsida; Euphorbiaceae; Euphorbiaceae; Euphorbiaceae;  
 OC Euphorbia; Euphorbia; Euphorbia; Euphorbia; Euphorbia; Euphorbia;  
 OX NCBI\_TaxID=10107;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yee J.-X.,  
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser B.F.,  
 RA Cowthorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P.I. OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.  
 DR SWISS-2DPAGE: P99031; MOUSE.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA: 1106 MW; E1E842C1240B145A CRG64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1 to 05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 KS 3  
 Db 5 KS 6

## RESULT 30

AKKX\_MOUSE STANDARD; PRT; 15 AA.  
 AC P29261;  
 DT 01-DEC-1993 (Rel. 34, Created)  
 DT 01-DEC-1993 (Rel. 34, Last sequence update)  
 DE Amyloid-like protein from liver tissue (Spec. 11 117) (Amyloid-like protein)  
 DE (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Vertebrata; Mammalia; Rodentia; Muridae; Muridae; Mus.  
 OC Spermophyta; Magnoliopsida; Euphorbiaceae; Euphorbiaceae; Euphorbiaceae;  
 OC Euphorbia; Euphorbia; Euphorbia; Euphorbia; Euphorbia; Euphorbia;  
 OX NCBI\_TaxID=10107;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yee J.-X.,  
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser B.F.,  
 RA Cowthorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P.I. OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.  
 DR SWISS-2DPAGE: P99031; MOUSE.  
 FT NON\_TER 9

CC INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HATH / HPCB FAMILY.  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1222 MW; 81BF67AB415B9D1 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SR 4  
 DB 5 SR 6

RESULT 31  
 ANGT\_CHICK STANDARD; PRI: 10 AA.  
 ID ANGT\_CHICK  
 AC P01618;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1,7]-angiotensin I); (Ang I) (Fragment).  
 DE (Fragment).  
 GN AGT OR SERPIN8.  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 CC NCBI\_TaxID=9031, 93934;  
 RN [1];  
 RP SEQUENCE.  
 RC SPECIES=Chicken; PubMed=4361802;  
 RX MEDLINE=74127845; PubMed=4361802;  
 RA Nakayama T., Nakajima T., Sakabe H.;  
 RT "Comparative studies on angiotensins. 3. Structure of [owl  
 RT angiotensin and its identification by DNS-method.;"  
 RL Chem. Pharm. Bull. 21:2085-2087(1973).  
 RP [2];  
 RP SEQUENCE.  
 RC SPECIES=C. japonica;  
 RX MEDLINE=90284684; PubMed=2191893;  
 RA Takai Y., Hasegawa Y.;  
 RT "Vasopressor and depressor effects of native angiotensins and  
 RT inhibition of these effects in the Japanese quail.;"  
 RL Gen. Comp. Endocrinol. 79:12-22(1990).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN I, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR: A60624; A60624.  
 DR PIR: A50917; A50917.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SR 10  
 DB 4 SR 10  
 RESULT 32  
 COXA\_ONMY STANDARD; PRI: 1 AA.  
 ID COXA\_ONMY  
 AC P83328;  
 DT 01-OCT-1994 (Rel. 01, Created)  
 DT 01-OCT-1994 (Rel. 01, Last sequence update)  
 DT 01-MAY-2000 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase (EC 1.1.3.1) (Enzyme)  
 DE Cytochrome c oxidase (EC 1.1.3.1) (Enzyme)  
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neogastropoda; Euteleostomi; Euteleostomi;  
 CC Percaridactylia; Salmoniformes; Salmoniformes; Salmoniformes;  
 CC NCBI\_TaxID=5227;  
 RN [1];  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=94101010; PubMed=94101010;  
 RA Frouin R., Kadanech B.;  
 RT "Identification of cytochrome c oxidase (EC 1.1.3.1) as a component of the  
 RT cytochrome c oxidase (EC 1.1.3.1) (Enzyme) from rainbow trout.;"  
 RL Eur. J. Biochem. 221:1111-1117(1994).  
 CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
 CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT  
 CC CHAINS. CATALYTIC ACTIVITY: 4 tetrahydrochrome c + O(2) -> 4 tetrahydrochrome  
 CC c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrion; Inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
 DR PIR: S43625; S43625;  
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane;  
 ET NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1344 MW; C5C6Q4A50254D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2  
 DB 3 AK 4

RESULT 33  
 COXQ\_SHEEP STANDARD; PRI: 10 AA.  
 ID COXQ\_SHEEP  
 AC P83337;  
 DT 01-OCT-1994 (Rel. 01, Created)  
 DT 01-OCT-1994 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase (EC 1.1.3.1) (Enzyme)  
 DE (Fragment).  
 CC Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Vitis  
 CC NCBI\_TaxID=9943;  
 RN [1];  
 RP SEQUENCE.  
 RC TISSUE=Heart; and Liver.  
 RX MEDLINE=94101010; PubMed=94101010;  
 RA Frouin R., Kadanech B.;  
 RT "Identification of cytochrome c oxidase (EC 1.1.3.1) as a component of the  
 RT cytochrome c oxidase (EC 1.1.3.1) (Enzyme) from rainbow trout.;"  
 RL Eur. J. Biochem. 221:1111-1117(1994).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 tetrahydrochrome c + O(2) -> 4 tetrahydrochrome  
 CC c + 2 H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.



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GS09_BACSU
ID GS09_BACSU STANDARD: PRT: 10 AA
AC P80243:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE General stress protein 9 (GSP9) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1].
RP SEQUENCE.
RC STRAIN=168 / 1558;
RX MEDLINE=94282319; PubMed=8012595;
RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,
  Schmid R., Mach H., Hecker M.
RT "Analysis of the induction of general stress proteins of Bacillus
  subtilis."
RL Microbiology 140:741-752(1994).
CC -1- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, DRYNESS
  LIMITATION AND OXYGEN LIMITATION.
CC -1- CAUTION: Could not be found in the genome of B.subtilis 168.
KW Heat shock.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1168 MW: 997664425EAZ00A CR664;

Query Match 18.2% Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SR 4
   11
DB 1 SR 2

RESULT 39
HTF_HELZE
ID HTF_HELZE STANDARD: PRT: 10 AA.
AC p16353:
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrichalemic hormone (Hez-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Heteroptera.
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Nucleonidea;
OC Noctuidae; Heliothinae; Helicoverpa
OX NCBI_TaxID=7113;
RN [1].
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=88126324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird J.G.,
  Tseng C.M., Zhang Y.S., Hayes D.K.
RT "Isolation and primary structure of a neuropeptide hormone from
  Heliothis zea with hypertrichalemic and adipogenic activities."
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC -1- FUNCTION: HYPERTRICHAEMIC FACTORS ARE NEUROPEPTIDES THAT
  ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH OF INSECTS.
  THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / HCH FAMILY.
DR PIR: A31571;
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH: 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1096 MW: 8E70367865A5B9E1 CR764;

Query Match 18.2% Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 SR 4
   11
DB 1 SR 2

RESULT 40
NSL_MYC29
ID NSL_MYC29 STANDARD: PRT: 10 AA
AC B81143:
DT 15-JUN-1994 (Rel. 38, Created)
DT 15-JUN-1994 (Rel. 38, Last sequence update)
DT 16-JUN-2003 (Rel. 40, Last annotation update)
LE 59 kDa non-specific mycelial protein (Proteinase).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
  Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1774;
RN [1].
RP SEQUENCE.
RC STRAIN H37Rv;

Query Match 18.2% Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 47
TKL4_LOCM1
ID TKL4_LOCM1 STANDARD: PRT: 10 AA.
AC P30250;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin IV (TK-IV).
OS Locustatachykinin (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91219696; PubMed=2132575;
RA Schoofs L., Holman G.M., Hayes T.K., Kechiansky J.P., Nachman P.J.,
RA de Loof A.;
RT "Locustatachykinin III and IV: two additional insect neuropeptides
RT with homology to peptides of the vertebrate tachykinin family."
RL Regul. Pept. 31:199-212(1990).
CC -|- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR: H60073; ECL04M.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1040 MW; 9E52CD71F9C87735 CRC64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9; Reqs:
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SL 10
DB 3 SL 4

RESULT 48
TKNL_SCYCA
ID TKNL_SCYCA STANDARD: PRT: 10 AA.
AC P08608;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Scyllorhinin I.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carharniiformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=66192829; PubMed=2422058;
RA Conlon J.M., Beacon C.F., O'Toole L., Tim L.J.
RA "Scyllorhinin I and II: two novel tachykinins from dogfish
RL (2).
RN [2]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balmont P.J., Conlon J.M.;
RA "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyllorhinus canicula".
RL Eur. J. Biochem. 214:469-474(1993).
CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.

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-|- SUBCELLULAR LOCATION: Secreted.
-|- SIMILARITY: RELATES TO THE TACHYKININ FAMILY.
IR PIR: A24867; A24867.
IR InfoPro: P0802040; Tachykinin I.
IR PROSITE: PS00267; TACHYKININ_1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1040 MW; 160023F9C87735 CRC64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9; Reqs:
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DB 1 AK 2

RESULT 49
TKNP_CHICK
ID TKNP_CHICK STANDARD: PRT: 10 AA.
AC P10853;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurtakinin A (Substance K) (Neurokinin A).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Accipitriformes; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=66242465; PubMed=2474263;
RA Conlon J.M., Katsoulis S., Szemad W.B., Tim L.J.
RA "Substance P and Neurtakinin A from chicken spinal dorsal horn."
RL Regul. Pept. 20:171-180(1988).
CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
-|- SUBCELLULAR LOCATION: Secreted.
-|- SIMILARITY: RELATES TO THE TACHYKININ FAMILY.
IR PIR: JN0024; JN0024.
IR InfoPro: I0002040; Tachykinin.
IR PIR: PF02262; Tachykinin_1.
IR PROSITE: PS00267; TACHYKININ_1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1144 MW; BAC00620CF0FAB17604;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9; Reqs:
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 11
DB 9 AK 11

RESULT 50
TKNR_GNFW
ID TKNR_GNFW STANDARD: PRT: 10 AA.
AC P28590;
DT 01-DEC-1992 (Rel. 23, Created)
DT 01-DEC-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurtakinin A (Substance K) (Neurokinin A).
OS Caracanthus myxus (Rainbow trout) (Salmo gairdneri); and
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei.

```



OC procaranthopterygii; Salmoniformes; Salmonidae; Carangiformes  
 OX NCBI\_TaxID=8022, 8049;  
 RN {}  
 RP SEQUENCE.  
 RC SPECIES=O. mykiss, and G. morhua;  
 RX TISSUE=Brain;  
 MEDLINE=92298992; PubMed=1375687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A related peptides from the brain  
 of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NERVE END-  
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR: S23186; S23186.  
 DR PIR: S23307; S23307.  
 DR InterPro: IP002040; Tachykinin.  
 DR Pfam: PF02202; Tachykinin; 1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION (BY SIMILARITY)  
 SQ SEQUENCE 10 AA: 1145 MW: 13684.62; GFEK440 GSG64;

Query Match 18.28; Score 23.25; Length 16.  
 Best Local Similarity 100.00; Pred. No. 1.7E+00;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0.

QY 7 NS 8  
 II  
 Db 4 NS 5

Search completed: September 30, 2003, 10:26:16  
 Job time : 8.25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model:

Run on: September 30, 2003, 10:07:04 : Search time 31.6667 Seconds  
(without alignments)  
69,639 Million cell updates/sec

Title: US-09-787-443-21

Perfect score: 11

Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4479

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :

SPTREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	14	3 Q8J1G2	Q8J1G2 asl1y1 quos
2	3	27.3	8	2 P77556	P77556 escherichia
3	3	27.3	9	2 Q45852	Q45852 elusoidium
4	3	27.3	9	4 Q9UKJ6	Q9UKJ6 homo sapien
5	3	27.3	9	4 Q8NHL3	Q8NHL3 homo sapien
6	3	27.3	9	6 Q9TRW2	Q9TRW2 oryctolagus
7	3	27.3	9	10 Q8S3C6	Q8S3C6 glycyne max
8	3	27.3	10	2 Q47651	Q47651 escherichia
9	3	27.3	10	2 Q9X533	Q9X533 escherichia
10	3	27.3	10	2 Q9X534	Q9X534 leclercia a
11	3	27.3	10	2 Q9F5W1	Q9F5W1 vibrio chol
12	3	27.3	10	3 Q8TG88	Q8TG88 pleuroleus c
13	3	27.3	10	5 Q8WPL6	Q8WPL6 okopileura
14	3	27.3	10	15 P82080	P82080 limnodynast
15	3	27.3	10	15 Q8UT83	Q8UT83 human immun
16	3	27.3	11	2 Q9R872	Q9R872 escherichia

Q8J1G2 asl1y1 quos	17	4	36.4	3	Q8J1G2
Q46228 salmonelela	18	3	27.3	3	Q46228
Q9UKJ6 okopileura	19	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	20	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	21	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	22	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	23	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	24	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	25	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	26	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	27	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	28	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	29	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	30	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	31	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	32	3	27.3	3	Q9UKJ6
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Q9UKJ6 okopileura	36	3	27.3	3	Q9UKJ6
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Q9UKJ6 okopileura	41	3	27.3	3	Q9UKJ6
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Q9UKJ6 okopileura	43	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	44	3	27.3	3	Q9UKJ6
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Q9UKJ6 okopileura	66	3	27.3	3	Q9UKJ6
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Q9UKJ6 okopileura	68	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	69	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	70	3	27.3	3	Q9UKJ6
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Q9UKJ6 okopileura	91	3	27.3	3	Q9UKJ6
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Q9UKJ6 okopileura	98	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	99	3	27.3	3	Q9UKJ6
Q9UKJ6 okopileura	100	3	27.3	3	Q9UKJ6

90	2	18.2	8	8	P93957	P93957 testucopsis	163	2	18.2	3	1	04136	09406 homo sapien
91	2	18.2	8	8	P92222	P92222 bromas iner	164	2	18.2	3	4	04197	09497 homo sapien
92	2	18.2	8	8	P92388	P92388 henrardia p	165	2	18.2	3	5	04588	08588 echinidia
93	2	18.2	8	8	P92441	P92441 thriopyrum	166	2	18.2	3	6	04112	02412 bos taurus
94	2	18.2	8	8	Q9QD00	Q9QD00 masoala mad	167	2	18.2	3	6	04113	09401 eubria fy
95	2	18.2	8	8	P92404	P92404 lophopyrum	168	2	18.2	3	6	04116	09405 aotus azara
96	2	18.2	8	8	P93961	P93961 psathyrosta	169	2	18.2	3	6	04117	09408 eotus apoll
97	2	18.2	8	8	P93970	P93970 eremopyrum	170	2	18.2	3	6	04119	09413 espra hira
98	2	18.2	8	8	P93955	P93955 testucopsis	171	2	18.2	3	6	04094	02804 bos taurus
99	2	18.2	8	8	P93965	P93965 secale stri	172	2	18.2	3	6	04112	09402 eallithrix
100	2	18.2	8	8	P92394	P92394 hordeum val	173	2	18.2	3	6	04180	09180 oryctolagus
101	2	18.2	8	8	P92382	P92382 hordeum bre	174	2	18.2	3	6	04189	09409 aotus fusc
102	2	18.2	8	8	P93966	P93966 aequilops sp	175	2	18.2	3	6	04185	09405 satinus fu
103	2	18.2	8	8	Q9T4V2	Q9T4V2 asterina pe	176	2	18.2	3	6	04183	09403 callitico 4
104	2	18.2	8	8	P92227	P92227 crithopsis	177	2	18.2	3	6	04187	09407 samira sci
105	2	18.2	8	8	P92373	P92373 baynaldia v	178	2	18.2	3	6	04184	09404 leucophae
106	2	18.2	8	8	P92211	P92211 atropyrum e	179	2	18.2	3	6	04187	09407 canis fami
107	2	18.2	8	8	P92428	P92428 peridictyot	180	2	18.2	3	6	04189	09409 leucophae
108	2	18.2	8	8	P92386	P92386 hordeum mar	181	2	18.2	3	6	04187	09407 peridictyot
109	2	18.2	8	8	P93959	P93959 hordeum ere	182	2	18.2	3	6	04189	09409 spinaetia el
110	2	18.2	8	8	P92219	P92219 australopyr	183	2	18.2	3	6	04189	09409 semactia el
111	2	18.2	8	8	P93985	P93985 aequilops bo	184	2	18.2	3	6	04189	09409 asteromyia
112	2	18.2	8	8	P92443	P92443 faenariaetia	185	2	18.2	3	6	04189	09409 iliospadix
113	2	18.2	8	8	Q94V82	Q94V82 varanus sal	186	2	18.2	3	6	04189	09406 sclerospere
114	2	18.2	8	8	P92391	P92391 heteranthel	187	2	18.2	3	6	04189	09406 varanus pl
115	2	18.2	8	8	P93981	P93981 crithodum	188	2	18.2	3	6	04189	09406 splenactia el
116	2	18.2	8	8	P93992	P93992 australopyr	189	2	18.2	3	6	04189	09406 calothidaria
117	2	18.2	8	8	Q9XN88	Q9XN88 boophilus m	190	2	18.2	3	6	04189	09406 crithodum
118	2	18.2	8	8	P92426	P92426 pseudoroqec	191	2	18.2	3	6	04189	09406 mus muscra
119	2	18.2	8	8	P92431	P92431 aequilops ta	192	2	18.2	3	6	04189	09406 mus muscra
120	2	18.2	8	8	Q94V87	Q94V87 varanus sal	193	2	18.2	3	6	04189	09406 mus muscra
121	2	18.2	8	8	Q94V85	Q94V85 varanus sal	194	2	18.2	3	6	04189	09406 mus muscra
122	2	18.2	8	8	P92422	P92422 psathyrosta	195	2	18.2	3	6	04189	09406 hepaticus 4
123	2	18.2	8	8	Q37854	Q37854 bacterioph	196	2	18.2	3	6	04189	09406 human betac
124	2	18.2	8	8	Q8H9K4	Q8H9K4 bacterioph	197	2	18.2	3	6	04189	09406 avian betac
125	2	18.2	8	8	Q8H9J9	Q8H9J9 bacterioph	198	2	18.2	3	6	04189	09406 avian betac
126	2	18.2	8	8	Q8H9J7	Q8H9J7 bacterioph	199	2	18.2	3	6	04189	09406 avian betac
127	2	18.2	8	8	Q8H9J5	Q8H9J5 bacterioph	200	2	18.2	3	6	04189	09406 avian betac
128	2	18.2	8	8	Q8H9J3	Q8H9J3 bacterioph	201	2	18.2	3	6	04189	09406 avian betac
129	2	18.2	8	8	Q8H9J1	Q8H9J1 bacterioph	202	2	18.2	3	6	04189	09406 avian betac
130	2	18.2	8	8	Q8H9I9	Q8H9I9 bacterioph	203	2	18.2	3	6	04189	09406 avian betac
131	2	18.2	8	8	Q8H9I8	Q8H9I8 bacterioph	204	2	18.2	3	6	04189	09406 avian betac
132	2	18.2	8	8	Q8H9I6	Q8H9I6 bacterioph	205	2	18.2	3	6	04189	09406 avian betac
133	2	18.2	8	8	Q8H9I4	Q8H9I4 bacterioph	206	2	18.2	3	6	04189	09406 avian betac
134	2	18.2	8	8	Q8H9I3	Q8H9I3 bacterioph	207	2	18.2	3	6	04189	09406 avian betac
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136	2	18.2	8	8	Q8H9H6	Q8H9H6 bacterioph	209	2	18.2	3	6	04189	09406 avian betac
137	2	18.2	8	8	Q8H9H5	Q8H9H5 bacterioph	210	2	18.2	3	6	04189	09406 avian betac
138	2	18.2	8	8	Q8H9H3	Q8H9H3 bacterioph	211	2	18.2	3	6	04189	09406 avian betac
139	2	18.2	8	8	Q8H9H3	Q8H9H3 bacterioph	212	2	18.2	3	6	04189	09406 avian betac
140	2	18.2	8	8	Q35835	Q35835 rattus sp.	213	2	18.2	3	6	04189	09406 avian betac
141	2	18.2	8	8	Q9QVJ8	Q9QVJ8 mus sp. nep	214	2	18.2	3	6	04189	09406 avian betac
142	2	18.2	8	8	Q60615	Q60615 mus musculu	215	2	18.2	3	6	04189	09406 avian betac
143	2	18.2	8	8	Q8H9M9	Q8H9M9 mus musculu	216	2	18.2	3	6	04189	09406 avian betac
144	2	18.2	8	8	Q9QVJ4	Q9QVJ4 rattus sp.	217	2	18.2	3	6	04189	09406 avian betac
145	2	18.2	8	8	Q62933	Q62933 rattus sp.	218	2	18.2	3	6	04189	09406 avian betac
146	2	18.2	8	8	Q62528	Q62528 mus spiretes	219	2	18.2	3	6	04189	09406 avian betac
147	2	18.2	8	8	Q8H9M5	Q8H9M5 polymyviru	220	2	18.2	3	6	04189	09406 avian betac
148	2	18.2	8	8	Q91U19	Q91U19 influenza a	221	2	18.2	3	6	04189	09406 avian betac
149	2	18.2	8	8	Q84271	Q84271 human papil	222	2	18.2	3	6	04189	09406 avian betac
150	2	18.2	8	8	Q91U21	Q91U21 influenza a	223	2	18.2	3	6	04189	09406 avian betac
151	2	18.2	8	8	Q84273	Q84273 human papil	224	2	18.2	3	6	04189	09406 avian betac
152	2	18.2	8	8	Q83332	Q83332 murine hepa	225	2	18.2	3	6	04189	09406 avian betac
153	2	18.2	8	8	P87488	P87488 oncorhynch	226	2	18.2	3	6	04189	09406 avian betac
154	2	18.2	8	8	Q9T7E8	Q9T7E8 escherichia	227	2	18.2	3	6	04189	09406 avian betac
155	2	18.2	8	8	Q9UE09	Q9UE09 homo sapien	228	2	18.2	3	6	04189	09406 avian betac
156	2	18.2	8	8	Q15891	Q15891 homo sapien	229	2	18.2	3	6	04189	09406 avian betac
157	2	18.2	8	8	Q16276	Q16276 homo sapien	230	2	18.2	3	6	04189	09406 avian betac
158	2	18.2	8	8	Q9BQ02	Q9BQ02 homo sapien	231	2	18.2	3	6	04189	09406 avian betac
159	2	18.2	8	8	Q9H4B1	Q9H4B1 homo sapien	232	2	18.2	3	6	04189	09406 avian betac
160	2	18.2	8	8	Q9H522	Q9H522 homo sapien	233	2	18.2	3	6	04189	09406 avian betac
161	2	18.2	8	8	Q9UQ40	Q9UQ40 homo sapien	234	2	18.2	3	6	04189	09406 avian betac
162	2	18.2	8	8	Q9BQ14	Q9BQ14 homo sapien	235	2	18.2	3	6	04189	09406 avian betac

236	2	18.2	10	4	060912	Q60912 homo sapien	369	2	18.2	11	2	077404	Q77404 escherichia
237	2	18.2	10	4	090C53	Q90C53 homo sapien	310	2	18.2	11	2	Q76003	Q76003 escherichia
238	2	18.2	10	4	Q9H115	Q9H115 homo sapien	311	2	18.2	11	2	Q76000	Q76000 escherichia
239	2	18.2	10	4	Q9UCP3	Q9UCP3 homo sapien	312	2	18.2	11	2	Q76000	Q76000 escherichia
240	2	18.2	10	4	Q9UCU6	Q9UCU6 homo sapien	313	2	18.2	11	2	P71228	P71228 escherichia
241	2	18.2	10	4	Q8N6B1	Q8N6B1 homo sapien	314	2	18.2	11	2	P75514	P75514 escherichia
242	2	18.2	10	5	Q9TXK1	Q9TXK1 dermatophag	315	2	18.2	11	2	Q47347	Q47347 escherichia
243	2	18.2	10	5	P82384	P82384 drosophila	316	2	18.2	11	2	Q47424	Q47424 escherichia
244	2	18.2	10	5	P82217	P82217 bombyx mori	317	2	18.2	11	2	Q76417	Q76417 escherichia
245	2	18.2	10	6	Q9TS43	Q9TS43 sus scrofa	318	2	18.2	11	2	Q76417	Q76417 escherichia
246	2	18.2	10	6	Q8M78	Q8M78 bos taurus q	319	2	18.2	11	2	Q76417	Q76417 escherichia
247	2	18.2	10	6	Q9TR48	Q9TR48 bos taurus q	320	2	18.2	11	2	Q76417	Q76417 escherichia
248	2	18.2	10	8	Q9TKF7	Q9TKF7 agonis gran	321	2	18.2	11	2	Q76417	Q76417 escherichia
249	2	18.2	10	8	Q9TKF9	Q9TKF9 metaleuca v	322	2	18.2	11	2	Q76417	Q76417 escherichia
250	2	18.2	10	8	Q9TKG2	Q9TKG2 callistemon	323	2	18.2	11	2	Q76417	Q76417 escherichia
251	2	18.2	10	8	Q9TKF5	Q9TKF5 agonis gra	324	2	18.2	11	2	Q76417	Q76417 escherichia
252	2	18.2	10	8	Q94VG5	Q94VG5 varanus gri	325	2	18.2	11	2	Q76417	Q76417 escherichia
253	2	18.2	10	8	Q9TKF1	Q9TKF1 homo looperi	326	2	18.2	11	2	Q76417	Q76417 escherichia
254	2	18.2	10	8	Q9TKF8	Q9TKF8 tristatopsis	327	2	18.2	11	2	Q76417	Q76417 escherichia
255	2	18.2	10	8	Q9TKF4	Q9TKF4 angasomyrin	328	2	18.2	11	2	Q76417	Q76417 escherichia
256	2	18.2	10	8	Q9TKF3	Q9TKF3 asferomyrin	329	2	18.2	11	2	Q76417	Q76417 escherichia
257	2	18.2	10	8	Q9TKF0	Q9TKF0 neofabricia	330	2	18.2	11	2	Q76417	Q76417 escherichia
258	2	18.2	10	8	Q9TKF0	Q9TKF0 kunzea arbi	331	2	18.2	11	2	Q76417	Q76417 escherichia
259	2	18.2	10	8	Q94VD5	Q94VD5 varanus oli	332	2	18.2	11	2	Q76417	Q76417 escherichia
260	2	18.2	10	8	Q9TP24	Q9TP24 ratius sp.	333	2	18.2	11	2	Q76417	Q76417 escherichia
261	2	18.2	10	8	P92707	P92707 platysaurus	334	2	18.2	11	2	Q76417	Q76417 escherichia
262	2	18.2	10	8	Q9TKF6	Q9TKF6 agonis obtu	335	2	18.2	11	2	Q76417	Q76417 escherichia
263	2	18.2	10	8	Q9THM7	Q9THM7 leptosperma	336	2	18.2	11	2	Q76417	Q76417 escherichia
264	2	18.2	10	8	P92733	P92733 tegevaria	337	2	18.2	11	2	Q76417	Q76417 escherichia
265	2	18.2	10	8	Q9TKF2	Q9TKF2 leptosperma	338	2	18.2	11	2	Q76417	Q76417 escherichia
266	2	18.2	10	8	Q9TKF3	Q9TKF3 leptosperma	339	2	18.2	11	2	Q76417	Q76417 escherichia
267	2	18.2	10	8	Q9TKF7	Q9TKF7 kunzea pulv	340	2	18.2	11	2	Q76417	Q76417 escherichia
268	2	18.2	10	8	Q9THM6	Q9THM6 leptosperma	341	2	18.2	11	2	Q76417	Q76417 escherichia
269	2	18.2	10	8	Q9TKF6	Q9TKF6 leptosperma	342	2	18.2	11	2	Q76417	Q76417 escherichia
270	2	18.2	10	8	P92576	P92576 bipes bipar	343	2	18.2	11	2	Q76417	Q76417 escherichia
271	2	18.2	10	8	Q9THM7	Q9THM7 leptosperma	344	2	18.2	11	2	Q76417	Q76417 escherichia
272	2	18.2	10	8	Q9TKF8	Q9TKF8 kunzea eric	345	2	18.2	11	2	Q76417	Q76417 escherichia
273	2	18.2	10	8	Q9TKF9	Q9TKF9 kunzea baxi	346	2	18.2	11	2	Q76417	Q76417 escherichia
274	2	18.2	10	8	Q8SL54	Q8SL54 aconium haw	347	2	18.2	11	2	Q76417	Q76417 escherichia
275	2	18.2	10	8	Q9TFV5	Q9TFV5 eublepharus	348	2	18.2	11	2	Q76417	Q76417 escherichia
276	2	18.2	10	8	Q35013	Q35013 megalodryne	349	2	18.2	11	2	Q76417	Q76417 escherichia
277	2	18.2	10	8	Q8SHN1	Q8SHN1 bradypodion	350	2	18.2	11	2	Q76417	Q76417 escherichia
278	2	18.2	10	8	Q9TKF1	Q9TKF1 neofabricia	351	2	18.2	11	2	Q76417	Q76417 escherichia
279	2	18.2	10	8	P92632	P92632 eromias ara	352	2	18.2	11	2	Q76417	Q76417 escherichia
280	2	18.2	10	8	Q9TKF4	Q9TKF4 leptosperma	353	2	18.2	11	2	Q76417	Q76417 escherichia
281	2	18.2	10	8	Q9TKG0	Q9TKG0 lophostemon	354	2	18.2	11	2	Q76417	Q76417 escherichia
282	2	18.2	10	8	P82136	P82136 spinacia ol	355	2	18.2	11	2	Q76417	Q76417 escherichia
283	2	18.2	10	8	Q8HUB4	Q8HUB4 anomobryum	356	2	18.2	11	2	Q76417	Q76417 escherichia
284	2	18.2	10	9	Q38217	Q38217 lactococcus	357	2	18.2	11	2	Q76417	Q76417 escherichia
285	2	18.2	10	10	Q9S926	Q9S926 glycine max	358	2	18.2	11	2	Q76417	Q76417 escherichia
286	2	18.2	10	10	Q8SAC2	Q8SAC2 amblystegiu	359	2	18.2	11	2	Q76417	Q76417 escherichia
287	2	18.2	10	10	P82434	P82434 nicotiana t	360	2	18.2	11	2	Q76417	Q76417 escherichia
288	2	18.2	10	10	P82438	P82438 nicotiana t	361	2	18.2	11	2	Q76417	Q76417 escherichia
289	2	18.2	10	10	Q8GUV6	Q8GUV6 capseila ru	362	2	18.2	11	2	Q76417	Q76417 escherichia
290	2	18.2	10	11	Q9QW81	Q9QW81 rattus norv	363	2	18.2	11	2	Q76417	Q76417 escherichia
291	2	18.2	10	11	Q63389	Q63389 rattus norv	364	2	18.2	11	2	Q76417	Q76417 escherichia
292	2	18.2	10	11	Q8VIL8	Q8VIL8 mus muscrau	365	2	18.2	11	2	Q76417	Q76417 escherichia
293	2	18.2	10	11	Q9JL15	Q9JL15 mus muscrau	366	2	18.2	11	2	Q76417	Q76417 escherichia
294	2	18.2	10	11	Q70580	Q70580 mus muscrau	367	2	18.2	11	2	Q76417	Q76417 escherichia
295	2	18.2	10	12	Q84140	Q84140 influenza v	368	2	18.2	11	2	Q76417	Q76417 escherichia
296	2	18.2	10	12	Q69347	Q69347 herpes simf	369	2	18.2	11	2	Q76417	Q76417 escherichia
297	2	18.2	10	12	P90391	P90391 tomato yrt	370	2	18.2	11	2	Q76417	Q76417 escherichia
298	2	18.2	10	13	Q42355	Q42355 brachydanio	371	2	18.2	11	2	Q76417	Q76417 escherichia
299	2	18.2	10	13	Q9PR09	Q9PR09 sparus ara	372	2	18.2	11	2	Q76417	Q76417 escherichia
300	2	18.2	10	13	Q73588	Q73588 gallus gall	373	2	18.2	11	2	Q76417	Q76417 escherichia
301	2	18.2	10	13	Q73594	Q73594 gallus gall	374	2	18.2	11	2	Q76417	Q76417 escherichia
302	2	18.2	10	13	Q8AXT7	Q8AXT7 xenopus lae	375	2	18.2	11	2	Q76417	Q76417 escherichia
303	2	18.2	10	15	Q86324	Q86324 rous sarcom	376	2	18.2	11	2	Q76417	Q76417 escherichia
304	2	18.2	10	15	Q86325	Q86325 rous sarcom	377	2	18.2	11	2	Q76417	Q76417 escherichia
305	2	18.2	10	15	Q9QKJ0	Q9QKJ0 human immun	378	2	18.2	11	2	Q76417	Q76417 escherichia
306	2	18.2	10	15	Q86326	Q86326 rous sarcom	379	2	18.2	11	2	Q76417	Q76417 escherichia
307	2	18.2	11	2	Q9R790	Q9R790 borrelia ga	380	2	18.2	11	2	Q76417	Q76417 escherichia
308	2	18.2	11	2	Q47602	Q47602 escherichia	381	2	18.2	11	2	Q76417	Q76417 escherichia



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Query Match: 36.4%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.9e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SRKG 6
DB 7 SRKG 10

RESULT 2
P77556
ID P77556 PRELIMINARY; PRT: 8 AA.
AC P77556;
DT 01-FEB-1997 (TrEMBLrel. 02, Created);
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update);
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update);
DE TRAY (Fragment);
CN TRAY;
OS Escherichia coli;
OC Plasmid IncFI; R1;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
OC Enterobacteriaceae; Escherichia;
OX NCBI_TaxID:562;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN-ECOR11;
RX MEDLINE-96400908; PubMed 8807284;
RA Boyd E.F., Hill C.W., Rich S.M., Hart, E.L.;
RT "Mosaic structure of plasmids from natural populations of Escherichia
coli.";
RL Genetics 141:1091-1100(1996);
DR EMBL: U50661; AAC44245.1; -;
DR EMBL: U50650; AAC44234.1; -;
DR EMBL: U50651; AAC44235.1; -;
DR EMBL: U50652; AAC44236.1; -;
DR EMBL: U50653; AAC44237.1; -;
DR EMBL: U50654; AAC44238.1; -;
DR EMBL: U50655; AAC44239.1; -;
DR EMBL: U50656; AAC44240.1; -;
DR EMBL: U50657; AAC44241.1; -;
DR EMBL: U50658; AAC44242.1; -;
DR EMBL: U50659; AAC44243.1; -;
DR EMBL: U50660; AAC44244.1; -;
KW Plasmid.
FT NON_TER
SQ SEQUENCE 8 AA: 834 MW; D335A5B0544735A1 CRR64;

Query Match: 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.4e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 SSL 10
DB 6 SSL 8

RESULT 3
Q45852
ID Q45852 PRELIMINARY; PRT: 9 AA.
AC Q45852;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update);
DE Chloramphenicol acetyltransferase (cat);
OS Clostridium butyricum;
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium;
OX NCBI_TaxID:1492;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE-93143268; PubMed-1489203;
RA Huggins A.S., Bannam T.L., Rood J.I.;

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Query Match: 36.4%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.9e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SRKG 6
DB 7 SRKG 10

RESULT 4
Q45852
ID Q45852 PRELIMINARY; PRT: 9 AA.
AC Q45852;
DT 01-MAY-2002 (TrEMBLrel. 02, Last sequence update);
DT 01-MAY-2002 (TrEMBLrel. 02, Last sequence update);
DT 01-MAY-2002 (TrEMBLrel. 02, Last sequence update);
DE K18203 (Fragment);
CN K18203;
OS Homo sapiens;
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Hominidae; Homo;
OX NCBI_TaxID:9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Zhang W., Li X., Li N.;
RT "A SPANISH STRAIN OF THE BACTERIAL PATHOGEN ESCHERICHIA COLI
SUBSP. TYPICUM FROM THE OCEANIC ISLAND OF CANARY ISLANDS";
LP EMBL: AF240147; AAC44013.1; -;
KW Escherichia;
FT NON_TER
SQ SEQUENCE 9 AA: 1272 MW; 32266335A55E94 CRR64;

Query Match: 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.4e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 KSK 4
DB 6 KSK 7

RESULT 5
Q45852
ID Q45852 PRELIMINARY; PRT: 9 AA.
AC Q45852;
DT 01-OCT-2002 (TrEMBLrel. 02, Created);
DT 01-OCT-2002 (TrEMBLrel. 02, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 02, Last sequence update);
DE K18203 (Fragment);
CN K18203;
OS Homo sapiens;
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Hominidae; Homo;
OX NCBI_TaxID:9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Zhang W., Li X., Li N.;
RT "A SPANISH STRAIN OF THE BACTERIAL PATHOGEN ESCHERICHIA COLI
SUBSP. TYPICUM FROM THE OCEANIC ISLAND OF CANARY ISLANDS";
LP EMBL: AF240147; AAC44013.1; -;
KW Escherichia;
FT NON_TER
SQ SEQUENCE 9 AA: 1272 MW; 32266335A55E94 CRR64;

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Query Match 27.3%, Score 3, DB 42, Length 50  
 Best Local Similarity 100.0%, Pred. No. 8, 3e-06  
 Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 9 SLM 11  
 Db 2 SLM 4

## RESULT 6

Q9TRW2 PRELIMINARY: PRT: 9 AA.  
 AC Q9TRW2:  
 DT 01-MAY-2000 (TRENBLrel, 13, Created)  
 DT 01-MAY-2000 (TRENBLrel, 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel, 21, Last annotation update)  
 DE CADESMON-PHOSPHORYLATION site (Fragment)  
 OS Oryctolagus cuniculus (Rabbit)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cytodactylus  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE:9,178498; PubMed:1698046;  
 RA Ikebe M., Hornick T.;  
 RT "Determination of the phosphorylation sites of smooth muscle caldesmon  
 by protein kinase C";  
 RL Arch. Biochem. Biophys. 288:538-542(1991).  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1018 MW: 809018105 6735A5 CRC64:

## Query Match

Best Local Similarity 100.0%, Score 3, DB 6, Length 50  
 Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 8 SLM 10  
 Db 2 SLM 4

## RESULT 7

Q8S3C6 PRELIMINARY: PRT: 9 AA.  
 AC Q8S3C6:  
 DT 01-JUN-2002 (TRENBLrel, 21, Created)  
 DT 01-JUN-2002 (TRENBLrel, 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel, 21, Last annotation update)  
 DE SNF RAD 54-like protein (Fragment)  
 OS Glycine max (Soybean)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolus; Glycine  
 OX NCBI\_TaxID:3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-cv. Forrest;  
 RX MEDLINE-21258784; PubMed-11361330;  
 RA Meksem K., Ruben E., Hylen D., Trivelpashvili K., Lightfoot D.A.,  
 RT "Conversion of AFLP bands into high-throughput DNA markers";  
 RL Mol. Genet. Genomics 265:207-214(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-cv. Forrest;  
 RA Meksem K., Lightfoot D., Gibson P.;  
 RT "Soybean Sudden Death Syndrome resistant soybeans: soybean cyst  
 nematode resistant soybeans and methods of breeding and identifying  
 resistant plants";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF489439; AAM14563.1;  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1070 MW: DC20A69735A2C699 CRC64:

## Query Match

Best Local Similarity 100.0%, Score 3, DB 10, Length 50  
 Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 9 SLM 11  
 Db 2 SLM 4

## RESULT 8

Q47451 PRELIMINARY: PRT: 9 AA.  
 AC Q47451:  
 DT 01-MAY-2000 (TRENBLrel, 13, Created)  
 DT 01-MAY-2000 (TRENBLrel, 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel, 21, Last annotation update)  
 DE CADESMON-PHOSPHORYLATION site (Fragment)  
 OS Oryctolagus cuniculus (Rabbit)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cytodactylus  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE-9,178498; PubMed-1698046;  
 RA Ikebe M., Hornick T.;  
 RT "Determination of the phosphorylation sites of smooth muscle caldesmon  
 by protein kinase C";  
 RL Arch. Biochem. Biophys. 288:538-542(1991).  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1018 MW: 809018105 6735A5 CRC64:

## Query Match

Best Local Similarity 100.0%, Score 3, DB 2, Length 50  
 Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 AKA 3  
 Db 1 AKA 3

## RESULT 9

Q47451 PRELIMINARY: PRT: 9 AA.  
 AC Q47451:  
 DT 01-MAY-2000 (TRENBLrel, 13, Created)  
 DT 01-MAY-2000 (TRENBLrel, 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel, 21, Last annotation update)  
 DE CADESMON-PHOSPHORYLATION site (Fragment)  
 OS Oryctolagus cuniculus (Rabbit)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cytodactylus  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN 200A;  
 RX MEDLINE-9726822; F0061406127;

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RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RT bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-209A:
RX MEDLINE-98027386; PubMed-9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RT gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-209A:
RX MEDLINE-20568355; PubMed-11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL: AF120964; AAD23783.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10
DB 6 SSL 8

RESULT 10
QX534 PRELIMINARY: PRT: 10 AA.
AC QX534:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Leclercia adcarboxylata.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
OC Enterobacteriaceae; Leclercia.
OX NCBI_TaxID=83655;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-742H:
RX MEDLINE-97208220; PubMed-9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RT bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-742H:
RX MEDLINE-98027386; PubMed-9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RT gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-742H:
RX MEDLINE-20568355; PubMed-11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL: AF120965; AAD23785.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 10;

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Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10
DB 6 SSL 8

RESULT 11
QX534 PRELIMINARY: PRT: 10 AA.
AC QX534:
DT 01-MAR-2001 (TREMBlrel. 20, Created)
DT 01-MAR-2001 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 20, Last annotation update)
DE Cap (Fragment).
GN CAP.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales.
OX NCBI_TaxID=696;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-9803:
RA RUI Y.Y., Kan B., Chao S.Y., Liu Y.Q., Li G.M.;
RT "PS region of Vibrio cholerae O1 (CTXphi). Includes rsh (PSB).
RT rshA (RSTA) and rshD (RSD) genes."
RI Submitted (SEP-2001) to the EMBL/Genbank/DBCLS databases.
DR EMBL: AF162794; AA127911.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1093 MW; 0F7CA443A7745A5 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10
DB 6 SSL 5

RESULT 12
QX534 PRELIMINARY: PRT: 1 AA.
AC QX534:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Manganese peroxidase (Fragment).
GN MNP.
OS Pleurotus ostreatus (cluster mushroom) (White rot fungus).
OC Eukaryota; Basidiomycota; Basidiomycetes; Agaricomycotina;
OC Agaricomycotina; Pleurothales; Pleurothales.
OX NCBI_TaxID=5322;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-F101.3A:
RA Cohen M., Vandenbergh, David Y.;
RT "The effect of Mn2+ on transcription of mnp genes in Pleurotus
RT ostreatus."
RL Submitted (OCT-2001) to the EMBL/Genbank/DBCLS databases.
DR EMBL: AF156435; AAM6367.1; -;
KW Peroxidase.
FT NON_TER 1
SQ SEQUENCE 1 AA; 100 MW; 0F900A3967E339 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 1;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10
DB 7 SSL 9

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DR EMBL: AJ001816; CAA05032.1; -
KW plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1221 MW; 92014864C2C69735 CRK64;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. Re-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SLM 11
Db 4 SLM 6

RESULT 17
09BJ6;
ID 09BJ61 PRELIMINARY; PRT: 11 AA.
AC 09BJ61;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE G-box binding factor (Fragment)
OS Dictyostellium discoideum (Slime mold)
OC Eukaryota; Mycetozoa; Dictyosteliales; Dictyostelium
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-2129081; PubMed-11397018;
RA Brown J.M., Fitel R.A.;
RT "Functional and regulatory analysis of the Dictyostellium G box binding
factor.";
RL Dev. Biol. 234:521-534(2001).
DR EMBL: AF337815; AAK21290.1; -
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1248 MW; 87356B5FD1E1E1F1 CRK64;

Query Match 27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. Re-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNS 8
Db 9 GNS 11

RESULT 18
09G622
ID 09G622 PRELIMINARY; PRT: 11 AA.
AC 09G622;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI.
OS Salvia horsfieldii.
OC Mitochondrion
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Anamniota; Iguanidae;
OC Salvia.
OX NCBI_TaxID=118233;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-22114082; PubMed-12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genome:
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-22114081; PubMed-12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-fetals migration: An example using Acrodont lizard

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R1 phylogenetic relationships.
R2 Syst. Biol. 49:257-277(2000).
DR EMBL: AF128470; AAK21290.1; -
KW Mitochondrion
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1248 MW; 5627C7E46641A7 CRK64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. Re-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SLM 10
Db 2 SLM 4

RESULT 19
09G616
ID 09G616 PRELIMINARY; PRT: 11 AA.
AC 09G616;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE Cytochrome c oxidase subunit I (Fragment)
OS Cytochrome c oxidase subunit I (Fragment)
OX NCBI_TaxID=118196;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-22114082; PubMed-12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genome:
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-22114081; PubMed-12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-fetals migration: An example using Acrodont lizard
phylogenetic relationships.
R2 Syst. Biol. 49:257-277(2000).
DR EMBL: AF128470; AAK21290.1; -
KW Mitochondrion
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1248 MW; 5627C7E46641A7 CRK64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. Re-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SLM 10
Db 2 SLM 4

RESULT 20
09G610
ID 09G610 PRELIMINARY; PRT: 11 AA.
AC 09G610;
DT 01-MAR-2001 (Tremblrel. 16, Created)

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OC Lepidosauria; Squamata; Iguania; Acrodontia; Agamididae; Eutrocoastal;  
 OC Ceratophora;  
 OX NCBI\_TaxID=118196;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2165505; PubMed=11796034;  
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.  
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus *Ceratophora*  
 RT Endemic to Sri Lanka.";  
 RL Mol. Phylogenet. Evol. 22:111-117(2002).  
 DR EMBL: AF364053; AAL68024.1;  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33649067 CRC64;

Query Match 27.3%; Score 3; ID 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

OY 8 SSL 10  
 III  
 DB 2 SSL 4

## RESULT 24

OC9613  
 ID Q9G613 PRELIMINARY; PRT; 11 AA.

AC Q9G613  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI  
 OS Cophotis ceylanica.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodontia; Agamididae; Dipsosaurus;  
 OC Cophotis.  
 OX NCBI\_TaxID=118202;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.  
 RT "Evolution and information content of the mitochondrial genome  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Arachchane N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.  
 RT "Evaluating Trans-Tethys migration: An example using Agamid lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL: AF128493; AAG00716.1;  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336491A7 CRC64;

Query Match 27.3%; Score 3; ID 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

OY 8 SSL 10  
 III  
 DB 2 SSL 4

## RESULT 25

OC9525  
 ID Q9G525 PRELIMINARY; PRT; 11 AA.

AC Q9G525  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI  
 OS Cophotis ceylanica.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodontia; Agamididae; Dipsosaurus;  
 OC Cophotis.  
 OX NCBI\_TaxID=118202;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.  
 RT "Evolution and information content of the mitochondrial genome  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Arachchane N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.  
 RT "Evaluating Trans-Tethys migration: An example using Agamid lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL: AF128493; AAG00716.1;  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336491A7 CRC64;

Query Match 27.3%; Score 3; ID 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8000;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

OY 8 SSL 10  
 III  
 DB 2 SSL 4

RESULT 26

OC9524  
 ID Q9G524 PRELIMINARY; PRT; 11 AA.

AC Q9G524  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI  
 OS Cophotis ceylanica.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodontia; Agamididae; Dipsosaurus;  
 OC Cophotis.  
 OX NCBI\_TaxID=118202;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.  
 RT "Evolution and information content of the mitochondrial genome  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Arachchane N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.  
 RT "Evaluating Trans-Tethys migration: An example using Agamid lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL: AF128493; AAG00716.1;  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336491A7 CRC64;

Query Match 27.3% Score 3; DB 0; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10  
 Db 2 SSL 4

## RESULT 27

054226 PRELIMINARY; PRT; 12 AA.  
 AC 054226;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Polyketide synthase (Fragment).  
 GN ERYA.  
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Pseudonocardiales; Pseudonocardaceae; Saccharopolyspora.  
 OX NCBI\_TaxID=1836;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL2338;  
 RA Salah-Bey K., Doumith M., Michel J.M., Haydock S., Corlies G.,  
 Leadlay P.F., Reynal M.C.;  
 RT "Targeted gene inactivation for the elucidation of shikimate  
 biosynthesis in the erythromycin producer, saccharopolyspora  
 erythraea.";  
 RL Submitted (JUL-1997) to the EMBL/GenBank/NCBI databases.  
 DR EMBL; Y1432; CAA74712.1;  
 FT NON\_TER 1  
 FT SEQUENCE 12 AA; 1282 MW; D4BA3E57E27747D CR664;

Query Match 27.3% Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8  
 Db 10 GNS 12

## RESULT 28

046747 PRELIMINARY; PRT; 12 AA.  
 AC 046747;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Malate dehydrogenase (Fragment).  
 GN MDH.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=W3110;  
 RX MEDLINE=96165273; PubMed=8576952;  
 RA Bass S., Gu Q., Christen A.;  
 RT "Multicopy suppressors of pro mutant, Escherichia coli, include two BTA  
 (DeqP) protease homologs (HhaAB), DksA, and a truncated alpha-  
 J. Bacteriol. 178:1154-1161(1996).  
 RL J. Bacteriol. 178:1154-1161(1996).  
 DR EMBL; U15661; AAC43994.1;  
 FT NON\_TER 1  
 FT SEQUENCE 12 AA; 1302 MW; D2DR6E5218A5B33D CR664;

Query Match 27.3% Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3  
 Db 5 AKS 3

## RESULT 29

047251 PRELIMINARY; PRT; 12 AA.  
 AC 047251;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 11, Last annotation update)  
 DE Biotin protein (Fragment).  
 GN BMT.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Enterobacter.  
 OX NCBI\_TaxID=562;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 8739;  
 RA Mellin P.M.; Zamboni R.A.; Adams A.L.; Thomas S.P.;  
 RT "Nucleotide sequence of genes encoding the biotin domain of  
 Escherichia coli BMT.";  
 DE EMBL; Y08444; CAA74712.1;  
 FT NON\_TER 1  
 FT SEQUENCE 12 AA; 1282 MW; D4BA3E57E27747D CR664;

Query Match 27.3% Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 1  
 Db 4 SSL 4

## RESULT 30

047251 PRELIMINARY; PRT; 12 AA.  
 AC 047251;  
 DT 01-MAY-2000 (TrEMBLrel. 11, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 11, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 11, Last annotation update)  
 DE Glucose large subunit (Fragment).  
 GN Helicobacter pylori.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Epsilonproteales;  
 OC Bacteroidetes; Bacteroidia; Bacteroidaceae; Bacteroides;  
 OX NCBI\_TaxID=242400;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J99;  
 RX MEDLINE=96165273; PubMed=8576952;  
 RA Tachibana T., Kato T., Wada K., Horiuchi T.,  
 FT "Cloning and characterization of the glucose large subunit  
 of Helicobacter pylori.";  
 RL J. Bacteriol. 178:1154-1161(1996).  
 DR EMBL; U15661; AAC43994.1;  
 FT NON\_TER 1  
 FT SEQUENCE 12 AA; 1302 MW; D2DR6E5218A5B33D CR664;

Query Match 27.3% Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSK 6  
 Db 6 SSK 3

## RESULT 31

026429

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ID O26429 PRELIMINARY; PRT: 12 AA.
AC O26429;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PROBOSCIPEDIA protein (Fragment).
GN PB.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92111389; PubMed=1684932;
RA Randazzo F.M., Cribbs D.L., Kaufman T.C.;
RT "Rescue and regulation of proboscipedia: a homeotic gene of the
RT Antennapedia Complex.";
RL Development 113:257-271(1991).
DR EMBL: S77929; AAB20845.1; -.
DR FlyBase; FBgn0012734; Dpse\pb.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA: 1377 MW: 4608DB18E355A5B3 CR664;

Query Match 27.3%; Score 3; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRK 5
DB 3 SRK 5

RESULT 32
ID Q8AEW7 PRELIMINARY; PRT: 12 AA.
AC Q8AEW7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (Fragment).
GN REV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HAART patient 28;
RA Saurva S.;
RT "Characterization of HIV-1 genes from AIDS patients on combination
RT therapy with discordance between viral load and CD4 T cell counts.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ496725; CAD43155.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA: C395423D2F4321AD CR664;

Query Match 27.3%; Score 3; DB 15; Length 12.
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9
DB 8 NSS 10

RESULT 33
ID Q9X3E1 PRELIMINARY; PRT: 13 AA.
AC Q9X3E1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Cytochrome b (Fragment).

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```

GN PFEB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorococcus; Prochlorococcus;
OC Prochlorococcus.
OX NCBI_TaxID=1226;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity of the prochlorococcus populations from a coastal
RT sorted from the Sargasso Sea and the Gulf Stream.";
RL Limnol. Oceanogr. 43:1316-1330(1998).
OR EMBL: AF070141; AAL2755.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA: 1144 MW: 673E8027A4666A3 CR664;

Query Match 27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRK 5
DB 3 SRK 5

RESULT 34
ID Q9DEE4 PRELIMINARY; PRT: 13 AA.
AC Q9DEE4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RAGB transcription factor (Fragment).
GN RAGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Primates; Vertebrata; Euteleostomi;
OC Mammalia; Eutera; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Orita K., Hirotsu H., Nishida H., Yoshida M.C., Ake S.;
RT "Molecular analysis of the breakpoint region of a 1.1 kb
RT translocation in Fugu's chromosome 2.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
OR EMBL: AB012624; AAA3835.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA: 629 MW: 62944FE7A64A5B4 CR664;

Query Match 27.3%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10
DB 7 SSL 9

RESULT 35
ID Q29823 PRELIMINARY; PRT: 13 AA.
AC Q29823;
DT 01-NOV-1999 (TrEMBLrel. 13, Created)
DT 01-NOV-1999 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2000 (TrEMBLrel. 19, Last annotation update)
DE GEF-1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Primates; Vertebrata; Euteleostomi;
OC Mammalia; Eutera; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144827; PubMed=858856;
RA Beck S., Abdulla S., Aderkott R.P., Guyane R.J., Gatt J.G.;

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RA Hosking L.K., Jackson A., Kelly A., Newell W.R., Sanson P.,  
 RA Radley E., Thorpe K.L., Trowsdale J.,  
 RT "Evolutionary dynamics of non-coding sequences within the Class II  
 region of the human HMC."  
 RL J. Mol. Biol. 255:11-13(1996).  
 DR EMBL: X87344; CAA60783.1;  
 SQ SEQUENCE 13 AA; 1512 MW; 1F8948507F9CA584 CRC64;

Query Match 27.3%; Score 3; Len 7; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9  
 Db 6 NSS 8

## RESULT 36

Q9AU99 PRELIMINARY: PRT; 13 AA.  
 AC Q9AU99;  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE Chalcone synthase (Fragment).  
 OS Aethionema grandiflora.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;  
 OC Eurosids II; Brassicales; Brassicaceae; Arabionoma.  
 OX NCBI\_TaxID=72657;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RP Koch M., Kroymann J., Haubold B., Weisshaar B., Mitchell-Olds F.,  
 RT "Phylogenetic analysis of promoter sequences from cruciferous  
 RT plants".  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF249000; AAK31935.1;  
 FT NON\_TER 13  
 FT SEQUENCE 13 AA; 1432 MW; 5C444963C4621AA7 CRC64;

Query Match 27.3%; Score 3; Len 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10  
 Db 4 SSL 6

## RESULT 37

Q9FS97 PRELIMINARY: PRT; 13 AA.  
 AC Q9FS97;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2  
 OS Silene noctiflora (night-flowering catchfly).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene  
 OX NCBI\_TaxID=39899;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RP Popp M., Oxelman B.,  
 RT "Inferring the history of the polyploid Silene acaqua  
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data".  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ296140; CAC13021.1;  
 FT NON\_TER 1  
 FT NON\_TER 13  
 FT SEQUENCE 13 AA; 1391 MW; D71753428A8B4AB2 CRC64;

Query Match 27.3%; Score 3; Len 10; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SSL 11  
 Db 3 SSL 5

## RESULT 38

Q9R274 PRELIMINARY: PRT; 14 AA.  
 AC Q9R274;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
 DE Flagellin A (TRENBLrel. 13)  
 OS Pseudomonas fluorescens  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Gammaproteobacteria;  
 OC Gammaproteobacteria; Gammaproteobacteria;  
 OX NCBI\_TaxID=1774;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RP Studer E.,  
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RA SEQUENCE FROM N.A.  
 RP Studer E., Bolmer M., Wimmeroff M., Löffler J., Schmid S.,  
 RA Gleditsia,  
 RT "REL and sequence databases: 1. Compilations of Rel and Carbohydrate  
 RT cell per. products applied and derived from environmental samples".  
 RL Food Sci. Technol. 23:67-71(1999).  
 DR EMBL: AJ146772; CAP6942.1;  
 DR EMBL: AJ146773; CAP6943.1;  
 DR EMBL: AJ146774; CAP6944.1;  
 FT NON\_TER 1  
 FT SEQUENCE 14 AA; 1563 MW; 2744637A724156 CRC64;

Query Match 27.3%; Score 3; Len 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9  
 Db 5 NSS 6

## RESULT 39

Q9A081 PRELIMINARY: PRT; 14 AA.  
 AC Q9A081;  
 DT 01-MAY-1996 (TRENBLrel. 1, Created)  
 DT 01-MAY-1996 (TRENBLrel. 1, Last sequence update)  
 DT 01-MAY-1996 (TRENBLrel. 1, Last annotation update)  
 DE RPB2  
 OS Saccharomyces cerevisiae (baker's yeast)  
 OC Eukaryota; Eukaryota; Opisthokonta; Eukaryota; Archaezoa;  
 OC Bacteria; Actinobacteria; Acidithiobacillus; Acidithiobacillus;  
 OC Pseudomonas fluorescens  
 OX NCBI\_TaxID=1774;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RP MBEZNE 9004740; 9004740;  
 RA Donadio S., Shalton A., Botchko S.,  
 RT "Distal end of a flagellin gene from Pseudomonas fluorescens  
 RT Saccharomyces cerevisiae".  
 RL J. Bacteriol. 172:4600-4601(1990).  
 DR EMBL: M29612; AAA88442.1;  
 KW Hydrothermal protein.  
 SQ SEQUENCE 14 AA; 1759 MW; 8C00004FEE96BE CRC64;

Query Match 27.3%; Score 3; Len 2; Length 14;

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Best Local Similarity 100.0%; Pred. No. 9, 7e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SLM 10
DB 8 SLM 10

RESULT 40
Q9NFK8 PRELIMINARY; PRT; 14 AA.
AC Q9NFK8
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DI 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE Mmcl protein (Fragment).
GN Mmcl.
OS Brugia pahangi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filariida; Onchocercidae; Brugia.
OX NCBI_TaxID=6280,
RN [1]
RA SEQUENCE FROM N.A.
RP Enes R.D., Thompson F., Devaney E.,
RT "A novel mRNA up-regulated in mammalian-derived microfilaria of
RL Brugia."
DR EMBL: AJ277950; CAB93515.1;
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1602 MW; 5C4C62C55AB89397 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 9, 7e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SLM 11
DB 6 SLM 8

RESULT 41
P82220 PRELIMINARY; PRT; 14 AA.
AC P82220;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DI 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Pilyrista; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RA STRAIN-XINHANG X KEMING; TISSUE: Body wall, mid gut;
RX MELLINE-21177481; PubMed11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five distinct
RT silkworm";
RL 1 Chuan Hsueh Pao 28:217-224(2001).
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1566 MW; 3F6E8265CA86778 CRC64;

Query Match 27.4%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 9, 7e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRK 5
DB 1 SRK 3

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## RESULT 48

005003 PRELIMINARY: PRT; 15 AA.  
AC 005003: Q52844;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DI 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Nodulation protein A, 3'END (Fragment) (Fragment).  
GN NODA.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NZB2213;  
RX MEDLINE=97002748; PubMed=8850088;  
RA Scott D.B., Young C.A., Collins-Emerson J.M., Terzaghi E.A.,  
RA Rockman E.S., Lewis P.E., Pankhurst C.E.  
RT "Novel and complex chromosomal arrangement of Rhizobium loti  
nodulation genes".  
RL Mol. Plant Microbe Interact. 9:187-197(1996).  
DR EMBL: X65620; CAA46574.1; -;  
DR EMBL: X65620; CAA46573.1; -;  
DR InterPro: IPR003484; Noda.  
DR Pfam: PF02474; Noda; 1.  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1689 MW; 0A729663327794R1 CR664;

Query Match 27.3% Score 3; DH 2; Length 15;  
Best local similarity 100.0%; Pred. No. le+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKG 6

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Db 10 RKG 12

## RESULT 49

081SC5 PRELIMINARY: PRT; 15 AA.  
AC 081SC5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DI 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE FCR3 varCSA ligand (Fragment).  
GN VAR.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Harposporidia; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22096013; PubMed=12100556;  
RA Vazquez-Macias A., Martinez Cruz P., Castaneda-Correa M.A.,  
RA Scheidegger C., Gysin J., Schert A., Hernandez-Kikus R.  
RT "A distinct 5' flanking var gene region regulates Plasmodium  
falciparum variant erythrocyte surface antigen expression in placental  
malaria".  
RL Mol. Microbiol. 45:155-167(2002).  
DR EMBL: AY135378; AAN1318.1; -;  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1435 MW; SDEC3C68839RF2E CR664;

Query Match 27.3% Score 3; DH 5; Length 15;  
Best local similarity 100.0%; Pred. No. le+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKS 3

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Db 12 AKS 14

## RESULT 50

0850F6 PRELIMINARY: PRT; 15 AA.  
AC 0850F6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE CRF15 (Fragment).  
GN CRF15.  
OS Rhizoglyphus sp. 10.  
OC Metazoa; Echinodermata; Echinozoa; Echinozoa; Echinozoa; Chytridiomycota;  
OC Phlebobranchia;  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=10;  
RX Medline=10;  
RA Terzaghi E.A., Young C.A., Collins-Emerson J.M., Terzaghi E.A.,  
RT "Hydrophobicity and the role of the hydrophobicity in the interaction of  
and an evolutionary link to the lower fungi".  
RL Mol. Biol. Evol. 19:100-105(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=10;  
RA Long F.R.  
RL Submission (1) (2) (3) (4) (5) (6) (7) (8) (9) (10) (11) (12) (13) (14) (15) (16) (17) (18) (19) (20) (21) (22) (23) (24) (25) (26) (27) (28) (29) (30) (31) (32) (33) (34) (35) (36) (37) (38) (39) (40) (41) (42) (43) (44) (45) (46) (47) (48) (49) (50) (51) (52) (53) (54) (55) (56) (57) (58) (59) (60) (61) (62) (63) (64) (65) (66) (67) (68) (69) (70) (71) (72) (73) (74) (75) (76) (77) (78) (79) (80) (81) (82) (83) (84) (85) (86) (87) (88) (89) (90) (91) (92) (93) (94) (95) (96) (97) (98) (99) (100) (101) (102) (103) (104) (105) (106) (107) (108) (109) (110) (111) (112) (113) (114) (115) (116) (117) (118) (119) (120) (121) (122) (123) (124) (125) (126) (127) (128) (129) (130) (131) (132) (133) (134) (135) (136) (137) (138) (139) (140) (141) (142) (143) (144) (145) (146) (147) (148) (149) (150) (151) (152) (153) (154) (155) (156) (157) (158) (159) (160) (161) (162) (163) (164) (165) (166) (167) (168) (169) (170) (171) (172) (173) (174) (175) (176) (177) (178) (179) (180) (181) (182) 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101	3	27.3	8	3	US-08-582-7760-20	Sequence 20, Appl	27.3	1	US-08-255-441A-4	Sequence 1, Appl
102	3	27.3	8	3	US-09-136-218-10	Sequence 10, Appl	27.3	1	US-08-277-187-2	Sequence 2, Appl
103	3	27.3	8	3	US-08-726-807B-16	Sequence 16, Appl	27.3	1	US-08-217-188A-19	Sequence 19, Appl
104	3	27.3	8	3	US-09-234-163-10	Sequence 10, Appl	27.3	1	US-08-215-455A-9	Sequence 9, Appl
105	3	27.3	8	3	US-08-434-831B-20	Sequence 20, Appl	27.3	1	US-08-215-455A-14	Sequence 14, Appl
106	3	27.3	8	3	US-08-444-618-409	Sequence 409, Appl	27.3	1	US-08-215-405A-24	Sequence 24, Appl
107	3	27.3	8	3	US-08-444-618-487	Sequence 487, Appl	27.3	1	US-08-215-405A-44	Sequence 44, Appl
108	3	27.3	8	3	US-08-444-818-486	Sequence 488, Appl	27.3	1	US-08-215-405A-60	Sequence 60, Appl
109	3	27.3	8	3	US-08-444-818-489	Sequence 489, Appl	27.3	1	US-08-215-405A-70	Sequence 70, Appl
110	3	27.3	8	3	US-08-444-818-490	Sequence 490, Appl	27.3	1	US-08-217-146-2	Sequence 2, Appl
111	3	27.3	8	3	US-08-444-818-491	Sequence 491, Appl	27.3	1	US-08-217-146A-2	Sequence 2, Appl
112	3	27.3	8	3	US-08-444-818-492	Sequence 492, Appl	27.3	1	US-08-217-146A-1	Sequence 1, Appl
113	3	27.3	8	3	US-09-258-754-12	Sequence 24, Appl	27.3	1	US-08-217-146A-25	Sequence 25, Appl
114	3	27.3	8	3	US-09-056-226-20	Sequence 20, Appl	27.3	1	US-08-217-146A-43	Sequence 43, Appl
115	3	27.3	8	3	US-08-901-379-10	Sequence 1, Appl	27.3	1	US-08-217-146A-50	Sequence 50, Appl
116	3	27.3	8	3	US-09-064-767-6	Sequence 6, Appl	27.3	1	US-08-217-146A-14	Sequence 14, Appl
117	3	27.3	8	3	US-09-068-767-7	Sequence 7, Appl	27.3	1	US-08-217-146A-59	Sequence 59, Appl
118	3	27.3	8	3	US-09-068-767-14	Sequence 14, Appl	27.3	1	US-08-217-146A-6	Sequence 6, Appl
119	3	27.3	8	3	US-09-068-767-24	Sequence 24, Appl	27.3	1	US-08-217-146A-19	Sequence 19, Appl
120	3	27.3	8	3	US-09-068-767-25	Sequence 25, Appl	27.3	1	US-08-217-146A-21	Sequence 21, Appl
121	3	27.3	8	3	US-09-042-107-12	Sequence 2, Appl	27.3	1	US-08-217-146A-23	Sequence 23, Appl
122	3	27.3	8	3	US-09-263-975-25	Sequence 25, Appl	27.3	1	US-08-217-146A-34	Sequence 34, Appl
123	3	27.3	8	3	US-09-263-975-26	Sequence 26, Appl	27.3	1	US-08-217-146A-35	Sequence 35, Appl
124	3	27.3	8	3	US-09-133-062D-25	Sequence 25, Appl	27.3	1	US-08-217-146A-36	Sequence 36, Appl
125	3	27.3	8	3	US-09-082-279H-176	Sequence 176, Appl	27.3	1	US-08-217-146A-37	Sequence 37, Appl
126	3	27.3	8	3	US-09-082-279H-1505	Sequence 1505, Appl	27.3	1	US-08-217-146A-38	Sequence 38, Appl
127	3	27.3	8	3	US-08-486-673B-31	Sequence 31, Appl	27.3	1	US-08-217-146A-39	Sequence 39, Appl
128	3	27.3	8	3	US-08-326-718-9	Sequence 9, Appl	27.3	1	US-08-217-146A-40	Sequence 40, Appl
129	3	27.3	8	3	US-07-963-329A-53	Sequence 53, Appl	27.3	1	US-08-217-146A-41	Sequence 41, Appl
130	3	27.3	8	3	US-07-963-329A-54	Sequence 54, Appl	27.3	1	US-08-217-146A-42	Sequence 42, Appl
131	3	27.3	8	3	US-09-556-111-53	Sequence 53, Appl	27.3	1	US-08-217-146A-43	Sequence 43, Appl
132	3	27.3	8	3	US-09-314-268-72	Sequence 72, Appl	27.3	1	US-08-217-146A-44	Sequence 44, Appl
133	3	27.3	8	3	US-09-314-268-73	Sequence 73, Appl	27.3	1	US-08-217-146A-45	Sequence 45, Appl
134	3	27.3	8	3	US-09-314-268-74	Sequence 74, Appl	27.3	1	US-08-217-146A-46	Sequence 46, Appl
135	3	27.3	8	3	US-09-314-268-75	Sequence 75, Appl	27.3	1	US-08-217-146A-47	Sequence 47, Appl
136	3	27.3	8	3	US-09-314-268-76	Sequence 76, Appl	27.3	1	US-08-217-146A-48	Sequence 48, Appl
137	3	27.3	8	3	US-09-314-268-77	Sequence 77, Appl	27.3	1	US-08-217-146A-49	Sequence 49, Appl
138	3	27.3	8	3	US-09-315-304B-1632	Sequence 1632, Appl	27.3	1	US-08-217-146A-50	Sequence 50, Appl
139	3	27.3	8	3	US-09-315-304B-1659	Sequence 1659, Appl	27.3	1	US-08-217-146A-51	Sequence 51, Appl
140	3	27.3	8	3	US-08-938-105-1	Sequence 1, Appl	27.3	1	US-08-217-146A-52	Sequence 52, Appl
141	3	27.3	8	3	US-09-524-435-5	Sequence 5, Appl	27.3	1	US-08-217-146A-53	Sequence 53, Appl
142	3	27.3	8	3	US-07-945-280B-15	Sequence 15, Appl	27.3	1	US-08-217-146A-54	Sequence 54, Appl
143	3	27.3	8	3	US-08-988-842-31	Sequence 31, Appl	27.3	1	US-08-217-146A-55	Sequence 55, Appl
144	3	27.3	8	3	US-09-104-337A-473	Sequence 473, Appl	27.3	1	US-08-217-146A-56	Sequence 56, Appl
145	3	27.3	8	3	US-09-129-192C-25	Sequence 25, Appl	27.3	1	US-08-217-146A-57	Sequence 57, Appl
146	3	27.3	8	3	US-09-129-192C-26	Sequence 26, Appl	27.3	1	US-08-217-146A-58	Sequence 58, Appl
147	3	27.3	8	3	US-09-266-764-11	Sequence 11, Appl	27.3	1	US-08-217-146A-59	Sequence 59, Appl
148	3	27.3	8	3	US-09-691-523A-11	Sequence 11, Appl	27.3	1	US-08-217-146A-60	Sequence 60, Appl
149	3	27.3	8	3	US-09-834-784-1278	Sequence 1278, Appl	27.3	1	US-08-217-146A-61	Sequence 61, Appl
150	3	27.3	8	3	US-09-834-784-1525	Sequence 1525, Appl	27.3	1	US-08-217-146A-62	Sequence 62, Appl
151	3	27.3	8	3	PCT-US92-0944A-54	Sequence 54, Appl	27.3	1	US-08-217-146A-63	Sequence 63, Appl
152	3	27.3	8	3	PCT-US92-0944A-54	Sequence 54, Appl	27.3	1	US-08-217-146A-64	Sequence 64, Appl
153	3	27.3	8	3	PCT-US93-03985-4	Sequence 4, Appl	27.3	1	US-08-217-146A-65	Sequence 65, Appl
154	3	27.3	8	3	PCT-US96-03473-19	Sequence 19, Appl	27.3	1	US-08-217-146A-66	Sequence 66, Appl
155	3	27.3	8	3	PCT-US96-11458-5	Sequence 5, Appl	27.3	1	US-08-217-146A-67	Sequence 67, Appl
156	3	27.3	8	3	5183745-7	Sequence 7, Appl	27.3	1	US-08-217-146A-68	Sequence 68, Appl
157	3	27.3	8	3	5194592-46	Sequence 46, Appl	27.3	1	US-08-217-146A-69	Sequence 69, Appl
158	3	27.3	8	3	5206152-13	Sequence 13, Appl	27.3	1	US-08-217-146A-70	Sequence 70, Appl
159	3	27.3	9	1	US-08-080-074-14	Sequence 14, Appl	27.3	1	US-08-217-146A-71	Sequence 71, Appl
160	3	27.3	9	1	US-07-930-644-6	Sequence 6, Appl	27.3	1	US-08-217-146A-72	Sequence 72, Appl
161	3	27.3	9	1	US-08-082-847-31	Sequence 31, Appl	27.3	1	US-08-217-146A-73	Sequence 73, Appl
162	3	27.3	9	1	US-08-082-847-32	Sequence 32, Appl	27.3	1	US-08-217-146A-74	Sequence 74, Appl
163	3	27.3	9	1	US-08-082-847-33	Sequence 33, Appl	27.3	1	US-08-217-146A-75	Sequence 75, Appl
164	3	27.3	9	1	US-08-082-847-34	Sequence 34, Appl	27.3	1	US-08-217-146A-76	Sequence 76, Appl
165	3	27.3	9	1	US-08-082-847-35	Sequence 35, Appl	27.3	1	US-08-217-146A-77	Sequence 77, Appl
166	3	27.3	9	1	US-08-082-847-36	Sequence 36, Appl	27.3	1	US-08-217-146A-78	Sequence 78, Appl
167	3	27.3	9	1	US-08-082-847-37	Sequence 37, Appl	27.3	1	US-08-217-146A-79	Sequence 79, Appl
168	3	27.3	9	1	US-08-082-847-38	Sequence 38, Appl	27.3	1	US-08-217-146A-80	Sequence 80, Appl
169	3	27.3	9	1	US-08-322-707-4	Sequence 4, Appl	27.3	1	US-08-217-146A-81	Sequence 81, Appl
170	3	27.3	9	1	US-08-178-570-22	Sequence 22, Appl	27.3	1	US-08-217-146A-82	Sequence 82, Appl
171	3	27.3	9	1	US-08-178-570-27	Sequence 27, Appl	27.3	1	US-08-217-146A-83	Sequence 83, Appl
172	3	27.3	9	1	US-08-178-570-28	Sequence 28, Appl	27.3	1	US-08-217-146A-84	Sequence 84, Appl
173	3	27.3	9	1	US-08-178-570-29	Sequence 29, Appl	27.3	1	US-08-217-146A-85	Sequence 85, Appl

247	3	27.3	9	3	US-08-159-139A-973	Sequence 973, App	320	3	27.3	3	US-08-159-139A-973	Sequence 973, App
248	3	27.3	9	3	US-08-159-139A-979	Sequence 979, App	321	3	27.3	3	US-08-159-139A-979	Sequence 979, App
249	3	27.3	9	3	US-08-159-139A-1220	Sequence 1223, App	322	3	27.3	3	US-08-159-139A-1220	Sequence 1223, App
250	3	27.3	9	3	US-09-015-968-5	Sequence 5, App	323	3	27.3	3	US-09-015-968-5	Sequence 5, App
251	3	27.3	9	3	US-08-667-725B-19	Sequence 19, App	324	3	27.3	3	US-08-667-725B-19	Sequence 19, App
252	3	27.3	9	3	US-09-231-797-67	Sequence 67, App	325	3	27.3	3	US-09-231-797-67	Sequence 67, App
253	3	27.3	9	3	US-08-817-177-16	Sequence 16, App	326	3	27.3	3	US-08-817-177-16	Sequence 16, App
254	3	27.3	9	3	US-08-931-645-50	Sequence 50, App	327	3	27.3	3	US-08-931-645-50	Sequence 50, App
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259	3	27.3	9	3	US-09-007-748-19	Sequence 19, App	332	3	27.3	3	US-09-007-748-19	Sequence 19, App
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297	3	27.3	9	4	US-07-963-429A-70	Sequence 70, App	370	3	27.3	3	US-07-963-429A-70	Sequence 70, App
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302	3	27.3	9	4	US-09-492-543-108	Sequence 108, App	375	3	27.3	3	US-09-492-543-108	Sequence 108, App
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305	3	27.3	9	4	US-09-492-543-171	Sequence 171, App	378	3	27.3	3	US-09-492-543-171	Sequence 171, App
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307	3	27.3	9	4	US-09-565-548-59	Sequence 59, App	380	3	27.3	3	US-09-565-548-59	Sequence 59, App
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309	3	27.3	9	4	US-09-339-511-2	Sequence 2, App	382	3	27.3	3	US-09-339-511-2	Sequence 2, App
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311	3	27.3	9	4	US-09-339-511-4	Sequence 4, App	384	3	27.3	3	US-09-339-511-4	Sequence 4, App
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314	3	27.3	9	4	US-09-302-305C-24	Sequence 24, App	387	3	27.3	3	US-09-302-305C-24	Sequence 24, App
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316	3	27.3	9	4	US-08-408-915-1	Sequence 1, App	389	3	27.3	3	US-08-408-915-1	Sequence 1, App
317	3	27.3	9	4	US-08-408-915-2	Sequence 2, App	390	3	27.3	3	US-08-408-915-2	Sequence 2, App
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; Patent No. 5747339
; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, Hiroto
; APPLICANT: FURE, Isao
; APPLICANT: MORI, Chisato
; APPLICANT: TAKAMIZAWA, Akaishi
; APPLICANT: YOSHIDA, Iwao
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armsstrong, Westernman, Hattori, McDaniel &
; ADDRESSEE: Naughton
; STREET: 1725 K St. N.W. Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,977
; FILING DATE: 18-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-167466
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-230921
; FILING DATE: 31-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-305605
; FILING DATE: 09-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,706
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/769,996
; FILING DATE: 02-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/635,451
; FILING DATE: 28-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens-Smith, Theresa M.
; REGISTRATION NUMBER: 36,281
; REFERENCE/DOCKET NUMBER: 9007030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-324-977-24

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Query Match 36.4% Score 4; DB 1; Length 9;
Best local Similarity 100.0%; Pred. No. 2 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 6 GNSS 9
Db 4 GNSS 7

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RESULT 3
US-08-384-616-24
; Sequence 24, Application US/08384616
; Patent No. 5847101

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; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, Hiroto
; APPLICANT: FURE, Isao
; APPLICANT: MORI, Chisato
; APPLICANT: TAKAMIZAWA, Akaishi
; APPLICANT: YOSHIDA, Iwao
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Westernman, Hattori, McDaniel &
; ADDRESSEE: Naughton
; STREET: 1725 K St. N.W. Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,977
; FILING DATE: 18-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-167466
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-230921
; FILING DATE: 31-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-305605
; FILING DATE: 09-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,706
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/769,996
; FILING DATE: 02-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/635,451
; FILING DATE: 28-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens-Smith, Theresa M.
; REGISTRATION NUMBER: 36,281
; REFERENCE/DOCKET NUMBER: 9007030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-384-616-24

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Query Match 36.4% Score 4; DB 1; Length 9;
Best local Similarity 100.0%; Pred. No. 2 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 GNSS 7

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RESULT 4
US-08-928-958-19
; Sequence 19, Application US/08928958
; Patent No. 5877282
; GENERAL INFORMATION:
; APPLICANT: NADEAU, STEVEN J.
; APPLICANT: CLEVELAND, JEFFERY S.
; APPLICANT: BLAKE, JAMES

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1 APPLICANT: HAFAR, OMAR K.
2 TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
3 TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
4 TITLE OF INVENTION: METHODS OF USE THEREOF
5 NUMBER OF SEQUENCES: 24
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: ROBINS & ASSOCIATES
8 STREET: 90 MIDDLEFIELD ROAD, SUITE 200
9 CITY: MENLO PARK
10 STATE: CA
11 COUNTRY: USA
12 ZIP: 94025
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/928,958
21 FILING DATE: 12-SEP-1997
22 CLASSIFICATION: 514
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 60/026978
25 FILING DATE: 20-SEP-1996
26 ATTORNEY/AGENT INFORMATION:
27 NAME: ROBINS, ROBERTA L.
28 REGISTRATION NUMBER: 33,208
29 REFERENCE/DOCKET NUMBER: 5998-0019
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (650) 325-7812
32 TELEFAX: (650) 325-7823
33 INFORMATION FOR SEQ ID NO: 19:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 9 amino acids
36 TYPE: amino acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: peptide
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41 US-08-928-958-19
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43 Query Match 36.4%, Score 4; LR 2; Length 9;
44 Best Local Similarity 100.0%; Pred. No. 2; Seq-05;
45 Matches 4; Conservative 0; Mismatches 0; In-1s 0; Gaps 0
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47 QY 2 KSRK 5
48 DB 1111
49 3 KSRK 6
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51 RESULT 5
52 US-09 072 429-19
53 Sequence 19, Application US/09072429
54 Patent No. 5962415
55 GENERAL INFORMATION:
56 APPLICANT: Nadler, Steven G.
57 TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
58 TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSCLOCATION AND AN
59 TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
60 NUMBER OF SEQUENCES: 24
61 CORRESPONDENCE ADDRESS:
62 ADDRESSEE: Bristol-Myers Squibb Company
63 STREET: P.O. Box 4000
64 CITY: Princeton
65 STATE: New Jersey
66 COUNTRY: USA
67 ZIP: 08543-4000
68 COMPUTER READABLE FORM:
69 MEDIUM TYPE: Floppy disk
70 COMPUTER: IBM PC compatible
71 OPERATING SYSTEM: PC-DOS/MS-DOS
72 SOFTWARE: PatentIn Release #1.0, Version #1.30
73 CURRENT APPLICATION DATA:
74 APPLICATION NUMBER: US/09/072,429

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1 FILING DATE: 4 MAY 1996
2 CLASSIFICATION: 514
3 ATTORNEY/AGENT INFORMATION:
4 NAME: KROTH, CLAUDIA A.
5 REGISTRATION NUMBER: 44,000
6 REFERENCE/DOCKET NUMBER: N 141
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (650) 325-7812
9 TELEFAX: (650) 325-7823
10 INFORMATION FOR SEQ ID NO: 19:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 9 amino acids
13 TYPE: amino acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 MOLECULE TYPE: peptide
17 INFORMATION FOR SEQ ID NO: 19:
18 US-09 072-429-19
19
20 Query Match 36.4%, Score 4; LR 2; Length 9;
21 Best Local Similarity 100.0%; Pred. No. 2; Seq-05;
22 Matches 4; Conservative 0; Mismatches 0; In-1s 0; Gaps 0
23
24 QY 2 KSRK 5
25 DB 1111
26 3 KSRK 6
27
28 RESULT 6
29 US-08-928-958-19
30 Sequence 19, Application US/08026978
31 Patent No. 5962415
32 GENERAL INFORMATION:
33 APPLICANT:
34 TITLE OF INVENTION: NEW HIV-1 VIRUS RESISTANT HIV-1 VIRUS INHIBITORS OF HIV-1
35 TITLE OF INVENTION: INHIBITORS OF HIV-1 VIRUS INHIBITORS OF HIV-1
36 NUMBER OF SEQUENCES: 19
37 CORRESPONDENCE ADDRESS:
38 ADDRESSEE: National Institutes of Health, and Statens Serum
39 STREET: 400 South Street, N.W.
40 CITY: Washington
41 STATE: DC
42 COUNTRY: USA
43 ZIP: 20034
44 COMPUTER READABLE FORM:
45 MEDIUM TYPE: Floppy disk
46 COMPUTER: IBM PC compatible
47 OPERATING SYSTEM: PC-DOS/MS-DOS
48 SOFTWARE: PatentIn Release #1.0, Version #1.30 (FPO)
49 CURRENT APPLICATION DATA:
50 APPLICATION NUMBER: US/08/928,958
51 FILING DATE: 20 APR 1997
52 CLASSIFICATION: 514
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: US/08/928,958
55 FILING DATE: 20 APR 1997
56 INFORMATION FOR SEQ ID NO: 19:
57 SEQUENCE CHARACTERISTICS:
58 LENGTH: 9 amino acids
59 TYPE: amino acid
60 TOPOLOGY: unknown
61 MOLECULE TYPE: peptide
62 INFORMATION FOR SEQ ID NO: 19:
63 US-08-928-958-19
64
65 Query Match 36.4%, Score 4; LR 2; Length 9;
66 Best Local Similarity 100.0%; Pred. No. 2; Seq-05;
67 Matches 4; Conservative 0; Mismatches 0; In-1s 0; Gaps 0
68
69 QY 5 KSRK 8
70 DB 1111

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DB 6 KGNS 9

## RESULT 7

US-08-904-686A-24  
: Sequence 24, Application US/08904686A  
: Patent No. 5998130  
: GENERAL INFORMATION:  
: APPLICANT: OKAYAMA, Hirolo  
: APPLICANT: FUKE, Isao  
: APPLICANT: MORI, Chisato  
: APPLICANT: TAKAMIZAWA, Akahisa  
: APPLICANT: YOSHIDA, Iwao  
: TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
: TITLE OF INVENTION: CONA AND ANTIGEN POLYPEPTIDE  
: NUMBER OF SEQUENCES: 50  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Armstrong, Westerman, Hattori, McLeod &  
: STREET: 1725 K St. N.W. Suite 1030  
: CITY: Washington  
: STATE: D.C.  
: COUNTRY: U.S.A.  
: ZIP: 20006  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb  
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: APPLICATION NUMBER: US/08/904,686A  
: FILING DATE: 01-AUG-1997  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/324,977  
: FILING DATE: 18-OCT-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-167466  
: FILING DATE: 25-JUN-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-230921  
: FILING DATE: 31-AUG-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-305605  
: FILING DATE: 09-NOV-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/099,706  
: FILING DATE: 30-JUL-1993  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/769,996  
: FILING DATE: 02-OCT-1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/635,451  
: FILING DATE: 28-DEC-1990  
: ATTORNEY/AGENT INFORMATION:  
: NAME: McLeod, Le-Nhung  
: REGISTRATION NUMBER: 31,541  
: REFERENCE/DOCKET NUMBER: 900703G  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202) 659-2910  
: TELEFAX: (202) 887-0357  
: INFORMATION FOR SEQ ID NO: 24:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 9 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
US-08-904-686A-24

Query Match 36.4%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 GNSS 9

DB 4 GNSS 2

RESULT 8  
US-09-415-850-24  
: Sequence 24, Application US/09415850  
: Patent No. 6231624  
: GENERAL INFORMATION:  
: APPLICANT: OKAYAMA, Hirolo  
: APPLICANT: FUKE, Isao  
: APPLICANT: MORI, Chisato  
: APPLICANT: TAKAMIZAWA, Akahisa  
: APPLICANT: YOSHIDA, Iwao  
: TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
: TITLE OF INVENTION: CONA AND ANTIGEN POLYPEPTIDE  
: NUMBER OF SEQUENCES: 50  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Armstrong, Westerman, Hattori, McLeod &  
: STREET: 1725 K St. N.W. Suite 1030  
: CITY: Washington  
: STATE: D.C.  
: COUNTRY: U.S.A.  
: ZIP: 20006  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0  
: SOFTWARE: ASCII  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/415,850A  
: FILING DATE:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/09/404,340  
: FILING DATE: 01-AUG-1997  
: APPLICATION NUMBER: US 09/423,977  
: FILING DATE: 18-OCT-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-167466  
: FILING DATE: 25-JUN-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-230921  
: FILING DATE: 31-AUG-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/099,706  
: FILING DATE: 30-JUL-1993  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/769,996  
: FILING DATE: 02-OCT-1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/635,451  
: FILING DATE: 28-DEC-1990  
: ATTORNEY/AGENT INFORMATION:  
: NAME: McLeod, Le-Nhung  
: REGISTRATION NUMBER: 31,541  
: REFERENCE/DOCKET NUMBER: 900703G  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202) 659-2910  
: TELEFAX: (202) 887-0357  
: INFORMATION FOR SEQ ID NO: 24:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 9 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
US-09-415-850-24

Query Match 46.4%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

```

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 6 GNSS 9
Db 4 GNSS 7

RESULT 9
US-09-257-490 8
Sequence 8: Application US/09/257490A
Patent No. 6248328
GENERAL INFORMATION:
APPLICANT: Dietrich, Ursula
APPLICANT: Von Briesen, Hagen
APPLICANT: Grez, Manuel
APPLICANT: Rubsam, Walqmann, Beiga
TITLE OF INVENTION: HIV-1 virus isolates of a subtype and its 4 Proteomorphs
TITLE OF INVENTION: diagnostics, a vaccine against HIV-1 virus isolates
TITLE OF INVENTION: of this subtype and method of producing same
TITLE OF INVENTION: the HIV-1 virus isolates
FILE REFERENCE: 10496/P58512051
CURRENT APPLICATION NUMBER: US/09/257,490A
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-257-490-8

Query Match 36.4%; Score 4: 145 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2,500.0;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 5 GNSS 8
Db 6 GNSS 9

RESULT 10
US-09-593-870A-58
Sequence 58: Application US/09/593870A
Patent No. 6548643
GENERAL INFORMATION:
APPLICANT: McKenzie, Ian F.C.
APPLICANT: Apostolopoulos, Vasso
APPLICANT: Pictersz, Geoff Allan
TITLE OF INVENTION: Antigen Carbohydrate Compounds and their
TITLE OF INVENTION: Use in Immunotherapy
FILE REFERENCE: 2368-McKenzie
CURRENT APPLICATION NUMBER: US/09/593,870A
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version: 4.0
SEQ ID NO 58
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-593-870A-58

Query Match 36.4%; Score 4: 145 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2,500.0;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 7 NSSL 10
Db 1 NSSL 4

RESULT 11

```

```

US-09-593-870A-58
Sequence 58: Application US/09/593870A
Patent No. 6548643
GENERAL INFORMATION:
APPLICANT: McKenzie, Ian F.C.
APPLICANT: Apostolopoulos, Vasso
APPLICANT: Pictersz, Geoff Allan
TITLE OF INVENTION: Antigen Carbohydrate Compounds and their
TITLE OF INVENTION: Use in Immunotherapy
FILE REFERENCE: 2368-McKenzie
CURRENT APPLICATION NUMBER: US/09/593,870A
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version: 4.0
SEQ ID NO 58
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-593-870A-58

Query Match 36.4%; Score 4: 145 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1,800.0;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 6 NSSL 11
Db 6 NSSL 9

RESULT 12
US-09-593-870A-58
Sequence 58: Application US/09/593870A
Patent No. 6548643
GENERAL INFORMATION:
APPLICANT: McKenzie, Ian F.C.
APPLICANT: Apostolopoulos, Vasso
APPLICANT: Pictersz, Geoff Allan
TITLE OF INVENTION: Antigen Carbohydrate Compounds and their
TITLE OF INVENTION: Use in Immunotherapy
FILE REFERENCE: 2368-McKenzie
CURRENT APPLICATION NUMBER: US/09/593,870A
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patent In Ver. 2.1

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```

; SEQ ID NO 48
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acids
; OTHER INFORMATION: encoded by bases 921-956 of pBKX-3X
US-09-391-546-48

Query Match          36.4%  Score 4;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2, 4e-02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 6 GNSS 9
    IIII
DB 8 GNSS 11

RESULT 13
US-08-836-075A-164
; Sequence 164; Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS A VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; NUMBER OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DUKREE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836.075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.4
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-075A-164

Query Match          36.4%  Score 4;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2, 4e-02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 6 GNSS 9
    IIII
DB 4 GNSS 7
```

```

RESULT 14
US-09-219-586-74
; Sequence 74; Application US/09/219.586
; Patent No. 621864
; GENERAL INFORMATION:
; APPLICANT: MITCHELL, WILLIAM W.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES
; TITLE OF INVENTION: AND THEIR USE
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; CURRENT APPLICATION NUMBER: US/09/219.586
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: US/97-04-04
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: US/97-04-04
; EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FASTSEQ FOR WINDOWS Version 1.3
; SEQ ID NO: 101
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-219-586-74

Query Match          36.4%  Score 4;  DB 4;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 2, 4e-02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1 ASK 4
    III
DB 6 ASK 9

RESULT 15
US-09-025-596-164
; Sequence 103; Application US/09/025.596
; Patent No. 634464
; GENERAL INFORMATION:
; APPLICANT: MITCHELL, WILLIAM W.
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: ANTIGENIC PEPTIDES
; TITLE OF INVENTION: AND THEIR USE
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; CURRENT APPLICATION NUMBER: US/09/025.596
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: US/97-04-04
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: US/97-04-04
; EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FASTSEQ FOR WINDOWS Version 1.3
; SEQ ID NO: 101
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-025-596-164

Query Match          36.4%  Score 4;  DB 4;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 2, 4e-02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 2 KSK 5
    IIII
DB 7 KSK 10

RESULT 16
US-09-025-596-164
; Sequence 103; Application US/09/025.596
; Patent No. 634464
; GENERAL INFORMATION:
; APPLICANT: MITCHELL, WILLIAM W.
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: ANTIGENIC PEPTIDES
; TITLE OF INVENTION: AND THEIR USE
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
```



STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,661  
FILING DATE: 06-MAY-1998  
CLASSIFICATION: 436

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/025,521  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: US 08/911,594  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 60/023,921  
FILING DATE: 14-AUG-1996  
APPLICATION NUMBER: US 09/025,176  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: US 09/025,174  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: US 60/045,739  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,779  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,780  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,784  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,787  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,689  
FILING DATE: 6-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O  
REGISTRATION NUMBER: 33,542  
REFERENCE/DOCKET NUMBER: VDB97-09pm  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-073-661-103

Query Match 36.4% Score 4: 10: 4: Length 14:  
Best Local Similarity 100.0% Pred. No. 2: 5: 0: 2:  
Matches 4: Conservative 0: Mismatches 0: Labels 0: Gaps 0:

QY 2 KSRK 5  
DB 7 KSRK 10

RESULT 20  
US-08-879-565-7  
Sequence 7, Application US/08879565A  
Patent No. 6093573  
GENERAL INFORMATION:  
APPLICANT: Beamer, Lesa J  
APPLICANT: Carroll, Stephen F  
APPLICANT: Eisenberg, David  
TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN

FILE REFERENCED: US/09/073,661  
CURRENT APPLICATION NUMBER: US/09/073,661A  
CURRENT FILING DATE: 06-MAY-1998  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FASTSEQ for Windows  
SEQ ID NO: 7  
LENGTH: 14  
TYPE: PR  
ORGANISM: Human  
FEATURES:  
OTHER INFORMATION: "FastSeq" made available sequentially in releases  
OTHER INFORMATION: "FastSeq" made available sequentially in releases  
US 08-879-565-7

Query Match 36.4% Score 4: 10: 4: Length 14:  
Best Local Similarity 100.0% Pred. No. 2: 5: 0: 2:  
Matches 4: Conservative 0: Mismatches 0: Labels 0: Gaps 0:

QY 2 KSRK 5  
DB 7 KSRK 10  
RESULT 21  
US 09-433-245A-10  
Sequence 10, Application US/09-433-245A  
Patent No. 642696  
GENERAL INFORMATION:  
APPLICANT: ELI LILLY AND COMPANY, NEW CASTLE  
TITLE OF INVENTION: LEVEL-DEPENDENT INTRACELLULAR ANTIGEN PRESENTATION  
FILE REFERENCED: US 09-433-245A  
CURRENT APPLICATION NUMBER: US/09-433-245A  
CURRENT FILING DATE: 09-04-1999  
PRIOR APPLICATION NUMBER: 60/104,864  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 60/142,267  
PRIOR FILING DATE: 1999-07-05  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent In Vitro 2.0  
SEQ ID NO: 10  
LENGTH: 14  
TYPE: PR  
ORGANISM: Unknown  
FEATURES:  
OTHER INFORMATION: "FastSeq" made available sequentially in releases  
OTHER INFORMATION: "FastSeq" made available sequentially in releases  
US 09-433-245A-10

Query Match 36.4% Score 4: 10: 4: Length 14:  
Best Local Similarity 100.0% Pred. No. 2: 5: 0: 2:  
Matches 4: Conservative 0: Mismatches 0: Labels 0: Gaps 0:

QY 2 KSRK 5  
DB 7 KSRK 10

RESULT 22  
US 09-252-404A-21  
Sequence 21, Application US/09-252-404A  
Patent No. 645376  
GENERAL INFORMATION:  
APPLICANT: KIM PLUM LTD  
APPLICANT: XERO ZION LTD  
TITLE OF INVENTION: METHODS and Compositions for Regulating  
TITLE OF INVENTION: Protein-Protein Interactions  
FILE REFERENCED: 1440,134 00  
CURRENT APPLICATION NUMBER: S/09/252,404A  
CURRENT FILING DATE: 1999-02-18  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 21  
LENGTH: 14

? TYPE: PRT  
? ORGANISM: Synthetic peptide  
US-09-252-404-21

Query Match 36.4% Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2, 50-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
|||||  
DB 11 AKSR 14

RESULT 23  
US-08-616-844-45  
? Sequence 45, Application US/08616844  
? Patent No. 5849578  
? GENERAL INFORMATION:  
? APPLICANT: FALH, DEAN A.  
? TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
? TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
? NUMBER OF SEQUENCES: 54  
? CORRESPONDENCE ADDRESS:  
? ADDRESSEE: PENNIE & EDMONDS  
? STREET: 1155 Avenue of the Americas  
? CITY: New York  
? STATE: New York  
? COUNTRY: USA  
? ZIP: 10016-2711  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? OPERATING SYSTEM: IBM PC compatible  
? SOFTWARE: Patent Release #1.0, Version #1.30  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: US/08/616,844  
? FILING DATE: 15-MAR-1996  
? CLASSIFICATION: 800  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US 08/599,654  
? FILING DATE: 09-FEB-1995  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US 08/485,573  
? FILING DATE: 07-JUN-1995  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US 08/386,844  
? FILING DATE: 10-FEB-1995  
? ATTORNEY/AGENT INFORMATION:  
? NAME: CORUZZI, LAURA A.  
? REGISTRATION NUMBER: 30,742  
? REFERENCE/DOCKET NUMBER: 7853-055  
? TELECOMMUNICATION INFORMATION:  
? TELEPHONE: (212) 790-9090  
? TELEFAX: (212) 869-8864  
? INFORMATION FOR SEQ ID NO: 45:  
? SEQUENCE CHARACTERISTICS:  
? LENGTH: 15 amino acids  
? TYPE: amino acid  
? STRANDEDNESS:  
? TOPOLOGY: unknown  
? MOLECULE TYPE: peptide  
US-08-616-844-45

Query Match 36.4% Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2, 70-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
|||||  
DB 9 AKSR 12

RESULT 24  
US-08-650-272-10  
? Sequence 16, Application US/08700000  
? Patent No. 5866124  
? GENERAL INFORMATION:  
? APPLICANT: BODLEY, N. GARY, JR.  
? APPLICANT: PUSKAS, BOB  
? APPLICANT: MURRAY, SCOTT  
? TITLE OF INVENTION: Method for controlling antibodies  
? NUMBER OF SEQUENCES: 2  
? CORRESPONDENCE ADDRESS:  
? ADDRESSEE: N. GARY BODLEY & COMPANY  
? STREET: 6000  
? CITY: East Rutherford  
? STATE: NJ  
? COUNTRY: USA  
? ZIP: 07073  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? OPERATING SYSTEM: IBM PC compatible  
? SOFTWARE: Patent Release #1.0, Version #1.30  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: US/08/650,272  
? FILING DATE:  
? CLASSIFICATION: 114  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US 08/616,844  
? FILING DATE: 17-MAR-1996  
? ATTORNEY/AGENT INFORMATION:  
? NAME: BODLEY, N. GARY, JR.  
? REGISTRATION NUMBER: 30,742  
? REFERENCE/DOCKET NUMBER: 7853-055  
? TELECOMMUNICATION INFORMATION:  
? TELEPHONE: 908-272-0110  
? TELEFAX: 908-272-0110  
? INFORMATION FOR SEQ ID NO: 16:  
? SEQUENCE CHARACTERISTICS:  
? LENGTH: 15 amino acids  
? TYPE: amino acid  
? STRANDEDNESS:  
? TOPOLOGY: unknown  
? MOLECULE TYPE: Peptide  
? REFERENCE: NO  
US-08-650-272-10

Query Match 36.4% Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2, 70-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSIM 11  
|||||  
DB 11 SSIM 14

RESULT 25  
US-08-599-654-45  
? Sequence 45, Application US/08700000  
? Patent No. 5862705  
? GENERAL INFORMATION:  
? APPLICANT: FALH, DEAN A.  
? TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
? TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
? NUMBER OF SEQUENCES: 54  
? CORRESPONDENCE ADDRESS:  
? ADDRESSEE: PENNIE & EDMONDS  
? STREET: 1155 Avenue of the Americas  
? CITY: New York  
? STATE: New York  
? COUNTRY: USA  
? ZIP: 10016-2711  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? SOFTWARE: IBM PC compatible

1 OPERATING SYSTEM: PC-DOS/MS-DOS  
 2 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 3 CURRENT APPLICATION DATA:  
 4 APPLICATION NUMBER: US/08/599,654  
 5 FILING DATE: 09-FEB-1995  
 6 CLASSIFICATION: 800  
 7 PRIOR APPLICATION DATA:  
 8 APPLICATION NUMBER: US 08/485,575  
 9 FILING DATE: 07-JUN-1995  
 10 PRIOR APPLICATION DATA:  
 11 APPLICATION NUMBER: US 08/386,844  
 12 FILING DATE: 10-FEB-1995  
 13 ATTORNEY/AGENT INFORMATION:  
 14 NAME: CORUZZI, LAURA A.  
 15 REGISTRATION NUMBER: 30,742  
 16 REFERENCE/DOCKET NUMBER: 7853-641  
 17 TELECOMMUNICATION INFORMATION:  
 18 TELEPHONE: (212) 790-9090  
 19 TELEFAX: (212) 869-8864  
 20 TELEX: 66141 PENNIF  
 21 INFORMATION FOR SEQ ID NO: 45:  
 22 SEQUENCE CHARACTERISTICS:  
 23 LENGTH: 15 amino acids  
 24 TYPE: amino acid  
 25 STRANDEDNESS:  
 26 TOPOLOGY: unknown  
 27 MOLECULE TYPE: peptide  
 28 US-08-599-654-45

Query Match 36.4% Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2 7853-641  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 DB 9 AKSR 12

## RESULT 2/6

US-08-944-868A-45  
 1 Sequence 45, Application US/08944868A  
 2 Patent No. 6018025  
 3 GENERAL INFORMATION:  
 4 APPLICANT: FALB, DEAN A.  
 5 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 6 TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 7 NUMBER OF SEQUENCES: 34  
 8 CORRESPONDENCE ADDRESS:  
 9 ADDRESSEE: PENNIE & EDMONDS  
 10 STREET: 1155 Avenue of the Americas  
 11 CITY: New York  
 12 STATE: New York  
 13 COUNTRY: USA  
 14 ZIP: 10036-2711  
 15 COMPUTER READABLE FORM:  
 16 MEDIUM TYPE: Floppy disk  
 17 COMPUTER: IBM PC compatible  
 18 OPERATING SYSTEM: PC-DOS/MS-DOS  
 19 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 20 CURRENT APPLICATION DATA:  
 21 APPLICATION NUMBER: US/08/944,868A  
 22 FILING DATE:  
 23 CLASSIFICATION:  
 24 PRIOR APPLICATION DATA:  
 25 APPLICATION NUMBER: 08/599,654  
 26 FILING DATE:  
 27 PRIOR APPLICATION DATA:  
 28 APPLICATION NUMBER: US 08/386,844  
 29 FILING DATE: 10-FEB-1995  
 30 ATTORNEY/AGENT INFORMATION:  
 31 NAME: CORUZZI, LAURA A.  
 32 REGISTRATION NUMBER: 30,742  
 33 REFERENCE/DOCKET NUMBER: 7853-041

1 OPERATING SYSTEM: PC-DOS/MS-DOS  
 2 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 3 CURRENT APPLICATION DATA:  
 4 APPLICATION NUMBER: US/08/599,654  
 5 FILING DATE: 09-FEB-1995  
 6 CLASSIFICATION: 800  
 7 PRIOR APPLICATION DATA:  
 8 APPLICATION NUMBER: US 08/485,575  
 9 FILING DATE: 07-JUN-1995  
 10 PRIOR APPLICATION DATA:  
 11 APPLICATION NUMBER: US 08/386,844  
 12 FILING DATE: 10-FEB-1995  
 13 ATTORNEY/AGENT INFORMATION:  
 14 NAME: CORUZZI, LAURA A.  
 15 REGISTRATION NUMBER: 30,742  
 16 REFERENCE/DOCKET NUMBER: 7853-641  
 17 TELECOMMUNICATION INFORMATION:  
 18 TELEPHONE: (212) 790-9090  
 19 TELEFAX: (212) 869-8864  
 20 TELEX: 66141 PENNIF  
 21 INFORMATION FOR SEQ ID NO: 45:  
 22 SEQUENCE CHARACTERISTICS:  
 23 LENGTH: 15 amino acids  
 24 TYPE: amino acid  
 25 STRANDEDNESS:  
 26 TOPOLOGY: unknown  
 27 MOLECULE TYPE: peptide  
 28 US-08-599-654-45  
 29 Query Match 36.4% Score 4; DB 2; Length 15;  
 30 Best Local Similarity 100.0%; Pred. No. 2 7853-641  
 31 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 2/7

US-08-296-848A-2  
 1 Sequence 45, Application US/08296848A  
 2 Patent No. 6018025  
 3 GENERAL INFORMATION:  
 4 APPLICANT: FALB, DEAN A.  
 5 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 6 TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 7 NUMBER OF SEQUENCES: 34  
 8 CORRESPONDENCE ADDRESS:  
 9 ADDRESSEE: PENNIE & EDMONDS  
 10 STREET: 1155 Avenue of the Americas  
 11 CITY: New York  
 12 STATE: New York  
 13 COUNTRY: USA  
 14 ZIP: 10036  
 15 COMPUTER READABLE FORM:  
 16 MEDIUM TYPE: Floppy disk  
 17 COMPUTER: IBM PC compatible  
 18 OPERATING SYSTEM: PC-DOS/MS-DOS  
 19 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 20 CURRENT APPLICATION DATA:  
 21 APPLICATION NUMBER: US/08/296,848A  
 22 FILING DATE: 26 AUG-1994  
 23 CLASSIFICATION: 424  
 24 ATTORNEY/AGENT INFORMATION:  
 25 NAME: MUSICK, N. J.  
 26 REGISTRATION NUMBER: 18,622  
 27 REFERENCE/DOCKET NUMBER: 111044  
 28 TELECOMMUNICATION INFORMATION:  
 29 TELEPHONE: (212) 790-9090  
 30 TELEFAX: (212) 869-8864  
 31 TELEX: 66141 PENNIF  
 32 INFORMATION FOR SEQ ID NO: 45:  
 33 SEQUENCE CHARACTERISTICS:  
 34 LENGTH: 15 amino acids  
 35 TYPE: amino acid  
 36 STRANDEDNESS:  
 37 TOPOLOGY: unknown  
 38 MOLECULE TYPE: peptide  
 39 US-08-296-848A-2

Query Match 36.4% Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2 7853-641  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AKSR 9

DB 4 AKSR 9





NAME: CORUZZI, LAURA A  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7853-104  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-09-944-496-45

Query Match 36.4% Score 4: DB 3: Length 15:  
 Best Local Similarity 100.0% Pred. No. 2.7e+02  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 AKSR 4  
 Db 9 AKSR 12

## RESULT 31

US-09-365-530-2  
 Sequence 2, Application US/09365530  
 Patent No. 6440423  
 GENERAL INFORMATION:  
 APPLICANT: Clements, John D.  
 APPLICANT: Dickinson, Bonny L.  
 TITLE OF INVENTION: MUTANT ENTEROTOXIN EFFECTIVE AS A  
 TITLE OF INVENTION: NON-TOXIC ORAL ADJUVANT  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/365,530  
 FILING DATE:  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/296,848  
 FILING DATE: 26-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mistock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 5113-046  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-365-530-2

Query Match 36.4% Score 4: DB 4: Length 15:  
 Best Local Similarity 100.0% Pred. No. 2.7e+02  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 AKSR 4  
 Db 9 AKSR 12

RESULT 32  
 US-09-365-530-2  
 Sequence 5, Application US/09365530  
 Patent No. 6440423  
 GENERAL INFORMATION:  
 APPLICANT: Clements, John D.  
 APPLICANT: Dickinson, Bonny L.  
 TITLE OF INVENTION: MUTANT ENTEROTOXIN EFFECTIVE AS A  
 TITLE OF INVENTION: NON-TOXIC ORAL ADJUVANT  
 NUMBER OF SEQUENCES:  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/365,530  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/296,848  
 FILING DATE: 26-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mistock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 5113-046  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-365-530-2

Query Match 36.4% Score 4: DB 4: Length 15:  
 Best Local Similarity 100.0% Pred. No. 2.7e+02  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 AKSR 4  
 Db 9 AKSR 12

RESULT 33  
 US-09-365-530-2  
 Sequence 9, Application US/09365530  
 Patent No. 6440423  
 GENERAL INFORMATION:  
 APPLICANT: Clements, John D.  
 APPLICANT: Dickinson, Bonny L.  
 TITLE OF INVENTION: MUTANT ENTEROTOXIN EFFECTIVE AS A  
 TITLE OF INVENTION: NON-TOXIC ORAL ADJUVANT  
 NUMBER OF SEQUENCES:  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/365,530  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/296,848  
 FILING DATE: 26-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mistock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 5113-046  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-365-530-2

Query Match 36.4% Score 4: DB 4: Length 15:  
 Best Local Similarity 100.0% Pred. No. 2.7e+02  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

? PRIOR FILING DATE: 1999-04-28  
 ? NUMBER OF SEQ ID NOS: 61  
 ? SOFTWARE: PatentIn version 3.1  
 ? SEQ ID NO 9  
 ? LENGTH: 15  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Histone fragment  
 US-09-561-490E-9

Query Match 36.4%; Score 4; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RGN 7  
 DB 2 RGN 5

RESULT 34  
 PCT-US93-06751-7  
 ? Sequence 7; Application PC/TUS9306751  
 ? GENERAL INFORMATION:  
 ? APPLICANT: P. Keller, A. J. Conley, A. R. Shaw, B. A. Arnold  
 ? TITLE OF INVENTION: Immunological Conjugates of OMPG and  
 ? TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization and Epitopes  
 ? NUMBER OF SEQUENCES: 146  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Merck & Co., Inc.  
 ? STREET: P.O. Box 2000  
 ? CITY: Rahway  
 ? STATE: NJ  
 ? COUNTRY: USA  
 ? ZIP: 07065  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: PCT/US93/06751  
 ? FILING DATE: 19930719  
 ? CLASSIFICATION:  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Moredith, Roy D.  
 ? REGISTRATION NUMBER: 30,777  
 ? REFERENCE/DOCKET NUMBER: 18614  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (908) 594-4678  
 ? TELEFAX: (908) 594-4720  
 ? TELEX: 138825

? INFORMATION FOR SEQ ID NO: 7:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 15 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: peptide  
 ? HYPOTHETICAL: NO  
 ? ANTI-SENSE: NO  
 ? IMMEDIATE SOURCE: Random Epitope Library Alpha  
 PCT-US93-06751-7

Query Match 36.4%; Score 4; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9  
 DB 4 GNSS 7

RESULT 35  
 PCT-US93-06751-4  
 ? Sequence 46; Application PC/TUS9306751  
 ? GENERAL INFORMATION:  
 ? APPLICANT: P. Keller, A. J. Conley, A. R. Shaw, B. A. Arnold  
 ? TITLE OF INVENTION: Immunological Conjugates of OMPG and  
 ? TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization and Epitopes  
 ? NUMBER OF SEQUENCES: 4  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Merck & Co., Inc.  
 ? STREET: P.O. Box 2000  
 ? CITY: Rahway  
 ? STATE: NJ  
 ? COUNTRY: USA  
 ? ZIP: 07065  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: PCT/US93/06751  
 ? FILING DATE: 19930719  
 ? CLASSIFICATION:  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Moredith, Roy D.  
 ? REGISTRATION NUMBER: 30,777  
 ? REFERENCE/DOCKET NUMBER: 18614  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (908) 594-4678  
 ? TELEFAX: (908) 594-4720  
 ? TELEX: 138825  
 ? INFORMATION FOR SEQ ID NO: 46:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 15 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: peptide  
 ? HYPOTHETICAL: NO  
 ? ANTI-SENSE: NO  
 ? IMMEDIATE SOURCE: Random Epitope Library Alpha  
 PCT-US93-06751-46

Query Match 36.4%; Score 4; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9  
 DB 4 GNSS 7

RESULT 36  
 PCT-US93-06751-21  
 ? Sequence 21; Application PC/TUS9306751  
 ? REFERENCE/DOCKET NUMBER: 18614  
 ? GENERAL INFORMATION:  
 ? APPLICANT: BURLON, James  
 ? APPLICANT: 16-80, 706-4000  
 ? APPLICANT: 16-80, 706-4000  
 ? TITLE OF INVENTION: SELECTED EPITOPES OF TISSUE KALLICREIN  
 ? NUMBER OF SEQUENCES: 141  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: BAKER & BELL, J.L.L.  
 ? STREET: 555 1st Street, N.W., Suite 500 East  
 ? CITY: Washington  
 ? STATE: D.C.  
 ? COUNTRY: U.S.A.  
 ? ZIP: 20004-1109  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible

```

? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/079,812
? FILING DATE: 22-JUN-1993
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
? NAME: Remenick, James
? REGISTRATION NUMBER: 36,902
? REFERENCE/DOCKET NUMBER: 16865-0118
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 639-7700
? TELEFAX: (202) 639-7832
? INFORMATION FOR SEQ ID NO: 21:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-079-812-21

```

```

Query Match 27.3% Score 3, DB 1, Length 8:
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 SIM 11
Db 2 SIM 4

```

## RESULT 37

```

? US-08-148-910-11
? Sequence 11, Application US/08148910
? Patent No. 5466593
? GENERAL INFORMATION:
? APPLICANT: Takeshi SHIMOMURA et al.
? TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein:
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Wenderoth, Lind & Ponack
? STREET: 805 Fifteenth Street, N.W., #700
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 5.25 inch.
? MEDIUM TYPE: 500 Kb Storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: Wordperfect
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/148,910
? FILING DATE: No. 5466593ember 5, 1993
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Warren M. Cheek, Jr.
? REGISTRATION NUMBER: 33,367
? REFERENCE/DOCKET NUMBER:
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-8850
? TELEFAX: 202-371-8856
? TELEX:
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear

```

```

? MOLECULE TYPE: Protein
? ORIGINAL SOURCE:
? ORGANISM: human
? US-08-148-910-11
? Query Match 27.3% Score 3, DB 1, Length 8:
? Best Local Similarity 100.0%, Pred. No. 2.5e+05;
? Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 SIM 11
Db 2 SIM 4

```

## RESULT 38

```

? US-08-082-847-7
? Sequence 7, Application US/08082847
? Patent No. 6492894
? GENERAL INFORMATION:
? APPLICANT: EILMER, ANDREW W.
? TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
? TITLE OF INVENTION: COMPOSING A PEPTIDE
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: THE EILMER & GAMBLE COMPANY
? STREET: P.O. BOX 99763
? CITY: CINCINNATI
? STATE: OHIO
? COUNTRY: USA
? ZIP: 45249-8763
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/082,847
? FILING DATE: 1994-02-25
? CLASSIFICATION: 560
? ATTORNEY/AGENT INFORMATION:
? NAME: CYRSTAN L. BEAHM, JR.
? REGISTRATION NUMBER: 54,114
? REFERENCE/DOCKET NUMBER: 434669
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 513-627-2838
? TELEFAX: 513-627-2700
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-082-847-7

```

```

Query Match 27.3% Score 3, DB 1, Length 8:
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 SIM 11
Db 4 SIM 4

```

## RESULT 39

```

? US-08-082-847-8
? Sequence 8, Application US/08082847
? Patent No. 6492894
? GENERAL INFORMATION:
? APPLICANT: EILMER, ANDREW W.
? TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
? TITLE OF INVENTION: COMPOSING A PEPTIDE

```

: NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082.847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 34,804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858  
 : TELEFAX: 513-627-0260  
 : INFORMATION FOR SEQ ID NO: 8:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-082-847-8

Query Match 27.3%, Score 3, DB 1, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 2 5e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SRK 5  
 DB 4 SRK 6

RESULT 40  
 US-08-082-847-9  
 : Sequence 9, Application US/08082847  
 : Patent No. 5492894  
 : GENERAL INFORMATION:  
 : APPLICANT: FULMER, ANDREW W.  
 : APPLICANT: BASCOM, CHARLES C.  
 : TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 : TITLE OF INVENTION: COMPOSING A PEPTIDE  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082.847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 34,804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858

: TELEFAX: 513-627-0260  
 : INFORMATION FOR SEQ ID NO: 8:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-082-847-9  
 : Query Match 27.3%, Score 3, DB 1, Length 8;  
 : Best Local Similarity 100.0%, Pred. No. 2 5e-05;  
 : Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SRK 5

DB 4 SRK 6

RESULT 41  
 US-08-082-847-10  
 : Sequence 1, Application US/08082847  
 : Patent No. 5492894  
 : GENERAL INFORMATION:  
 : APPLICANT: FULMER, ANDREW W.  
 : APPLICANT: BASCOM, CHARLES C.  
 : TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 : TITLE OF INVENTION: COMPOSING A PEPTIDE  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082.847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 34,804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858  
 : TELEFAX: 513-627-0260  
 : INFORMATION FOR SEQ ID NO: 8:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-082-847-11

Query Match 27.3%, Score 3, DB 1, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 2 5e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SRK 5

DB 4 SRK 6

RESULT 42  
 US-08-082-847-27  
 : Sequence 27, Application US/08082847  
 : Patent No. 5492894  
 : GENERAL INFORMATION:  
 : APPLICANT: FULMER, ANDREW W.  
 : APPLICANT: BASCOM, CHARLES C.  
 : TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 : TITLE OF INVENTION: COMPOSING A PEPTIDE  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082.847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 34,804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858

1 APPLICANT: FULMER, ANDREW W.  
 2 APPLICANT: BASCOM, CHARLES C.  
 3 TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 4 TITLE OF INVENTION: COMPRISING A PEPTIDE  
 5 NUMBER OF SEQUENCES: 38  
 6 CORRESPONDENCE ADDRESS:  
 7 ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 8 STREET: P. O. BOX 398707  
 9 CITY: CINCINNATI  
 10 STATE: OHIO  
 11 COUNTRY: USA  
 12 ZIP: 45239-8707  
 13 MEDIUM TYPE: Floppy disk  
 14 COMPUTER: IBM PC compatible  
 15 OPERATING SYSTEM: PC-DOS/MS-DOS  
 16 SOFTWARE: Patent In Release #1.0, Version 1.0  
 17 CURRENT APPLICATION DATA:  
 18 APPLICATION NUMBER: US/08/082,847  
 19 FILING DATE: 19930625  
 20 CLASSIFICATION: 530  
 21 ATTORNEY/AGENT INFORMATION:  
 22 NAME: CORSTANJE, BRAHM J.  
 23 REGISTRATION NUMBER: 34,804  
 24 REFERENCE/DOCKET NUMBER: 4346CK  
 25 TELECOMMUNICATION INFORMATION:  
 26 TELEPHONE: 513-627-2858  
 27 TELEFAX: 513-627-0260  
 28 INFORMATION FOR SEQ ID NO: 27:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 TOPOLOGY: linear  
 33 MOLECULE TYPE: peptide  
 34 UN-08-082-847-27

Query Match 27.38; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Prod. No. 2,500,005;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0

Qy 3 SRK 5  
III  
Db 3 SRK 5

RESULT 43  
US-08-082 847-28  
Sequence 28, Application US/08082847  
Patent No. 5492894  
GENERAL INFORMATION:  
APPLICANT: FULMER, ANDREW W.  
APPLICANT: BASCOM, CHARLES C.  
TITLE OF INVENTION: COMPOSITIONS FOR REVEALING WEAVERIES  
TITLE OF INVENTION: COMPRISING A PEPTIDE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
STREET: P. O. BOX 398707  
CITY: CINCINNATI  
STATE: OHIO  
COUNTRY: USA  
ZIP: 45239-8707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,847  
FILING DATE: 19930625  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: CORSTANJE, BRAHM J.

```

US-08-082-847-30
: Sequence 30, Application US/08082847
: Patent No. 5492894
: GENERAL INFORMATION:
: APPLICANT: FULMER, ANDREW W.
: APPLICANT: BASCOM, CHARLES C.
: TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
: TITLE OF INVENTION: COMPOSING A PEPTIDE
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: THE PROCTER & GAMBLE COMPANY
: STREET: P. O. BOX 398707
: CITY: CINCINNATI
: STATE: OHIO
: COUNTRY: USA
: ZIP: 45239-8707
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/082,847
: FILING DATE: 19930625
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: CORSTANJE, BRAHM J.
: REGISTRATION NUMBER: 34,804
: REFERENCE/DOCKET NUMBER: 4364CR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 513-627-2858
: TELEFAX: 513-627-0260
: INFORMATION FOR SEQ ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-082-847-30

```

```

Query Match      27.3% Score 57 88 11 Length 81
Best Local Similarity 100.0% Pred. No. 2 5e-25
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gap 2 0

```

QY 3 SRK 5  
111  
Db 5 SRK 7

```

RESULT 46
US-07-747 735-15
: Sequence 15, Application US/07747785
: Patent No. 549467;
: GENERAL INFORMATION:
: APPLICANT: LAI, Ching-Juh
: APPLICANT: MEN, Ruhe
: APPLICANT: BRAY, Michael
: TITLE OF INVENTION: FLAVIVIRUS ENVELOPE PROTEINS WITH
: TITLE OF INVENTION: INCREASED IMMUNOGENICITY FOR USE IN IMMUNIZATION AGAINST
: TITLE OF INVENTION: VIRUS INFECTION
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cushman, Darby & Cushman
: STREET: 1615 L Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20016-5601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25

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[illegible]

STRANDEDNESS: UNKNOWN  
 TOPOLOGY: UNKNOWN  
 MOLECULE TYPE: PEPTIDE  
 HYPOTHETICAL: NO  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:

Query Match 27.3% Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2,50,05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 SSL 10  
 DB 5 SSL 7

RESULT 48  
 US-08-210-266A-7  
 Sequence 7, Application US/08210266A  
 Patent No. 5545619  
 GENERAL INFORMATION:  
 APPLICANT: Atkinson, John P.  
 APPLICANT: Hourcade, Dennis  
 APPLICANT: Krych, Malgorzata  
 TITLE OF INVENTION: Modified Complement System  
 TITLE OF INVENTION: Regulators  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 2800 One Atlantic Center, 1201 West Peachtree  
 STREET: Street  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: US  
 ZIP: 30309-3450  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: DOS/MS-DOS  
 SOFTWARE: Patent No. 5545619, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/210-266A  
 FILING DATE: 1998-09-08  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/06-514  
 FILING DATE: 1998-09-08  
 ATTORNEY/AGENT: INFORMATION  
 NAME: Pabst, Patricia L.  
 REGISTRATION NUMBER: 41,283  
 REFERENCE/DECKET NUMBER: 1,000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404) 554-2944  
 TELEFAX: (404) 554-2944  
 INFORMATION FOR SEQ ID NO:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MEDIUM TYPE: Floppy disk  
 US-08-210-266A-7

Query Match 100.0% Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2,50,05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 7 NSS 9  
 DB 1 NSS 5

RESULT 49  
 US-08-097-938-41  
 Sequence 61, Application US/0097938  
 Patent No. 5929774  
 GENERAL INFORMATION:  
 APPLICANT: SUNELIN, DEAN  
 APPLICANT: SUNELIN, DEAN  
 TITLE OF INVENTION: RECOMBINANT 120 RECEPTOR AND ITS  
 TITLE OF INVENTION: ADONEX AND ANTAGONISTS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Mark D. A. Finkler  
 STREET: 2000 Pennsylvania Ave., N.W., Ste. 5500  
 CITY: Washington, DC  
 COUNTRY: USA  
 ZIP: 20006-1812  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: DOS/MS-DOS  
 SOFTWARE: Patent No. 5929774, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/97-938  
 FILING DATE: 2000-09-19  
 CLASSIFICATION: 4-3  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MURSHIEL, KATE H.  
 REGISTRATION NUMBER: 29,279  
 REFERENCE/DECKET NUMBER: 2,000-2066-00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 867-1361  
 TELEFAX: (202) 867-1361  
 TELEX: 90-4330  
 INFORMATION FOR SEQ ID NO: 41  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 US-08-097-938-41

Search completed: 09/29/03 11:28:59  
 Job time: 13,967 secs

Query Match 27.3% Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NSS 9  
 III  
 DB 3 NSS 5

RESULT 50  
 US-07-958-903A-53  
 : Sequence 53, Application US/07958903A  
 : Patent No. 5652214  
 : GENERAL INFORMATION:  
 : APPLICANT: Lewis, Michael E.  
 : APPLICANT: Kauer, James C.  
 : APPLICANT: Smith, Kevin R.  
 : APPLICANT: Callison, Kathleen V.  
 : APPLICANT: Baldino, Frank  
 : APPLICANT: Neff, Nicola  
 : APPLICANT: Iqbal, Mohamed  
 : TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION  
 : TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND  
 : TITLE OF INVENTION: ANALOGS  
 : NUMBER OF SEQUENCES: 56  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Fish & Richardson  
 : STREET: 225 Franklin Street  
 : CITY: Boston  
 : STATE: Massachusetts  
 : COUNTRY: U.S.A.  
 : ZIP: 02110-2804  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 : COMPUTER: IBM PS/2 Model 502 or 55SX  
 : OPERATING SYSTEM: MS-DOS (Version 5.0)  
 : SOFTWARE: WordPerfect (Version 5.1)  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/07/958,903A  
 : FILING DATE: October 7, 1992  
 : CLASSIFICATION: 514  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/361,595  
 : FILING DATE: June 5, 1989  
 : APPLICATION NUMBER: 07/534,139  
 : FILING DATE: June 5, 1990  
 : APPLICATION NUMBER: 07/869,913  
 : FILING DATE: April 15, 1992  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Clark, Paul T.  
 : REGISTRATION NUMBER: 30,162  
 : REFERENCE/DCKET NUMBER: 02655/003604  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617) 542-5070  
 : TELEFAX: (617) 542-8906  
 : TELEX: 200154  
 : INFORMATION FOR SEQ ID NO: 53:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8  
 : TYPE: amino acid  
 : STRANDEDNESS:  
 : TOPOLOGY: linear  
 : US-07-958-903A-53

Query Match 27.3% Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKS 3  
 III  
 DB 5 AKS 7



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run On: September 30, 2003, 10:10:03 ; Search time 21.5 seconds  
(without alignments)  
77.413 million col: updates/sec

**Title:** US-09-787-443-21

perfect score:

Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 566894 seqs, 151307093 residues

Word size : 32 bits

Total number of hits satisfying chosen parameters: 1488.

Minimum DB seq	length: 8
Maximum DB seq	length: 15

### Post-processing: Listing first 500 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCMMB.pcp.p
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pcp.p
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.p
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCMMB.pcp.p
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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp.p
- 8: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCMMB.pcp.p
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCMMB.pcp.p
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCMMB.pcp.p
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pcp.p
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCMMB.pcp.p
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCMMB.pcp.p
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCMMB.pcp.p
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.p
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pcp.p
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCMMB.pcp.p

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5	45.5	14	12	US-10-138-473-165 Sequence 125, Appl
2	4	36.4	8	11	US-09-725-470A-127 Sequence 127, Appl
3	4	36.4	8	11	US-09-726-470A-235 Sequence 235, Appl
4	4	36.4	4	12	US-10-231-894-19 Sequence 19, Appl
5	4	36.4	8	14	US-10-112-527-7 Sequence 7, Appl
6	4	36.4	9	11	US-09-876-904A-74 Sequence 74, Appl
7	4	36.4	9	12	US-10-315-920-16 Sequence 16, Appl
8	4	36.4	9	15	US-10-040-862-9703 Sequence 9703, Ap
9	4	36.4	9	15	US-10-040-862-9745 Sequence 9745, Ap
10	4	36.4	9	15	US-10-040-862-9811 Sequence 9811, Ap
11	4	36.4	9	15	US-10-040-862-9587 Sequence 9587, Ap
12	4	36.4	9	15	US-10-040-862-10270 Sequence 10270, A
13	4	36.4	9	15	US-10-040-862-10370 Sequence 10370, A
14	4	36.4	9	15	US-10-040-862-10390 Sequence 10390, A
15	4	36.4	10	11	US-09-572-404B-66 Sequence 66, Appl



[illegible]

[illegible]

? PRIOR APPLICATION NUMBER: US 60/116,673  
 ? PRIOR FILING DATE: 1999-01-21  
 ? PRIOR APPLICATION NUMBER: DK 1998 01281  
 ? PRIOR FILING DATE: 1998-10-18  
 ? PRIOR APPLICATION NUMBER: US 60/070,488  
 ? PRIOR FILING DATE: 1998-01-05  
 ? PRIOR APPLICATION NUMBER: DK 1997 01277  
 ? PRIOR FILING DATE: 1997-11-10  
 ? PRIOR APPLICATION NUMBER: US 60/044,624  
 ? PRIOR FILING DATE: 1997-04-18  
 ? PRIOR APPLICATION NUMBER: DK 1997 00376  
 ? PRIOR FILING DATE: 1997-04-02  
 ? NUMBER OF SEQ ID NOS: 174  
 ? SOFTWARE: PatentIn version 3.1  
 ? SEQ ID NO: 165  
 ? LENGTH: 14  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: N-terminal sequence of IB42  
 US-10-138-473-165

Query Match 45.5%; Score 5; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSL 10  
 Db 2 GNSL 6

## RESULT 2

US-09-726-470A-127  
 ? Sequence 127, Application US/09726470A  
 ? Publication No. US20030036528A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? CURRENT FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928123.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: PatentIn Ver. 2.1  
 ? SEQ ID NO 127  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with three amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? FEATURE:  
 ? NAME/KEY: SITE  
 ? LOCATION: (8)  
 ? OTHER INFORMATION: p-Fluorophenylalanine  
 US-09-726-470A-127

Query Match 36.4%; Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 56+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 Db 2 AKSR 5

## RESULT 3

US-09-726-470A-245  
 ? Sequence 235, Application US/09726470A  
 ? Publication No. US20030036528A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? CURRENT FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928123.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: PatentIn version 2.1  
 ? SEQ ID NO 245  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: Peptide  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with three amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 US-09-726-470A-245

Query Match 46.4%; Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 56+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 Db 2 AKSR 5

## RESULT 4

US-10-231-894-179  
 ? Sequence 19, Application US/09726470A  
 ? Publication No. US20030036528A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? TITLE OF INVENTION: p21 Peptides and Methods of Treatment of Diseases  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/10/231,894  
 ? CURRENT FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928123.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 64  
 ? SOFTWARE: PatentIn Ver. 2.1  
 ? SEQ ID NO 179  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Human  
 US-10-231-894-179

Query Match 66.4%; Score 4; DB 12; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 56+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSKR 5  
 Db 1 KSKR 4

RESULT 5  
 US-10-112-527-7



Query Match 36.4% Score 4: 66/15; Length 9  
 Best Local Similarity 100.0%; Pred. No. 60/05;  
 Matches 4: Conservative 0; Mismatches 0; In-dels 0; Deletions 0

Oy 6 GNSS 9  
 Db 5 GNSS 8

## RESULT 9

US-10-040-862-9765  
 : Sequence 9765, Application US/10040862  
 : Publication No. US20030078396A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Gaiger, Alexander  
 : APPLICANT: Aldate, Paul A.  
 : APPLICANT: Mannion, Jane  
 : APPLICANT: Retter, Marc  
 : APPLICANT: Corixa Corporation  
 : TITLE OF INVENTION: Compositions and Methods for the Detection of a Leukemia and T-Cell  
 : TITLE OF INVENTION: Hematological Malignancies

: FILE REFERENCE: 014058-013520G5  
 : CURRENT APPLICATION NUMBER: US/10/040.862  
 : CURRENT FILING DATE: 2001-11-06  
 : PRIOR APPLICATION NUMBER: US 60/186,126  
 : PRIOR FILING DATE: 2000-03-01  
 : PRIOR APPLICATION NUMBER: US 60/190,479  
 : PRIOR FILING DATE: 2000-03-17  
 : PRIOR APPLICATION NUMBER: US 60/200,545  
 : PRIOR FILING DATE: 2000-04-27  
 : PRIOR APPLICATION NUMBER: US 60/200,303  
 : PRIOR FILING DATE: 2000-04-26  
 : PRIOR APPLICATION NUMBER: US 60/200,779  
 : PRIOR FILING DATE: 2000-04-28  
 : PRIOR APPLICATION NUMBER: US 60/200,959  
 : PRIOR FILING DATE: 2000-05-01  
 : PRIOR APPLICATION NUMBER: US 60/202,084  
 : PRIOR FILING DATE: 2000-05-04  
 : PRIOR APPLICATION NUMBER: US 60/206,201  
 : PRIOR FILING DATE: 2000-05-22  
 : PRIOR APPLICATION NUMBER: US 60/218,950  
 : PRIOR FILING DATE: 2000-07-14  
 : PRIOR APPLICATION NUMBER: US 60/222,903  
 : PRIOR FILING DATE: 2000-08-03  
 : PRIOR APPLICATION NUMBER: US 60/223,416  
 : PRIOR FILING DATE: 2000-08-04  
 : PRIOR APPLICATION NUMBER: US 60/223,376  
 : PRIOR FILING DATE: 2000-08-07  
 : PRIOR APPLICATION NUMBER: US 09/796,692  
 : PRIOR FILING DATE: 2001-03-01  
 : NUMBER OF SEQ ID NOS: 10467  
 : SOFTWARE: FastSeq for Windows Version 3.0  
 : SEQ ID NO 9765  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-040-862-9765

Query Match 36.4% Score 4: 66/15; Length 9  
 Best Local Similarity 100.0%; Pred. No. 60/05;  
 Matches 4: Conservative 0; Mismatches 0; In-dels 0; Deletions 0

Oy 6 GNSS 9  
 Db 5 GNSS 8

## RESULT 10

US-10-040-862-9811  
 : Sequence 9811, Application US/10040862  
 : Publication No. US20030078396A1  
 : GENERAL INFORMATION:

: APPLICANT: Gaiger, Alexander  
 : APPLICANT: Aldate, Paul A.  
 : APPLICANT: Mannion, Jane  
 : APPLICANT: Retter, Marc  
 : APPLICANT: Corixa Corporation  
 : TITLE OF INVENTION: Compositions and Methods for the Detection of a Leukemia and T-Cell  
 : TITLE OF INVENTION: Hematological Malignancies  
 : FILE REFERENCE: 014058-013520G5  
 : CURRENT APPLICATION NUMBER: US/10/040.862  
 : CURRENT FILING DATE: 2001-11-06  
 : PRIOR APPLICATION NUMBER: US 60/186,126  
 : PRIOR FILING DATE: 2000-03-01  
 : PRIOR APPLICATION NUMBER: US 60/190,479  
 : PRIOR FILING DATE: 2000-03-17  
 : PRIOR APPLICATION NUMBER: US 60/200,545  
 : PRIOR FILING DATE: 2000-04-27  
 : PRIOR APPLICATION NUMBER: US 60/200,303  
 : PRIOR FILING DATE: 2000-04-26  
 : PRIOR APPLICATION NUMBER: US 60/200,779  
 : PRIOR FILING DATE: 2000-04-28  
 : PRIOR APPLICATION NUMBER: US 60/200,959  
 : PRIOR FILING DATE: 2000-05-01  
 : PRIOR APPLICATION NUMBER: US 60/202,084  
 : PRIOR FILING DATE: 2000-05-04  
 : PRIOR APPLICATION NUMBER: US 60/206,201  
 : PRIOR FILING DATE: 2000-05-22  
 : PRIOR APPLICATION NUMBER: US 60/218,950  
 : PRIOR FILING DATE: 2000-07-14  
 : PRIOR APPLICATION NUMBER: US 60/222,903  
 : PRIOR FILING DATE: 2000-08-03  
 : PRIOR APPLICATION NUMBER: US 60/223,416  
 : PRIOR FILING DATE: 2000-08-04  
 : PRIOR APPLICATION NUMBER: US 60/223,376  
 : PRIOR FILING DATE: 2000-08-07  
 : PRIOR APPLICATION NUMBER: US 09/796,692  
 : PRIOR FILING DATE: 2001-03-01  
 : NUMBER OF SEQ ID NOS: 10467  
 : SOFTWARE: FastSeq for Windows Version 3.0  
 : SEQ ID NO 9811  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-040-862-9811

Query Match 36.4% Score 4: 66/15; Length 9  
 Best Local Similarity 100.0%; Pred. No. 60/05;  
 Matches 4: Conservative 0; Mismatches 0; In-dels 0; Deletions 0

Oy 6 GNSS 9  
 Db 5 GNSS 8

RESULT 11  
 US-10-040-862-9812  
 : Sequence 9812, Application US/10040862  
 : Publication No. US20030078396A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Gaiger, Alexander  
 : APPLICANT: Aldate, Paul A.  
 : APPLICANT: Mannion, Jane  
 : APPLICANT: Retter, Marc  
 : APPLICANT: Corixa Corporation  
 : TITLE OF INVENTION: Compositions and Methods for the Detection of a Leukemia and T-Cell  
 : TITLE OF INVENTION: Hematological Malignancies  
 : FILE REFERENCE: 014058-013520G5  
 : CURRENT APPLICATION NUMBER: US/10/040.862  
 : CURRENT FILING DATE: 2001-11-06  
 : PRIOR APPLICATION NUMBER: US 60/186,126  
 : PRIOR FILING DATE: 2000-03-01  
 : PRIOR APPLICATION NUMBER: US 60/190,479  
 : PRIOR FILING DATE: 2000-03-17  
 : PRIOR APPLICATION NUMBER: US 60/200,545  
 : PRIOR FILING DATE: 2000-04-27  
 : PRIOR APPLICATION NUMBER: US 60/200,303  
 : PRIOR FILING DATE: 2000-04-26  
 : PRIOR APPLICATION NUMBER: US 60/200,779  
 : PRIOR FILING DATE: 2000-04-28  
 : PRIOR APPLICATION NUMBER: US 60/200,959  
 : PRIOR FILING DATE: 2000-05-01  
 : PRIOR APPLICATION NUMBER: US 60/202,084  
 : PRIOR FILING DATE: 2000-05-04  
 : PRIOR APPLICATION NUMBER: US 60/206,201  
 : PRIOR FILING DATE: 2000-05-22  
 : PRIOR APPLICATION NUMBER: US 60/218,950  
 : PRIOR FILING DATE: 2000-07-14  
 : PRIOR APPLICATION NUMBER: US 60/222,903  
 : PRIOR FILING DATE: 2000-08-03  
 : PRIOR APPLICATION NUMBER: US 60/223,416  
 : PRIOR FILING DATE: 2000-08-04  
 : PRIOR APPLICATION NUMBER: US 60/223,376  
 : PRIOR FILING DATE: 2000-08-07  
 : PRIOR APPLICATION NUMBER: US 09/796,692  
 : PRIOR FILING DATE: 2001-03-01  
 : NUMBER OF SEQ ID NOS: 10467  
 : SOFTWARE: FastSeq for Windows Version 3.0  
 : SEQ ID NO 9812  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-040-862-9812

? PRIOR FILING DATE: 2000-04-27  
 ? PRIOR APPLICATION NUMBER: US 60/200,103  
 ? PRIOR FILING DATE: 2000-04-28  
 ? PRIOR APPLICATION NUMBER: US 60/200,774  
 ? PRIOR FILING DATE: 2000-04-28  
 ? PRIOR APPLICATION NUMBER: US 60/200,599  
 ? PRIOR FILING DATE: 2000-05-01  
 ? PRIOR APPLICATION NUMBER: US 60/202,084  
 ? PRIOR FILING DATE: 2000-05-04  
 ? PRIOR APPLICATION NUMBER: US 60/206,261  
 ? PRIOR FILING DATE: 2000-05-22  
 ? PRIOR APPLICATION NUMBER: US 60/218,950  
 ? PRIOR FILING DATE: 2000-07-14  
 ? PRIOR APPLICATION NUMBER: US 60/222,903  
 ? PRIOR FILING DATE: 2000-08-03  
 ? PRIOR APPLICATION NUMBER: US 60/223,416  
 ? PRIOR FILING DATE: 2000-08-04  
 ? PRIOR APPLICATION NUMBER: US 60/223,378  
 ? PRIOR FILING DATE: 2000-08-07  
 ? PRIOR APPLICATION NUMBER: US 05/796,652  
 ? PRIOR FILING DATE: 2001-03-01  
 ? NUMBER OF SEQ. ID NOS: 10467  
 ? SOFTWARE: FastSeq for Windows Version 4.0  
 ? SEQ. ID NO 9987  
 ? LENGTH: 9  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US-10-040-862 5987

Query Match: 36.4%; Score 4; 98 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9  
 Db 1111  
 6 GNSS 9

## RESULT 12

US-10-040-862-10270  
 ? Sequence 10270, Application US/10040872  
 ? Publication No. US20030078396A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Galquer, Alexander  
 ? APPLICANT: Algate, Paul A.  
 ? APPLICANT: Mannion, Jane  
 ? APPLICANT: Rottler, Marc  
 ? APPLICANT: Corixa Corporation  
 ? TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
 ? TITLE OF INVENTION: Hematological Malignancies  
 ? FILE REFERENCE: 014058-01352005  
 ? CURRENT APPLICATION NUMBER: US/10/040,862  
 ? CURRENT FILING DATE: 2001-11-06  
 ? PRIOR APPLICATION NUMBER: US 60/186,126  
 ? PRIOR FILING DATE: 2000-03-01  
 ? PRIOR APPLICATION NUMBER: US 60/190,479  
 ? PRIOR FILING DATE: 2000-03-17  
 ? PRIOR APPLICATION NUMBER: US 60/200,545  
 ? PRIOR FILING DATE: 2000-04-27  
 ? PRIOR APPLICATION NUMBER: US 60/200,403  
 ? PRIOR FILING DATE: 2000-04-28  
 ? PRIOR APPLICATION NUMBER: US 60/200,774  
 ? PRIOR FILING DATE: 2000-04-28  
 ? PRIOR APPLICATION NUMBER: US 60/200,994  
 ? PRIOR FILING DATE: 2000-05-01  
 ? PRIOR APPLICATION NUMBER: US 60/202,084  
 ? PRIOR FILING DATE: 2000-05-04  
 ? PRIOR APPLICATION NUMBER: US 60/206,261  
 ? PRIOR FILING DATE: 2000-05-22  
 ? PRIOR APPLICATION NUMBER: US 60/218,950  
 ? PRIOR FILING DATE: 2000-07-14  
 ? PRIOR APPLICATION NUMBER: US 60/222,903  
 ? PRIOR FILING DATE: 2000-08-03

? PRIOR APPLICATION NUMBER: US 60/200,103  
 ? PRIOR FILING DATE: 2000-04-27  
 ? PRIOR APPLICATION NUMBER: US 60/200,774  
 ? PRIOR FILING DATE: 2000-04-28  
 ? PRIOR APPLICATION NUMBER: US 60/200,599  
 ? PRIOR FILING DATE: 2000-05-01  
 ? PRIOR APPLICATION NUMBER: US 60/202,084  
 ? PRIOR FILING DATE: 2000-05-04  
 ? PRIOR APPLICATION NUMBER: US 60/206,261  
 ? PRIOR FILING DATE: 2000-05-22  
 ? PRIOR APPLICATION NUMBER: US 60/218,950  
 ? PRIOR FILING DATE: 2000-07-14  
 ? PRIOR APPLICATION NUMBER: US 60/222,903  
 ? PRIOR FILING DATE: 2000-08-03  
 ? PRIOR APPLICATION NUMBER: US 60/223,416  
 ? PRIOR FILING DATE: 2000-08-04  
 ? PRIOR APPLICATION NUMBER: US 60/223,378  
 ? PRIOR FILING DATE: 2000-08-07  
 ? PRIOR APPLICATION NUMBER: US 05/796,652  
 ? PRIOR FILING DATE: 2001-03-01  
 ? NUMBER OF SEQ. ID NOS: 10467  
 ? SOFTWARE: FastSeq for Windows Version 4.0  
 ? SEQ. ID NO 9987  
 ? LENGTH: 9  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US-10-040 862 10270

Query Match: 36.4%; Score 4; 98 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9  
 Db 1111  
 6 GNSS 9

## RESULT 14

US-10-040-862-10270  
 ? Sequence 10270, Application US/10040872  
 ? Publication No. US20030078396A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Galquer, Alexander  
 ? APPLICANT: Algate, Paul A.  
 ? APPLICANT: Mannion, Jane  
 ? APPLICANT: Rottler, Marc  
 ? APPLICANT: Corixa Corporation  
 ? TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
 ? TITLE OF INVENTION: Hematological Malignancies  
 ? FILE REFERENCE: 014058-01352005  
 ? CURRENT APPLICATION NUMBER: US/10/040,862  
 ? CURRENT FILING DATE: 2001-11-06  
 ? PRIOR APPLICATION NUMBER: US 60/186,126  
 ? PRIOR FILING DATE: 2000-03-01  
 ? PRIOR APPLICATION NUMBER: US 60/190,479  
 ? PRIOR FILING DATE: 2000-03-17  
 ? PRIOR APPLICATION NUMBER: US 60/200,545  
 ? PRIOR FILING DATE: 2000-04-27  
 ? PRIOR APPLICATION NUMBER: US 60/200,403  
 ? PRIOR FILING DATE: 2000-04-28  
 ? PRIOR APPLICATION NUMBER: US 60/200,774  
 ? PRIOR FILING DATE: 2000-04-28  
 ? PRIOR APPLICATION NUMBER: US 60/200,994  
 ? PRIOR FILING DATE: 2000-05-01

Query Match: 36.4%; Score 4; 98 15; Length 9;



Best Local Similarity 100.0%; Pred. No. 50-05;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9  
|||||  
Db 6 GNSS 9

## RESULT 14

US-10-040-862-10390  
Sequence 10390, Application US/10040862  
Publication No. US20030078396A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Retter, Marc  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Compositions and Methods for the treatment of disorders and therapies  
TITLE OF INVENTION: Hematological Malignancies  
FILE REFERENCE: 014058-013520US  
CURRENT APPLICATION NUMBER: US/10/040.862  
PRIOR FILING DATE: 2001-11-06  
PRIOR APPLICATION NUMBER: US 60/186,124  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,304  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: US 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: US 60/223,378  
PRIOR FILING DATE: 2000-08-07  
PRIOR APPLICATION NUMBER: US 09/796,692  
PRIOR FILING DATE: 2001-03-01  
NUMBER OF SEQ ID NOS: 10467  
SOFTWARE: FastSeq for Windows Version 5.0  
SEQ ID NO 10390  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-040-862-10390

Query Match 36.4%; Score 4; Seq. Id. 100.0%;

Best Local Similarity 100.0%; Pred. No. 66-66;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9  
|||||  
Db 6 GNSS 9

## RESULT 15

US-09-572-404B-66  
Sequence 66, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: 014058-013520US  
CURRENT APPLICATION NUMBER: US/10/040.862  
NUMBER OF SEQ ID NOS: 4200  
SOFTWARE: Proteom Ltd  
SEQ ID NO 66  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: SEQ ID NO 66 is a part of a protein of 1000 amino acids, and is a part of a protein of 1000 amino acids, and is a part of a protein of 1000 amino acids.  
US-09-572-404B-66

Query Match 100.0%; Score 4; Seq. Id. 100.0%;  
Best Local Similarity 100.0%; Pred. No. 66-66;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9  
|||||  
Db 6 GNSS 9

## RESULT 16

US-09-572-404B-496  
Sequence 496, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: 014058-013520US  
CURRENT APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 4200  
SOFTWARE: Proteom Ltd  
SEQ ID NO 496  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: SEQ ID NO 496 is a part of a protein of 1000 amino acids, and is a part of a protein of 1000 amino acids, and is a part of a protein of 1000 amino acids.  
US-09-572-404B-496

Query Match 100.0%; Score 4; Seq. Id. 100.0%;  
Best Local Similarity 100.0%; Pred. No. 496-496;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9  
|||||  
Db 6 GNSS 9

## RESULT 17

US-09-572-404B-764  
Sequence 764, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: 014058-013520US  
CURRENT APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 4200  
SOFTWARE: Proteom Ltd  
SEQ ID NO 764  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: Sequence 764 is a part of a protein of 1000 amino acids, and is a part of a protein of 1000 amino acids, and is a part of a protein of 1000 amino acids.  
US-09-572-404B-764

QY 6 GNSS 9  
|||||  
Db 6 GNSS 9

Query Match 36.4% Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 50-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSSL 10  
 IIII  
 DB 7 NSSL 10

## RESULT 18

US-09-572-404B-1297  
 ; Sequence 1297, Application US/09572404B  
 ; Publication No. US20030078374A1

## GENERAL INFORMATION:

; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572.404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 1297

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in CACNA1S OR CACNA1C OR CACNA1D OR CACNA1E OR CACNA1F OR CACNA1G OR CACNA1H OR CACNA1I OR CACNA1J OR CACNA1K OR CACNA1L OR CACNA1M OR CACNA1N OR CACNA1O OR CACNA1P OR CACNA1Q OR CACNA1R OR CACNA1S OR CACNA1T OR CACNA1U OR CACNA1V OR CACNA1W OR CACNA1X OR CACNA1Y OR CACNA1Z in this patent.

US-09-572-404B-1297

Query Match 36.4% Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 50-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 IIII  
 DB 7 AKSR 10

## RESULT 19

US-09-572-404B-2994  
 ; Sequence 2994, Application US/09572404B  
 ; Publication No. US20030078374A1

## GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572.404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 2994

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in SFRS3 OR SFRS3B OR SFRS3C OR SFRS3D OR SFRS3E OR SFRS3F OR SFRS3G OR SFRS3H OR SFRS3I OR SFRS3J OR SFRS3K OR SFRS3L OR SFRS3M OR SFRS3N OR SFRS3O OR SFRS3P OR SFRS3Q OR SFRS3R OR SFRS3S OR SFRS3T OR SFRS3U OR SFRS3V OR SFRS3W OR SFRS3X OR SFRS3Y OR SFRS3Z in this patent.

US-09-572-404B-2994

Query Match 36.4% Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 50-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5  
 IIII  
 DB 3 KSRK 6

## RESULT 20

US-09-572-404B-3130

; Sequence 3130, Application US/09572404B

; Publication No. US20030078374A1

## GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572.404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 3130

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in SFRS3 OR SFRS3B OR SFRS3C OR SFRS3D OR SFRS3E OR SFRS3F OR SFRS3G OR SFRS3H OR SFRS3I OR SFRS3J OR SFRS3K OR SFRS3L OR SFRS3M OR SFRS3N OR SFRS3O OR SFRS3P OR SFRS3Q OR SFRS3R OR SFRS3S OR SFRS3T OR SFRS3U OR SFRS3V OR SFRS3W OR SFRS3X OR SFRS3Y OR SFRS3Z in this patent.

US-09-572-404B-3130

Query Match 36.4% Score 4; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 50-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSRK 4  
 IIII  
 DB 3 KSRK 6

## RESULT 21

US-09-572-270A-253

; Sequence 253, Application US/09572404B

; Publication No. US20030078374A1

## GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572.404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 1445

; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 253

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Atorhizis Thallium

; OTHER INFORMATION: Sequence located in AT1A at 2+38 and may interact with

US-09-572-270A-253

Query Match 36.4% Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 50-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSSL 10  
 IIII  
 DB 1 NSSL 4

## RESULT 22

US-09-572-270A-862

; Sequence 862, Application US/09572404B

; Publication No. US20030078374A1

## GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572.404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 1144

; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 862

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Atorhizis Thallium

; OTHER INFORMATION: Sequence located in TOP2 at 18-27 and may interact with

US-09-572-270A-862

Query Match 36.4% Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 ||||  
 DB 3 AKSR 6

## RESULT 23

US-09-876-904A-83  
 ; Sequence 83, Application US/09876904A  
 ; Publication No. US2003007279A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PUSONEMIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPIDOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876.904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210.925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 83  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic T-DNA-linked Viro2  
 ; OTHER INFORMATION: endonuclease of the Agrobacterium tumefaciens tumor-inducing  
 ; OTHER INFORMATION: plasmid  
 US-09-876-904A-83

Query Match 36.4% Score 4; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRKG 6  
 ||||  
 DB 4 SRKG 7

## RESULT 24

US-10-211-088-246  
 ; Sequence 246, Application US/10211088  
 ; Publication No. US20030104479A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bright, Gary R.  
 ; APPLICANT: Premkumar, D. David  
 ; APPLICANT: Chen, Yih-Tai  
 ; TITLE OF INVENTION: No. 10-22-US  
 ; FILE REFERENCE: 01-1022-088  
 ; CURRENT APPLICATION NUMBER: US/10/211.088  
 ; CURRENT FILING DATE: 2002-10-15  
 ; PRIOR APPLICATION NUMBER: 60/309,395  
 ; PRIOR FILING DATE: 2001-08-01  
 ; PRIOR APPLICATION NUMBER: 60/341,589  
 ; PRIOR FILING DATE: 2001-12-13  
 ; NUMBER OF SEQ ID NOS: 366  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 246  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Nuclear localization signal  
 US-10-211-088-246

Query Match 36.4% Score 4; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SRKG 6  
 ||||  
 DB 4 SRKG 7

## RESULT 25

US-09-880-748-2773  
 ; Sequence 2773, Application US/0980748  
 ; Publication No. US2003007279A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert et al  
 ; TITLE OF INVENTION: Anticodons that immunospecifically bind keys  
 ; FILE REFERENCE: PFG-3  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; NUMBER OF SEQ ID NOS: 4299  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2773  
 ; LENGTH: 12  
 ; TYPE: PRI  
 ; ORGANISM: Homo Sapiens  
 US-09-880-748-2773

Query Match 36.4% Score 4; DB 11; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSIM 11  
 ||||  
 DB 3 SSIM 7

## RESULT 26

US-09-880-748-4015  
 ; Sequence 4015, Application US/0980748  
 ; Publication No. US2003007279A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert et al  
 ; TITLE OF INVENTION: Anticodons that immunospecifically bind keys  
 ; FILE REFERENCE: PFG-3  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/210.925  
 ; NUMBER OF SEQ ID NOS: 4299  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4015  
 ; LENGTH: 12  
 ; TYPE: PRI  
 ; ORGANISM: Homo Sapiens  
 US-09-880-748-4015

Query Match 36.4% Score 4; DB 11; Length 12;

Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSLM 11  
||||  
Db 3 SSLM 6

## RESULT 27

US-09-880-748-3016  
; Sequence 3016, Application US/99880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind H-Ys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 3016  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-3016

Query Match 36.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSLM 11  
||||  
Db 3 SSLM 6

## RESULT 28

US-10-190-082-538  
; Sequence 538, Application US/10190082  
; Publication No. US20030148264A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Lawrence A.  
; APPLICANT: Sidhu, Sachdev S.  
; APPLICANT: Heid, Heike A.  
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
; FILE REFERENCE: P1905R1  
; CURRENT APPLICATION NUMBER: US/10/190,082  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/303,644  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 683  
; SEQ ID NO: 538  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-190-082-538

Query Match 36.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKSR 4

Qy 2 AKSR 4  
|||||

## RESULT 29

US-10-190-082-538  
; Sequence 538, Application US/10190082  
; Publication No. US20030148264A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Lawrence A.  
; APPLICANT: Sidhu, Sachdev S.  
; APPLICANT: Heid, Heike A.  
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
; FILE REFERENCE: P1905R1  
; CURRENT APPLICATION NUMBER: US/10/190,082  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/303,644  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 683  
; SEQ ID NO: 538  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-190-082-538

Query Match 36.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AKSR 4  
|||||

## RESULT 30

US-10-294-444-117  
; Sequence 444, Application US/1029444A  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: JEN OVERSEAS LTD.  
; TITLE OF INVENTION: INHIBITORS OF THE PDZ DOMAIN PROTEIN  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/10/294,444  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334,242  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 444  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Isolated from random sept. phage library  
; OTHER INFORMATION: Isolated from random sept. phage library  
US-10-294-444-117

Query Match 36.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NNS 11  
|||||

## RESULT 31

US-10-294-444-117  
; Sequence 444, Application US/1029444A  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
US-10-294-444-117

```
1 APPLICANT: Belcher, Angela M
2 APPLICANT: Smalley, Richard E.
3 APPLICANT: Ryan, Esther
4 APPLICANT: Lee, Seung-wuk
5 TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
6 FILE REFERENCE: 119227-1066
7 CURRENT APPLICATION NUMBER: US/10/254,445A
8 CURRENT FILING DATE: 2003-02-19
9 PRIOR APPLICATION NUMBER: 60/1425,664
10 PRIOR FILING DATE: 2001-09-28
11 NUMBER OF SEQ ID NOS: 245
12 SOFTWARE: PatentIn version 3.1
13 SEQ ID NO 157
14 LENGTH: 12
15 TYPE: PRT
16 ORGANISM: artificial sequence
17 FEATURE:
18 OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage library
19 US-10-254-446A-157

Query Match      36.4%  Score 4: DB 15: Fourth 12:
Best Local Similarity 100.0%  Pred. NO. 5, de-02:
Matches      4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY      8 SSSL 11
DB      6 SSSL 9

RESULT 32
US-09-851-138-164
Sequence 164, Application US/09851138
Publication No. US20020183508A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HERPESVIRUS VIRUS GEN-TYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
AGENTS
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DIERKE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,138
FILING DATE: 09-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,075
FILING DATE: <unknown>
APPLICATION NUMBER: EP 94870166.4
FILING DATE: 21 Oct 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS-004
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
```

```
US-09-851-138-164
Query Match      36.4%  Score 4: DB 15: Fourth 12:
Best Local Similarity 100.0%  Pred. NO. 5, de-02:
Matches      4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY      6 SSSL 9
DB      4 SSSL 9

RESULT 33
US-10-254-446A-157
Sequence 164, Application US/10/254,445A
Publication No. US20020183508A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HERPESVIRUS VIRUS GEN-TYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
AGENTS
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DIERKE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/254,445A
FILING DATE: 09-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,075
FILING DATE: <unknown>
APPLICATION NUMBER: EP 94870166.4
FILING DATE: 21 Oct 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS-004
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
```

RESULT 35  
 US-10-153-244-173  
 : Sequence 173, Application US/10153244  
 : Publication No. US20030144191A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Bristol-Myers Squibb Company  
 : TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER  
 : FILE REFERENCE: D0144 NP  
 : CURRENT APPLICATION NUMBER: US/10/153,244  
 : PRIOR FILING DATE: 2002-05-22  
 : PRIOR APPLICATION NUMBER: US 60/292,599  
 : PRIOR FILING DATE: 2001-05-22  
 : PRIOR APPLICATION NUMBER: US 60/362,944  
 : PRIOR FILING DATE: 2002-03-08  
 : NUMBER OF SEQ ID NOS: 335  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 173  
 : LENGTH: 13  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-153-244-173

Query Match 36.4%, Score 4; bp 12, Length 13;  
 Best Local Similarity 100.0%, Pred. No. 6, 2+0+0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5  
 Db 5 KSRK 8

RESULT 36  
 US-10-153-244-223  
 : Sequence 223, Application US/10153244  
 : Publication No. US20030144191A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Bristol-Myers Squibb Company  
 : TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER  
 : FILE REFERENCE: D0144 NP  
 : CURRENT APPLICATION NUMBER: US/10/153,244  
 : CURRENT FILING DATE: 2002-05-22  
 : PRIOR APPLICATION NUMBER: US 60/292,599  
 : PRIOR FILING DATE: 2001-05-22  
 : PRIOR APPLICATION NUMBER: US 60/362,944  
 : PRIOR FILING DATE: 2002-03-08  
 : NUMBER OF SEQ ID NOS: 335  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 223  
 : LENGTH: 13  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-153-244-223

Query Match 36.4%, Score 4; bp 12, Length 13;  
 Best Local Similarity 100.0%, Pred. No. 6, 2+0+0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5  
 Db 5 KSRK 8

RESULT 37  
 US-10-100-785-101  
 : Sequence 101, Application US/10100785  
 : Publication No. US20030171348A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Mitchell, William M.  
 : Stratton, Charles W.

US-10-100-785-101  
 : Sequence 101, Application US/10100785  
 : Publication No. US20030171348A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Mitchell, William M.  
 : Stratton, Charles W.  
 : TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER  
 : FILE REFERENCE: D0144 NP  
 : CURRENT APPLICATION NUMBER: US/10/153,244  
 : PRIOR FILING DATE: 2002-05-22  
 : PRIOR APPLICATION NUMBER: US 60/292,599  
 : PRIOR FILING DATE: 2001-05-22  
 : PRIOR APPLICATION NUMBER: US 60/362,944  
 : PRIOR FILING DATE: 2002-03-08  
 : NUMBER OF SEQ ID NOS: 335  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 101  
 : LENGTH: 13  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-100-785-101

Query Match 36.4%, Score 4; bp 12, Length 13;  
 Best Local Similarity 100.0%, Pred. No. 6, 2+0+0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5  
 Db 5 KSRK 8

RESULT 38  
 US-10-100-785-101

: Sequence 103, Application US/10100785  
 : Publication No. US20030171348A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Mitchell, William M.  
 : Stratton, Charles W.  
 : TITLE OF INVENTION: DIAGNOSIS AND MANAGEMENT OF  
 : INFECTION CAUSED BY CHLAMYDIA  
 : NUMBER OF SEQUENCES: 114  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 : STREET: Two Millia Drive  
 : CITY: Lexington  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02173  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: Windows 95  
 : SOFTWARE: FastSeq for Windows Version 2.0E  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/10/100,785  
 : FILING DATE: 19-Mar-2002  
 : CLASSIFICATION: <Unknown>  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 09/073,661  
 : FILING DATE: 06-MAY-1998  
 : APPLICATION NUMBER: US 09/025,521  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 08/911,543  
 : FILING DATE: 14-AUG-1997  
 : APPLICATION NUMBER: US 60/023,921  
 : FILING DATE: 14-AUG-1996  
 : APPLICATION NUMBER: US 09/025,176  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 09/025,174  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 60/045,739  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,779  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,760  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,764  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,787  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,689  
 : FILING DATE: 6-MAY-1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Carroll, Alice O.  
 : REGISTRATION NUMBER: 33,542  
 : REFERENCE/DOCKET NUMBER: VDB97 09pm  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 781-861-6240  
 : TELEFAX: 781-861-9540  
 : TELEX: <Unknown>  
 : INFORMATION FOR SEQ ID NO: 103:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 13 amino acids  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 103:  
 : US-10-100-785-103

Query Match 36.4%; Score 4; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6,2e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5  
 ||||

: Sequence 104, Application US/10100785  
 : Publication No. US20030171348A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Mitchell, William M.  
 : Stratton, Charles W.  
 : TITLE OF INVENTION: DIAGNOSIS AND MANAGEMENT OF  
 : INFECTION CAUSED BY CHLAMYDIA  
 : NUMBER OF SEQUENCES: 114  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 : STREET: Two Millia Drive  
 : CITY: Lexington  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02173  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: Windows 95  
 : SOFTWARE: FastSeq for Windows Version 2.0E  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/10/100,785  
 : FILING DATE: 19-Mar-2002  
 : CLASSIFICATION: <Unknown>  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 09/073,661  
 : FILING DATE: 06-MAY-1998  
 : APPLICATION NUMBER: US 09/025,521  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 08/911,543  
 : FILING DATE: 14-AUG-1997  
 : APPLICATION NUMBER: US 60/023,921  
 : FILING DATE: 14-AUG-1996  
 : APPLICATION NUMBER: US 09/025,176  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 09/025,174  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 60/045,739  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,779  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,760  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,764  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,787  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,689  
 : FILING DATE: 6-MAY-1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Carroll, Alice O.  
 : REGISTRATION NUMBER: 33,542  
 : REFERENCE/DOCKET NUMBER: VDB97 09pm  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 781-861-6240  
 : TELEFAX: 781-861-9540  
 : TELEX: <Unknown>  
 : INFORMATION FOR SEQ ID NO: 103:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 13 amino acids  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 103:  
 : US-10-100-785-103

Query Match 36.4%; Score 4; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6,2e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5  
 ||||

: Sequence 105, Application US/10100785  
 : Publication No. US20030171348A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Mitchell, William M.  
 : Stratton, Charles W.  
 : TITLE OF INVENTION: DIAGNOSIS AND MANAGEMENT OF  
 : INFECTION CAUSED BY CHLAMYDIA  
 : NUMBER OF SEQUENCES: 114  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 : STREET: Two Millia Drive  
 : CITY: Lexington  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02173  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: Windows 95  
 : SOFTWARE: FastSeq for Windows Version 2.0E  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/10/100,785  
 : FILING DATE: 19-Mar-2002  
 : CLASSIFICATION: <Unknown>  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 09/073,661  
 : FILING DATE: 06-MAY-1998  
 : APPLICATION NUMBER: US 09/025,521  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 08/911,543  
 : FILING DATE: 14-AUG-1997  
 : APPLICATION NUMBER: US 60/023,921  
 : FILING DATE: 14-AUG-1996  
 : APPLICATION NUMBER: US 09/025,176  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 09/025,174  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 60/045,739  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,779  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,760  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,764  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,787  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,689  
 : FILING DATE: 6-MAY-1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Carroll, Alice O.  
 : REGISTRATION NUMBER: 33,542  
 : REFERENCE/DOCKET NUMBER: VDB97 09pm  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 781-861-6240  
 : TELEFAX: 781-861-9540  
 : TELEX: <Unknown>  
 : INFORMATION FOR SEQ ID NO: 103:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 13 amino acids  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 103:  
 : US-10-100-785-103

Query Match 36.4%; Score 4; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6,2e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5  
 ||||

: Sequence 106, Application US/10100785  
 : Publication No. US20030171348A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Mitchell, William M.  
 : Stratton, Charles W.  
 : TITLE OF INVENTION: DIAGNOSIS AND MANAGEMENT OF  
 : INFECTION CAUSED BY CHLAMYDIA  
 : NUMBER OF SEQUENCES: 114  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 : STREET: Two Millia Drive  
 : CITY: Lexington  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02173  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: Windows 95  
 : SOFTWARE: FastSeq for Windows Version 2.0E  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/10/100,785  
 : FILING DATE: 19-Mar-2002  
 : CLASSIFICATION: <Unknown>  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 09/073,661  
 : FILING DATE: 06-MAY-1998  
 : APPLICATION NUMBER: US 09/025,521  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 08/911,543  
 : FILING DATE: 14-AUG-1997  
 : APPLICATION NUMBER: US 60/023,921  
 : FILING DATE: 14-AUG-1996  
 : APPLICATION NUMBER: US 09/025,176  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 09/025,174  
 : FILING DATE: 18-FEB-1998  
 : APPLICATION NUMBER: US 60/045,739  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,779  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,760  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,764  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,787  
 : FILING DATE: 6-MAY-1997  
 : APPLICATION NUMBER: US 60/045,689  
 : FILING DATE: 6-MAY-1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Carroll, Alice O.  
 : REGISTRATION NUMBER: 33,542  
 : REFERENCE/DOCKET NUMBER: VDB97 09pm  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 781-861-6240  
 : TELEFAX: 781-861-9540  
 : TELEX: <Unknown>  
 : INFORMATION FOR SEQ ID NO: 103:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 13 amino acids  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 103:  
 : US-10-100-785-103

Query Match 36.4%; Score 4; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6,2e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5  
 ||||

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? GENERAL INFORMATION:
? APPLICANT: Osbourn, Anne E
? APPLICANT: Haralampidis, Kosmas
? APPLICANT: Bryan, Gregory T
? TITLE OF INVENTION: Plant Gene
? FILE REFERENCE: 0380-P02892US0
? CURRENT APPLICATION NUMBER: US/10/168.445
? CURRENT FILING DATE: 2002-10-30
? PRIOR APPLICATION NUMBER: PCT/GB00/04908
? PRIOR FILING DATE: 2000-12-20
? PRIOR APPLICATION NUMBER: GB 9930394.3
? PRIOR FILING DATE: 1999-12-22
? PRIOR APPLICATION NUMBER: GB 0020217.6
? PRIOR FILING DATE: 2000-08-16
? NUMBER OF SEQ ID NOS: 219
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 89
? LENGTH: 13
? TYPE: PRT
? ORGANISM: Avena sativa
US-10-168-445-89

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Query Match          36.4%   Score 4; DB 12; Length 13
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 NSSL 10
    1111
DB 3 NSSL 6

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RESULT 42
US-10-156-820-11
? Sequence 11; Application US/10156820
? Publication No. US20020150558A1
? GENERAL INFORMATION:
? APPLICANT: Boulanger, Pierre
? APPLICANT: Hong, Saw See
? APPLICANT: Katayan, Lucie
? TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
? FILE REFERENCE: 032751-036
? CURRENT APPLICATION NUMBER: US/10/156.820
? CURRENT FILING DATE: 2002-06-30
? PRIOR APPLICATION NUMBER: PCT/FR98/00184
? PRIOR FILING DATE: 1998-01-30
? PRIOR APPLICATION NUMBER: FR 97/01005
? PRIOR FILING DATE: 1997-01-30
? PRIOR APPLICATION NUMBER: FR 97/11166
? PRIOR FILING DATE: 1997-09-09
? NUMBER OF SEQ ID NOS: 98
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 11
? LENGTH: 13
? TYPE: PRT
? ORGANISM: Mastadenovirus, serotype 2
US-10-156-820-11

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Query Match          36.4%   Score 4; DB 14; Length 13
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 NSSL 10
    1111
DB 1 NSSL 4

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RESULT 43
US-10-256-865-21
? Sequence 21; Application US/10256865
? Publication No. US20030049672A1
? GENERAL INFORMATION:
? APPLICANT: Kun Ping Lu
? APPLICANT: Xiao Zhen Zhou

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? TITLE OF INVENTION: Methods and compositions for polypeptides
? FILE REFERENCE: 0445-1041-11
? CURRENT APPLICATION NUMBER: US/10/256.865
? CURRENT FILING DATE: 2002-10-26
? PRIOR APPLICATION NUMBER: FR 97/01005
? PRIOR FILING DATE: 1997-01-30
? NUMBER OF SEQ ID NOS: 42
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 21
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Syntheris Inc
US-10-256-865-21

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```

Query Match          36.4%   Score 4; DB 15; Length 14
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ASSE 3
    1
DB 1 ASSE 13

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RESULT 44
US-10-123-604-27
? Sequence 27; Application US/1020004
? Publication No. US2002000047A1
? GENERAL INFORMATION:
? APPLICANT: Bristol-Myers Squibb Company

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? TITLE OF INVENTION: Polymorphic, Les Proben-Two Novel Human G-Protein-Coupled Receptors
? FILE REFERENCE: 0014-00
? CURRENT APPLICATION NUMBER: US/10/123.604
? CURRENT FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 00/258,319
? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 00/258,319
? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 00/258,319
? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 00/258,319
? PRIOR FILING DATE: 2001-04-11
? NUMBER OF SEQ ID NOS: 226
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 27
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-123-604-27

```

```

Query Match          36.4%   Score 4; DB 15; Length 14
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NSSL 1
    1
DB 1 NSSL 13

```

```

RESULT 45
US-10-120-604-20
? Sequence 20; Application US/1020004
? Publication No. US2002000047A1
? GENERAL INFORMATION:

```

```

? APPLICANT: Bristol-Myers Squibb Company
? TITLE OF INVENTION: Polymorphic, Les Proben-Two Novel Human G-Protein-Coupled Receptors
? FILE REFERENCE: 0014-00
? CURRENT APPLICATION NUMBER: US/10/120.604
? CURRENT FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 00/258,319

```



1 PRIOR APPLICATION NUMBER: US 60/283,161  
2 PRIOR FILING DATE: 2001-04-11  
3 PRIOR APPLICATION NUMBER: US 60/288,458  
4 PRIOR FILING DATE: 2001-05-03  
5 PRIOR APPLICATION NUMBER: US 60/300,619  
6 PRIOR FILING DATE: 2001-06-25  
7 NUMBER OF SEQ ID NOS: 226  
8 SOFTWARE: PatentIn version 3.0  
9 SEQ ID NO 28  
10 LENGTH: 14  
11 TYPE: PRT  
12 ORGANISM: Homo sapiens  
13 US-10-120-604-28

Query Match 36.4% Score 4: DB 15: Length 14:  
Best Local Similarity 100.0% Pred. No. 6,600,023  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
1111  
DB 6 NSSL 9

RESULT 46  
US-10-120-604-70  
1 Sequence 70: Application US/10120604  
2 Publication No. US20030096347A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Bristol-Myers Squibb Company  
5 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
6 FILE REFERENCE: D0143NP  
7 CURRENT APPLICATION NUMBER: US/10/120,604  
8 CURRENT FILING DATE: 2002-04-11  
9 PRIOR APPLICATION NUMBER: US 60/283,145  
10 PRIOR FILING DATE: 2001-04-11  
11 PRIOR APPLICATION NUMBER: US 60/283,161  
12 PRIOR FILING DATE: 2001-04-11  
13 PRIOR APPLICATION NUMBER: US 60/288,458  
14 PRIOR FILING DATE: 2001-05-03  
15 PRIOR APPLICATION NUMBER: US 60/300,619  
16 PRIOR FILING DATE: 2001-06-25  
17 NUMBER OF SEQ ID NOS: 226  
18 SOFTWARE: PatentIn version 3.0  
19 SEQ ID NO 70  
20 LENGTH: 14  
21 TYPE: PRT  
22 ORGANISM: Homo sapiens  
23 US-10-120-604-70

Query Match 36.4% Score 4: DB 15: Length 14:  
Best Local Similarity 100.0% Pred. No. 6,600,023  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
1111  
DB 7 NSSL 10

RESULT 47  
US-10-120-604-71  
1 Sequence 71: Application US/10120604  
2 Publication No. US20030096347A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Bristol-Myers Squibb Company  
5 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
6 FILE REFERENCE: D0143NP  
7 CURRENT APPLICATION NUMBER: US/10/120,604  
8 CURRENT FILING DATE: 2002-04-11  
9 PRIOR APPLICATION NUMBER: US 60/283,145  
10 PRIOR FILING DATE: 2001-04-11  
11 PRIOR APPLICATION NUMBER: US 60/283,161  
12 PRIOR APPLICATION NUMBER: US 60/283,161

1 PRIOR FILING DATE: 2001-04-11  
2 PRIOR APPLICATION NUMBER: US 60/288,458  
3 PRIOR FILING DATE: 2001-05-03  
4 PRIOR APPLICATION NUMBER: US 60/300,619  
5 PRIOR FILING DATE: 2001-06-25  
6 NUMBER OF SEQ ID NOS: 226  
7 SOFTWARE: PatentIn version 3.0  
8 SEQ ID NO 71  
9 LENGTH: 14  
10 TYPE: PRT  
11 ORGANISM: Homo sapiens  
12 US-10-120-604-71

Query Match 36.4% Score 4: DB 15: Length 14:  
Best Local Similarity 100.0% Pred. No. 6,600,023  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
1111  
DB 6 NSSL 9

RESULT 48  
US-10-120-604-72  
1 Sequence 72: Application US/10120604  
2 Publication No. US20030096347A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Bristol-Myers Squibb Company  
5 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
6 FILE REFERENCE: D0143NP  
7 CURRENT APPLICATION NUMBER: US/10/120,604  
8 CURRENT FILING DATE: 2002-04-11  
9 PRIOR APPLICATION NUMBER: US 60/283,145  
10 PRIOR FILING DATE: 2001-04-11  
11 PRIOR APPLICATION NUMBER: US 60/283,161  
12 PRIOR FILING DATE: 2001-04-11  
13 PRIOR APPLICATION NUMBER: US 60/288,458  
14 PRIOR FILING DATE: 2001-05-03  
15 PRIOR APPLICATION NUMBER: US 60/300,619  
16 PRIOR FILING DATE: 2001-06-25  
17 NUMBER OF SEQ ID NOS: 226  
18 SOFTWARE: PatentIn version 3.0  
19 SEQ ID NO 86  
20 LENGTH: 14  
21 TYPE: PRT  
22 ORGANISM: Homo sapiens  
23 US-10-120-604-72

Query Match 36.4% Score 4: DB 15: Length 14:  
Best Local Similarity 100.0% Pred. No. 6,600,023  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
1111  
DB 7 NSSL 10

RESULT 49  
US-10-120-604-87  
1 Sequence 49: Application US/10120604  
2 Publication No. US20030096347A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Bristol-Myers Squibb Company  
5 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
6 FILE REFERENCE: D0143NP  
7 CURRENT APPLICATION NUMBER: US/10/120,604  
8 CURRENT FILING DATE: 2002-04-11  
9 PRIOR APPLICATION NUMBER: US 60/283,145  
10 PRIOR FILING DATE: 2001-04-11  
11 PRIOR APPLICATION NUMBER: US 60/283,161  
12 PRIOR FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: US 60/288,458
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-87

Query Match 36.4%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pos. N. 1; Pos. E. 1;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 NSSL 10
DB 6 NSSL 9

RESULT 50
US-10-086-816A-10
; Sequence 10, Application US/046816A
; Publication No. US20030106075A1
; GENERAL INFORMATION:
; APPLICANT: CILILAR, TOMAS
; TITLE OF INVENTION: NOVEL GENE ENCODING HEMANIN ANION TRANSFER
; FILE REFERENCE: 240,1PCD
; CURRENT APPLICATION NUMBER: US/10/086,816A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/330,245
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/112,267
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 60/088,864
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Immunogenic peptide
US-10-086-816A-10

Query Match 36.4%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pos. N. 1; Pos. E. 1;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SRKG 6
DB 7 SRKG 10

Search completed: September 30, 2003, 10:34:28
Job time : 23.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 41.0833 seconds  
(without alignments)  
42.459 Million cell updates/sec

Title: US-09-787-443-22

Perfect score: 11

Sequence: 1 ARKSRDWTALK 11

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27522

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
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- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
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- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	21	AA88550 NCAM Igl binding p
2	11	100.0	11	23	ABG69350 Human neural cell
3	5	45.5	8	23	AB874692 Transcription fact
4	5	45.5	8	23	AB874740 Transcription fact
5	5	45.5	8	23	AB874743 Transcription fact
6	5	45.5	8	23	AB874756 Transcription fact
7	5	45.5	14	22	AA957433 Human peptidase #708
8	4	36.4	8	15	AAR72176 Hepatitis C Virus
9	4	36.4	8	15	AAR72177 Hepatitis C Virus

10	4	36.4	11	24	AA872177 Hepatitis C Virus
11	4	36.4	11	24	AA872178 Hepatitis C Virus
12	4	36.4	11	24	AA872179 Hepatitis C Virus
13	4	36.4	11	24	AA872180 Hepatitis C Virus
14	4	36.4	11	24	AA872181 Hepatitis C Virus
15	4	36.4	11	24	AA872182 Hepatitis C Virus
16	4	36.4	11	24	AA872183 Hepatitis C Virus
17	4	36.4	11	24	AA872184 Hepatitis C Virus
18	4	36.4	11	24	AA872185 Hepatitis C Virus
19	4	36.4	11	24	AA872186 Hepatitis C Virus
20	4	36.4	11	24	AA872187 Hepatitis C Virus
21	4	36.4	11	24	AA872188 Hepatitis C Virus
22	4	36.4	11	24	AA872189 Hepatitis C Virus
23	4	36.4	11	24	AA872190 Hepatitis C Virus
24	4	36.4	11	24	AA872191 Hepatitis C Virus
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26	4	36.4	11	24	AA872193 Hepatitis C Virus
27	4	36.4	11	24	AA872194 Hepatitis C Virus
28	4	36.4	11	24	AA872195 Hepatitis C Virus
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30	4	36.4	11	24	AA872197 Hepatitis C Virus
31	4	36.4	11	24	AA872198 Hepatitis C Virus
32	4	36.4	11	24	AA872199 Hepatitis C Virus
33	4	36.4	11	24	AA872200 Hepatitis C Virus
34	4	36.4	11	24	AA872201 Hepatitis C Virus
35	4	36.4	11	24	AA872202 Hepatitis C Virus
36	4	36.4	11	24	AA872203 Hepatitis C Virus
37	4	36.4	11	24	AA872204 Hepatitis C Virus
38	4	36.4	11	24	AA872205 Hepatitis C Virus
39	4	36.4	11	24	AA872206 Hepatitis C Virus
40	4	36.4	11	24	AA872207 Hepatitis C Virus
41	4	36.4	11	24	AA872208 Hepatitis C Virus
42	4	36.4	11	24	AA872209 Hepatitis C Virus
43	4	36.4	11	24	AA872210 Hepatitis C Virus
44	4	36.4	11	24	AA872211 Hepatitis C Virus
45	4	36.4	11	24	AA872212 Hepatitis C Virus
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47	4	36.4	11	24	AA872214 Hepatitis C Virus
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49	4	36.4	11	24	AA872216 Hepatitis C Virus
50	4	36.4	11	24	AA872217 Hepatitis C Virus
51	4	36.4	11	24	AA872218 Hepatitis C Virus
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53	4	36.4	11	24	AA872220 Hepatitis C Virus
54	4	36.4	11	24	AA872221 Hepatitis C Virus
55	4	36.4	11	24	AA872222 Hepatitis C Virus
56	4	36.4	11	24	AA872223 Hepatitis C Virus
57	4	36.4	11	24	AA872224 Hepatitis C Virus
58	4	36.4	11	24	AA872225 Hepatitis C Virus
59	4	36.4	11	24	AA872226 Hepatitis C Virus
60	4	36.4	11	24	AA872227 Hepatitis C Virus
61	4	36.4	11	24	AA872228 Hepatitis C Virus
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63	4	36.4	11	24	AA872230 Hepatitis C Virus
64	4	36.4	11	24	AA872231 Hepatitis C Virus
65	4	36.4	11	24	AA872232 Hepatitis C Virus
66	4	36.4	11	24	AA872233 Hepatitis C Virus
67	4	36.4	11	24	AA872234 Hepatitis C Virus
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69	4	36.4	11	24	AA872236 Hepatitis C Virus
70	4	36.4	11	24	AA872237 Hepatitis C Virus
71	4	36.4	11	24	AA872238 Hepatitis C Virus
72	4	36.4	11	24	AA872239 Hepatitis C Virus
73	4	36.4	11	24	AA872240 Hepatitis C Virus
74	4	36.4	11	24	AA872241 Hepatitis C Virus
75	4	36.4	11	24	AA872242 Hepatitis C Virus
76	4	36.4	11	24	AA872243 Hepatitis C Virus
77	4	36.4	11	24	AA872244 Hepatitis C Virus
78	4	36.4	11	24	AA872245 Hepatitis C Virus
79	4	36.4	11	24	AA872246 Hepatitis C Virus
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81	4	36.4	11	24	AA872248 Hepatitis C Virus
82	4	36.4	11	24	AA872249 Hepatitis C Virus

83	4	36.4	14	23	ABB07294	Human histone H3 F	156	8	27.3	8	27	HIV A02 super motif
84	4	36.4	15	17	AAR97895	Japan cedar pollen	157	8	27.3	8	27	HIV A02 super motif
85	4	36.4	15	17	AAR97896	Japan cedar pollen	158	8	27.3	8	27	HIV A02 super motif
86	4	36.4	15	20	AA070446	New noctuid anis	159	8	27.3	8	27	HIV A02 super motif
87	4	36.4	15	21	AA070446	T cell antigen rec	160	8	27.3	8	27	HIV A02 super motif
88	4	36.4	15	21	AA070446	T cell antigen rec	161	8	27.3	8	27	HIV A02 super motif
89	4	36.4	15	22	AA070446	Human Kazal type I	162	8	27.3	8	27	HIV A02 super motif
90	4	36.4	15	22	AA070446	Human phospholipase	163	8	27.3	8	27	HIV A02 super motif
91	4	36.4	15	22	AA070446	Interleukin 2 recep	164	8	27.3	8	27	HIV A02 super motif
92	4	36.4	15	22	AA070446	Antigenesis prote	165	8	27.3	8	27	HIV A02 super motif
93	4	36.4	15	22	AA070446	Immunogenic peptid	166	8	27.3	8	27	HIV A02 super motif
94	4	36.4	15	22	AA070446	N-terminal of reov	167	8	27.3	8	27	HIV A02 super motif
95	4	36.4	15	23	AA070446	Histone H3 dist. acc	168	8	27.3	8	27	HIV A02 super motif
96	4	36.4	15	23	AA070446	H84 g. plasmodia	169	8	27.3	8	27	HIV A02 super motif
97	4	36.4	15	23	AA070446	Karyoplastic peptid	170	8	27.3	8	27	HIV A02 super motif
98	4	36.4	15	24	ABR30373	Human cancer relat	171	8	27.3	8	27	HIV A02 super motif
99	4	36.4	15	24	ABR30373	Human cancer relat	172	8	27.3	8	27	HIV A02 super motif
100	4	36.4	15	24	ABR30501	Human cancer relat	173	8	27.3	8	27	HIV A02 super motif
101	4	36.4	15	24	ABR30502	Human cancer relat	174	8	27.3	8	27	HIV A02 super motif
102	4	36.4	15	24	ABR30685	Human cancer relat	175	8	27.3	8	27	HIV A02 super motif
103	4	36.4	15	24	ABR30691	Human cancer relat	176	8	27.3	8	27	HIV A02 super motif
104	4	36.4	15	24	ABR31261	Human cancer relat	177	8	27.3	8	27	HIV A02 super motif
105	4	36.4	15	24	ABR31262	Human cancer relat	178	8	27.3	8	27	HIV A02 super motif
106	4	36.4	15	24	ABR31314	Human cancer relat	179	8	27.3	8	27	HIV A02 super motif
107	3	27.3	8	7	AAP60494	Peptide with Fe re	180	8	27.3	8	27	HIV A02 super motif
108	3	27.3	8	13	AAR33141	Select binder of F	181	8	27.3	8	27	HIV A02 super motif
109	3	27.3	8	14	AAR33077	Human cytomegalov	182	8	27.3	8	27	HIV A02 super motif
110	3	27.3	8	14	AAR35999	Hepatitis C virus	183	8	27.3	8	27	HIV A02 super motif
111	3	27.3	8	14	AAR36000	Hepatitis C virus	184	8	27.3	8	27	HIV A02 super motif
112	3	27.3	8	14	AAR36001	Hepatitis C virus	185	8	27.3	8	27	HIV A02 super motif
113	3	27.3	8	14	AAR36002	Hepatitis C virus	186	8	27.3	8	27	HIV A02 super motif
114	3	27.3	8	14	AAR36003	Hepatitis C virus	187	8	27.3	8	27	HIV A02 super motif
115	3	27.3	8	14	AAR36004	Hepatitis C virus	188	8	27.3	8	27	HIV A02 super motif
116	3	27.3	8	14	AAR3467	Sc/SSA epitope 285	189	8	27.3	8	27	HIV A02 super motif
117	3	27.3	8	15	AAR72179	Hepatitis C virus	190	8	27.3	8	27	HIV A02 super motif
118	3	27.3	8	15	AAR72173	Hepatitis C virus	191	8	27.3	8	27	HIV A02 super motif
119	3	27.3	8	15	AAR58338	Hypotensive polype	192	8	27.3	8	27	HIV A02 super motif
120	3	27.3	8	15	AAR61039	Dynorphin-like po	193	8	27.3	8	27	HIV A02 super motif
121	3	27.3	8	16	AAR21334	Cereagan precursor	194	8	27.3	8	27	HIV A02 super motif
122	3	27.3	8	16	AAR73354	Human TSH receptor	195	8	27.3	8	27	HIV A02 super motif
123	3	27.3	8	16	AAR73355	Human TSH receptor	196	8	27.3	8	27	HIV A02 super motif
124	3	27.3	8	16	AAR73356	Human TSH receptor	197	8	27.3	8	27	HIV A02 super motif
125	3	27.3	8	16	AAR77244	C-peptide 1/2 Junc	198	8	27.3	8	27	HIV A02 super motif
126	3	27.3	8	16	AAR64595	PF-1 peptide 4.3.11	199	8	27.3	8	27	HIV A02 super motif
127	3	27.3	8	17	AAR96814	N-glycanase Iga	200	8	27.3	8	27	HIV A02 super motif
128	3	27.3	8	17	AAR96815	Human laminin b2	201	8	27.3	8	27	HIV A02 super motif
129	3	27.3	8	18	AAR30602	CAEV immunogen	202	8	27.3	8	27	HIV A02 super motif
130	3	27.3	8	19	AA020217	Human beta-amyloid	203	8	27.3	8	27	HIV A02 super motif
131	3	27.3	8	19	AA064273	mgp2.7 peptide sub	204	8	27.3	8	27	HIV A02 super motif
132	3	27.3	8	19	AA056994	Enzyme inhibitor p	205	8	27.3	8	27	HIV A02 super motif
133	3	27.3	8	19	AA056995	Enzyme inhibitor p	206	8	27.3	8	27	HIV A02 super motif
134	3	27.3	8	19	AA057001	Enzyme inhibitor p	207	8	27.3	8	27	HIV A02 super motif
135	3	27.3	8	20	AA042587	Human IgE peptide	208	8	27.3	8	27	HIV A02 super motif
136	3	27.3	8	20	AA025226	HIV gag protein gp	209	8	27.3	8	27	HIV A02 super motif
137	3	27.3	8	20	AA016056	Human keratin K5	210	8	27.3	8	27	HIV A02 super motif
138	3	27.3	8	20	AA034877	Predicted binding	211	8	27.3	8	27	HIV A02 super motif
139	3	27.3	8	20	AA034884	Predicted binding	212	8	27.3	8	27	HIV A02 super motif
140	3	27.3	8	20	AA010144	I cell epitope/MHC	213	8	27.3	8	27	HIV A02 super motif
141	3	27.3	8	21	AA081137	Peptide monomer	214	8	27.3	8	27	HIV A02 super motif
142	3	27.3	8	21	AA08128	Peptide derived fr	215	8	27.3	8	27	HIV A02 super motif
143	3	27.3	8	21	AA03780	Fibrinogen fragmen	216	8	27.3	8	27	HIV A02 super motif
144	3	27.3	8	21	AA03781	Fibrinogen fragmen	217	8	27.3	8	27	HIV A02 super motif
145	3	27.3	8	21	AA01920	Peptide sequence	218	8	27.3	8	27	HIV A02 super motif
146	3	27.3	8	21	AA084390	N-terminal peptide	219	8	27.3	8	27	HIV A02 super motif
147	3	27.3	8	21	AA085203	Human IgE mutant	220	8	27.3	8	27	HIV A02 super motif
148	3	27.3	8	21	AA085220	Human IgE mutant	221	8	27.3	8	27	HIV A02 super motif
149	3	27.3	8	21	AA082893	Antigenic peptide	222	8	27.3	8	27	HIV A02 super motif
150	3	27.3	8	21	AA085421	Oncophila shaker	223	8	27.3	8	27	HIV A02 super motif
151	3	27.3	8	21	AA067468	PF70 peptide havin	224	8	27.3	8	27	HIV A02 super motif
152	3	27.3	8	21	AA089404	Core polypeptide	225	8	27.3	8	27	HIV A02 super motif
153	3	27.3	8	21	AA089405	Core polypeptide	226	8	27.3	8	27	HIV A02 super motif
154	3	27.3	8	21	AA066381	HLA-B8-binding HIV	227	8	27.3	8	27	HIV A02 super motif
155	3	27.3	8	22	ABP11993	HIV A02 super motif	228	8	27.3	8	27	HIV A02 super motif

229	3	27.3	8	22	AAB011182	Human, gene 2, encod	302	3	27.3	4	25	AAY40745	Active site of superm
230	3	27.3	8	22	AAB72647	Mammalian interfer	303	3	27.3	4	25	AAY26557	beta 1, alpha 1, and
231	3	27.3	8	22	AAB72649	Mammalian interfer	304	3	27.3	4	25	AAY26558	beta 1, alpha 1, and
232	3	27.3	8	22	AAB72650	Mammalian interfer	305	3	27.3	4	25	AAY26559	HIV Env gp120 prote
233	3	27.3	8	22	AAB72651	Mammalian interfer	306	3	27.3	4	20	AAY26560	beta 1, alpha 1, and
234	3	27.3	8	22	AAB77805	Core polypeptide 1	307	3	27.3	4	20	AAY40871	HIV gp120 gp120
235	3	27.3	8	22	AAB77806	Core polypeptide 2	308	3	27.3	4	20	AAY40872	HIV gp120 gp120
236	3	27.3	8	22	AAB77807	Core polypeptide 3	309	3	27.3	4	20	AAY40873	HIV gp120 gp120
237	3	27.3	8	22	AAB76079	Tumor associated	310	3	27.3	4	20	AAY40874	Antigenic site of
238	3	27.3	8	22	AAB55198	Anti-RSV F1 p178	311	3	27.3	4	20	AAY40875	T cell epitope/RNP
239	3	27.3	8	23	AB060421	Protease binding p	312	3	27.3	4	21	AAR24124	HIV class 1 motif
240	3	27.3	8	23	AB060426	Protease binding p	313	3	27.3	4	21	AAR24125	Tyrosine kinase BL
241	3	27.3	8	23	AB26630	Yeast GPAL amino t	314	3	27.3	4	21	AAR24126	Human CASp19 prot
242	3	27.3	8	23	AB26630	Yeast GPAL amino t	315	3	27.3	4	21	AAR24127	Human CASp19 prot
243	3	27.3	8	23	AB015653	MHC class 1 molecu	316	3	27.3	4	21	AAR24128	Epitope derived fr
244	3	27.3	8	23	AB098394	West Nile virus ca	317	3	27.3	4	21	AAY40876	Human MHC class 1
245	3	27.3	8	23	AB064041	Synthetic vascular	318	3	27.3	4	21	AAY40877	Peptide R 5 from 1
246	3	27.3	8	23	ABJ00179	Human albumin fusi	319	3	27.3	4	21	AAY40878	Anti platelet alve
247	3	27.3	8	23	ABG34988	Her2/neu derived H	320	3	27.3	4	21	AAY40879	Anti platelet alve
248	3	27.3	8	23	AB857484	Human prostate can	321	3	27.3	4	21	AAY40880	HIV A2 binding pep
249	3	27.3	8	23	AB846360	HIV A2-specific pr	322	3	27.3	4	21	AAY40881	Helicase-peptide
250	3	27.3	8	23	AB846400	Desmoglein-2 CAR s	323	3	27.3	4	21	AAY40882	Helicase-peptide
251	3	27.3	8	23	AB846400	Desmoglein-2 CAR s	324	3	27.3	4	21	AAY40883	Helicase-peptide
252	3	27.3	8	24	AB064634	Transcription fact	325	3	27.3	4	21	AAY40884	Helicase-peptide
253	3	27.3	8	24	ABJ19997	Motif-specific and	326	3	27.3	4	21	AAY40885	Helicase-peptide
254	3	27.3	8	24	ABJ19997	MHC binding peptid	327	3	27.3	4	21	AAY40886	Helicase-peptide
255	3	27.3	9	10	ABP75021	Proteome analysis	328	3	27.3	4	21	AAY40887	Helicase-peptide
256	3	27.3	9	12	AAR90875	Proposed 1 cell ep	329	3	27.3	4	21	AAY40888	Helicase-peptide
257	3	27.3	9	12	AAR11570	Native HIV core pr	330	3	27.3	4	21	AAY40889	Helicase-peptide
258	3	27.3	9	14	AAR22408	CMV gB epitope 559	331	3	27.3	4	21	AAY40890	Helicase-peptide
259	3	27.3	9	14	AAR44992	Anti histamine and	332	3	27.3	4	21	AAY40891	Helicase-peptide
260	3	27.3	9	14	AAR54617	Tryptic peptide #1	333	3	27.3	4	21	AAR54618	Helicase-peptide
261	3	27.3	9	14	AAR34778	Listeria p60 pepid	334	3	27.3	4	21	AAR54619	Helicase-peptide
262	3	27.3	9	14	AAR41615	CAD tryptic peptid	335	3	27.3	4	21	AAR54620	Helicase-peptide
263	3	27.3	9	15	AAY38004	TRP-44, Syntheti	336	3	27.3	4	21	AAR54621	Helicase-peptide
264	3	27.3	9	15	AAY38040	Hepatitis B virus	337	3	27.3	4	21	AAR54622	Helicase-peptide
265	3	27.3	9	15	AAY38241	HIV-derived HIV-bi	338	3	27.3	4	21	AAR54623	Helicase-peptide
266	3	27.3	9	15	AAY59226	Peptide fragment (	339	3	27.3	4	21	AAR54624	Helicase-peptide
267	3	27.3	9	16	AAB59198	Peptide fragment (	340	3	27.3	4	21	AAR54625	Helicase-peptide
268	3	27.3	9	16	AAR21445	HSV 2 glycoprotein	341	3	27.3	4	21	AAR54626	Helicase-peptide
269	3	27.3	9	16	AAR78786	RapB (772-180) pe	342	3	27.3	4	21	AAR54627	Helicase-peptide
270	3	27.3	9	16	AAR75532	N. alata arabinoga	343	3	27.3	4	21	AAR54628	Helicase-peptide
271	3	27.3	9	16	AAR71853	A. alternata allera	344	3	27.3	4	21	AAR54629	Helicase-peptide
272	3	27.3	9	16	AAR77243	C-epsilon-1/2, junc	345	3	27.3	4	21	AAR54630	Helicase-peptide
273	3	27.3	9	16	AAR71794	Peptide, neutralisi	346	3	27.3	4	21	AAR54631	Helicase-peptide
274	3	27.3	9	16	AAR64596	RP-1 peptide 41 fr	347	3	27.3	4	21	AAR54632	Helicase-peptide
275	3	27.3	9	17	AAR49584	Human leucocyte an	348	3	27.3	4	21	AAR54633	Helicase-peptide
276	3	27.3	9	17	AAR49509	Human leucocyte ac	349	3	27.3	4	21	AAR54634	Helicase-peptide
277	3	27.3	9	17	AAR49502	Human leucocyte an	350	3	27.3	4	21	AAR54635	Helicase-peptide
278	3	27.3	9	17	AAR49418	Human leucocyte an	351	3	27.3	4	21	AAR54636	Helicase-peptide
279	3	27.3	9	17	AAR06952	Human leucocyte an	352	3	27.3	4	21	AAR54637	Helicase-peptide
280	3	27.3	9	18	AAR39717	Autocrine mobility	353	3	27.3	4	21	AAR54638	Helicase-peptide
281	3	27.3	9	18	AAR39717	HIV peptide #1 sup	354	3	27.3	4	21	AAR54639	Helicase-peptide
282	3	27.3	9	18	AAR39532	HIV 1 psi peptide	355	3	27.3	4	21	AAR54640	Helicase-peptide
283	3	27.3	9	18	AAR43854	Specific human leu	356	3	27.3	4	21	AAR54641	Helicase-peptide
284	3	27.3	9	18	AAR29254	Immunomodulatory p	357	3	27.3	4	21	AAR54642	Helicase-peptide
285	3	27.3	9	18	AAR36830	Immunogenic peptid	358	3	27.3	4	21	AAR54643	Helicase-peptide
286	3	27.3	9	18	AAR21611	Immunogenic peptid	359	3	27.3	4	21	AAR54644	Helicase-peptide
287	3	27.3	9	19	AAY20633	Antibiotic potent	360	3	27.3	4	21	AAR54645	Helicase-peptide
288	3	27.3	9	19	AAY20633	Human neurofilamen	361	3	27.3	4	21	AAR54646	Helicase-peptide
289	3	27.3	9	19	AAY20633	Human neurofilamen	362	3	27.3	4	21	AAR54647	Helicase-peptide
290	3	27.3	9	19	AAY20633	Denque virus type	363	3	27.3	4	21	AAR54648	Helicase-peptide
291	3	27.3	9	19	AAY56409	Nuclear localisati	364	3	27.3	4	21	AAR54649	Helicase-peptide
292	3	27.3	9	19	AAY45573	Amino-terminal pro	365	3	27.3	4	21	AAR54650	Helicase-peptide
293	3	27.3	9	20	AAY52104	CAL4 activation do	366	3	27.3	4	21	AAR54651	Helicase-peptide
294	3	27.3	9	20	AAY53312	Bcr-Abi epitope (a	367	3	27.3	4	21	AAR54652	Helicase-peptide
295	3	27.3	9	20	AAY45574	Immunogenic peptid	368	3	27.3	4	21	AAR54653	Helicase-peptide
296	3	27.3	9	20	AAY45609	Immunogenic peptid	369	3	27.3	4	21	AAR54654	Helicase-peptide
297	3	27.3	9	20	AAY45813	Immunogenic peptid	370	3	27.3	4	21	AAR54655	Helicase-peptide
298	3	27.3	9	20	AAY46453	Immunogenic peptid	371	3	27.3	4	21	AAR54656	Helicase-peptide
299	3	27.3	9	20	AAY46901	Immunogenic peptid	372	3	27.3	4	21	AAR54657	Helicase-peptide
300	3	27.3	9	20	AAY47754	Immunogenic peptid	373	3	27.3	4	21	AAR54658	Helicase-peptide
301	3	27.3	9	20	AAY48014	Immunogenic peptid	374	3	27.3	4	21	AAR54659	Helicase-peptide

375	3	27.3	9	22	ABP21513	HIV A03 motif pol	448	1	27.3	1	22	AA007296	HLA-B *2703 noname
376	3	27.3	9	22	ABP21537	HIV A03 motif pol	449	3	27.3	1	22	AA007413	HLA-A *202 noname
377	3	27.3	9	22	ABP21757	HIV A03 motif pol	450	3	27.3	1	22	AA007438	HLA-A *203 noname
378	3	27.3	9	22	ABP21889	HIV A03 motif rev	451	3	27.3	1	22	AA007450	HLA-B *0702 noname
379	3	27.3	9	22	ABP21891	HIV A03 motif rev	452	3	27.3	1	22	AA007459	HLA-B *2705 noname
380	3	27.3	9	22	ABP22981	HIV A11 motif nef	453	3	27.3	1	22	AA007462	HLA-B *2705 noname
381	3	27.3	9	22	ABP22983	HIV A11 motif nef	454	3	27.3	1	22	AA007463	HLA-A *201 noname
382	3	27.3	9	22	ABP23075	HIV A11 motif pol	455	3	27.3	1	22	AA007487	HLA-A1 nonamer #74
383	3	27.3	9	22	ABP23188	HIV A11 motif pol	456	3	27.3	1	22	AA007499	HLA-B *2705 noname
384	3	27.3	9	22	ABP23318	HIV A11 motif pol	457	3	27.3	1	22	AA007509	HLA-A *0203 noname
385	3	27.3	9	22	ABP23319	HIV A11 motif pol	458	3	27.3	1	22	AA007510	HLA-A *0203 noname
386	3	27.3	9	22	ABP23422	HIV A11 motif pol	459	3	27.3	1	22	AA007511	HLA-A *0203 noname
387	3	27.3	9	22	ABP23443	HIV A11 motif pol	460	3	27.3	1	22	AA007512	HLA-A1 nonamer #42
388	3	27.3	9	22	ABP23444	HIV A11 motif pol	461	3	27.3	1	22	AA007513	HLA-B *0702 noname
389	3	27.3	9	22	ABP23618	HIV A11 motif pol	462	3	27.3	1	22	AA007514	HLA-B *0702 noname
390	3	27.3	9	22	ABP23718	HIV A11 motif rev	463	3	27.3	1	22	AA007515	HLA-A26 nonamer #2
391	3	27.3	9	22	ABP23720	HIV A11 motif rev	464	3	27.3	1	22	AA007516	HLA-A26 nonamer #1
392	3	27.3	9	22	ABP23721	HIV A11 motif rev	465	3	27.3	1	22	AA007517	HLA-B8 nonamer #1
393	3	27.3	9	22	ABP24211	HIV A24 motif pol	466	3	27.3	1	22	AA007518	HLA-B8 nonamer #59
394	3	27.3	9	22	ABP24211	HIV A24 motif pol	467	3	27.3	1	22	AA007519	HLA-B *510 noname
395	3	27.3	9	22	ABP24262	HIV derived peptide	468	3	27.3	1	22	AA007520	HLA-B *510 noname
396	3	27.3	9	22	ABP25243	HIV derived peptide	469	3	27.3	1	22	AA007521	HLA-B *510 noname
397	3	27.3	9	22	AA070112	Human Calcitonin R	470	3	27.3	1	22	AA007522	HLA-B8 nonamer #11
398	3	27.3	9	22	AA068120	Human Breast Cancer	471	3	27.3	1	22	AA007523	HLA-A *0202 noname
399	3	27.3	9	22	AB002200	Viral core polypep	472	3	27.3	1	22	AA007524	HLA-A *0202 noname
400	3	27.3	9	22	AAG68072	Antitumor cancer	473	3	27.3	1	22	AA007525	HLA-A26 nonamer #2
401	3	27.3	9	22	AA068996	Vaccine related MR	474	3	27.3	1	22	AA007526	HLA-B *51 noname
402	3	27.3	9	22	AA024228	Human MHC class I	475	3	27.3	1	22	AA007527	HLA-A26 nonamer #2
403	3	27.3	9	22	AA026616	Human Leukocyte Aa	476	3	27.3	1	22	AA007528	HLA-A26 nonamer #2
404	3	27.3	9	22	AA026949	Human Leukocyte Aa	477	3	27.3	1	22	AA007529	HLA-B *510 noname
405	3	27.3	9	22	AA082770	Human Telomerase 1	478	3	27.3	1	22	AA007530	HLA-A26 nonamer #3
406	3	27.3	9	22	AA082771	Human Telomerase 1	479	3	27.3	1	22	AA007531	HLA-A26 nonamer #3
407	3	27.3	9	22	AA022177	HIV peptide SEQ ID	480	3	27.3	1	22	AA007532	HLA-B8 nonamer #25
408	3	27.3	9	22	AA022310	HIV peptide SEQ ID	481	3	27.3	1	22	AA007533	HLA-B8 nonamer #25
409	3	27.3	9	22	AA022311	HIV peptide SEQ ID	482	3	27.3	1	22	AA007534	HLA-A *203 noname
410	3	27.3	9	22	AA022312	HIV peptide SEQ ID	483	3	27.3	1	22	AA007535	HLA-B8 nonamer #3
411	3	27.3	9	22	AA022394	HIV peptide SEQ ID	484	3	27.3	1	22	AA007536	HLA-A *203 noname
412	3	27.3	9	22	AA022395	HIV peptide SEQ ID	485	3	27.3	1	22	AA007537	HLA-A27 nonamer #3
413	3	27.3	9	22	AA022496	HIV peptide SEQ ID	486	3	27.3	1	22	AA007538	HLA-A *0203 noname
414	3	27.3	9	22	AA022541	HIV peptide SEQ ID	487	3	27.3	1	22	AA007539	HLA-B *510 noname
415	3	27.3	9	22	AA022542	HIV peptide SEQ ID	488	3	27.3	1	22	AA007540	HLA-B *510 noname
416	3	27.3	9	22	AA022594	HIV peptide SEQ ID	489	3	27.3	1	22	AA007541	HLA-B *510 noname
417	3	27.3	9	22	AA022595	HIV peptide SEQ ID	490	3	27.3	1	22	AA007542	HLA-B8 nonamer #3
418	3	27.3	9	22	AA022596	HIV peptide SEQ ID	491	3	27.3	1	22	AA007543	HLA-B8 nonamer #3
419	3	27.3	9	22	AA022597	HIV peptide SEQ ID	492	3	27.3	1	22	AA007544	HLA-A27 nonamer #3
420	3	27.3	9	22	AA022598	HIV peptide SEQ ID	493	3	27.3	1	22	AA007545	HLA-A *0203 noname
421	3	27.3	9	22	AA022599	HIV peptide SEQ ID	494	3	27.3	1	22	AA007546	HLA-B *510 noname
422	3	27.3	9	22	AA022600	HIV peptide SEQ ID	495	3	27.3	1	22	AA007547	HLA-B *510 noname
423	3	27.3	9	22	AA022601	HIV peptide SEQ ID	496	3	27.3	1	22	AA007548	HLA-B *510 noname
424	3	27.3	9	22	AA022602	HIV peptide SEQ ID	497	3	27.3	1	22	AA007549	HLA-B *510 noname
425	3	27.3	9	22	AA022603	HIV peptide SEQ ID	498	3	27.3	1	22	AA007550	HLA-B *510 noname
426	3	27.3	9	22	AA022604	HIV peptide SEQ ID	499	3	27.3	1	22	AA007551	HLA-B *510 noname
427	3	27.3	9	22	AA022605	HIV peptide SEQ ID	500	3	27.3	1	22	AA007552	HLA-B *510 noname
428	3	27.3	9	22	AA022606	HIV peptide SEQ ID	501	3	27.3	1	22	AA007553	HLA-B *510 noname
429	3	27.3	9	22	AA022607	HIV peptide SEQ ID	502	3	27.3	1	22	AA007554	HLA-B *510 noname
430	3	27.3	9	22	AA022608	HIV peptide SEQ ID	503	3	27.3	1	22	AA007555	HLA-B *510 noname
431	3	27.3	9	22	AA022609	HIV peptide SEQ ID	504	3	27.3	1	22	AA007556	HLA-B *510 noname
432	3	27.3	9	22	AA022610	HIV peptide SEQ ID	505	3	27.3	1	22	AA007557	HLA-B *510 noname
433	3	27.3	9	22	AA022611	HIV peptide SEQ ID	506	3	27.3	1	22	AA007558	HLA-B *510 noname
434	3	27.3	9	22	AA022612	HIV peptide SEQ ID	507	3	27.3	1	22	AA007559	HLA-B *510 noname
435	3	27.3	9	22	AA022613	HIV peptide SEQ ID	508	3	27.3	1	22	AA007560	HLA-B *510 noname
436	3	27.3	9	22	AA022614	HIV peptide SEQ ID	509	3	27.3	1	22	AA007561	HLA-B *510 noname
437	3	27.3	9	22	AA022615	HIV peptide SEQ ID	510	3	27.3	1	22	AA007562	HLA-B *510 noname
438	3	27.3	9	22	AA022616	HIV peptide SEQ ID	511	3	27.3	1	22	AA007563	HLA-B *510 noname
439	3	27.3	9	22	AA022617	HIV peptide SEQ ID	512	3	27.3	1	22	AA007564	HLA-B *510 noname
440	3	27.3	9	22	AA022618	HIV peptide SEQ ID	513	3	27.3	1	22	AA007565	HLA-B *510 noname
441	3	27.3	9	22	AA022619	HIV peptide SEQ ID	514	3	27.3	1	22	AA007566	HLA-B *510 noname
442	3	27.3	9	22	AA022620	HIV peptide SEQ ID	515	3	27.3	1	22	AA007567	HLA-B *510 noname
443	3	27.3	9	22	AA022621	HIV peptide SEQ ID	516	3	27.3	1	22	AA007568	HLA-B *510 noname
444	3	27.3	9	22	AA022622	HIV peptide SEQ ID	517	3	27.3	1	22	AA007569	HLA-B *510 noname
445	3	27.3	9	22	AA022623	HIV peptide SEQ ID	518	3	27.3	1	22	AA007570	HLA-B *510 noname
446	3	27.3	9	22	AA022624	HIV peptide SEQ ID	519	3	27.3	1	22	AA007571	HLA-B *510 noname
447	3	27.3	9	22	AA022625	HIV peptide SEQ ID	520	3	27.3	1	22	AA007572	HLA-B *510 noname

A: USMPLHS

FESTUJ 1

AA007550

HLA-A\*2703 noname

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XX

XX

XX OS Synthetic.  
XX PN W0200018801-A2.  
XX PD 06-APR-2000.  
XX PF 23 SEP-1999; 99WO-DK00500.  
XX PR 29-SEP-1998; 98DK-0001232.  
XX PR 29-APR-1999; 98DK-0000592.  
XX PA (RONN/) RONN I C B.  
XX PA (BOCK/) BOCK E.  
XX PA (HOLM/) HOLM A.  
XX PA (OLSE/) OLSEN M.  
XX PA (OSTE/) OSTERGAARD S.  
XX PA (JENSEN) JENSEN P H.  
XX PA (POUL/) POULSEN F H.  
XX PA (SORO/) SOROKA V.  
XX PA (RALE/) RALETS I.  
XX PA (BERE/) BEREZIN V.  
XX PI Ronn ICh, Bock E, Holm A, Olsen M, OSTERGAARD S, Jensen PH,  
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
XX DR WPI: 2000-293111/25.  
XX PT Compositions that bind neural cell adhesion molecules useful for  
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's  
XX PS Example 4: Page 25; 119pp; English.  
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule  
XX CC NCAM is found in three forms, two of which are transmembrane forms, while  
XX CC the third is attached via a lipid anchor to the cell membrane. All three  
XX CC NCAM forms have an extracellular structure consisting five immunoglobulin  
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the  
XX CC N-terminal. The present sequence represents a peptide which binds to the  
XX CC NCAM Ig1 domain. The peptide can be used in a compound which binds to the  
XX CC NCAM Ig1/2 domains, and is capable of stimulating or promoting neurite  
XX CC outgrowth from NCAM presenting cells, and is also capable of promoting the  
XX CC proliferation of NCAM presenting cells. The compound may be used in  
XX CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
XX CC The compound may in particular be used to treat diseases of the central  
XX CC and peripheral nervous systems such as post operative nerve damage,  
XX CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
XX CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
XX CC demyelias, sclerosis, nerve degeneration associated with diabetes,  
XX CC mellitus, disorders affecting the circadian clock or neuro-muscular;  
XX CC transmission and schizophrenia. Conditions affecting the muscles may also  
XX CC be treated with the compound, such as conditions associated with impaired  
XX CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
XX CC liver and bowel may also be treated using the compound. The compound is  
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to  
XX CC learn, and to stimulate the memory of a subject.  
XX SQ Sequence 11 AA:  
Query Match 100.0%; Score 11; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8 5e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
QY 1 ARKSRDMTA1K 11  
| | | | | | | | | | | |  
Db 1 ARKSRDMTA1K 11  
RESULT 2  
ABG69350

XX AA: Sequence 11 AA:  
XX AB: 21 SEP-1999; 99WO-DK00500.  
XX DT 06-APR-2000.  
XX PF 23 SEP-1999; 99WO-DK00500.  
XX PR 29-SEP-1998; 98DK-0001232.  
XX PR 29-APR-1999; 98DK-0000592.  
XX PA (RONN/) RONN I C B.  
XX PA (BOCK/) BOCK E.  
XX PA (HOLM/) HOLM A.  
XX PA (OLSE/) OLSEN M.  
XX PA (OSTE/) OSTERGAARD S.  
XX PA (JENSEN) JENSEN P H.  
XX PA (POUL/) POULSEN F H.  
XX PA (SORO/) SOROKA V.  
XX PA (RALE/) RALETS I.  
XX PA (BERE/) BEREZIN V.  
XX PI Ronn ICh, Bock E, Holm A, Olsen M, OSTERGAARD S, Jensen PH,  
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
XX DR WPI: 2000-293111/25.  
XX PT Compositions that bind neural cell adhesion molecules useful for  
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's  
XX PS Example 4: Page 25; 119pp; English.  
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule  
XX CC NCAM is found in three forms, two of which are transmembrane forms, while  
XX CC the third is attached via a lipid anchor to the cell membrane. All three  
XX CC NCAM forms have an extracellular structure consisting five immunoglobulin  
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the  
XX CC N-terminal. The present sequence represents a peptide which binds to the  
XX CC NCAM Ig1 domain. The peptide can be used in a compound which binds to the  
XX CC NCAM Ig1/2 domains, and is capable of stimulating or promoting neurite  
XX CC outgrowth from NCAM presenting cells, and is also capable of promoting the  
XX CC proliferation of NCAM presenting cells. The compound may be used in  
XX CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
XX CC The compound may in particular be used to treat diseases of the central  
XX CC and peripheral nervous systems such as post operative nerve damage,  
XX CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
XX CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
XX CC demyelias, sclerosis, nerve degeneration associated with diabetes,  
XX CC mellitus, disorders affecting the circadian clock or neuro-muscular;  
XX CC transmission and schizophrenia. Conditions affecting the muscles may also  
XX CC be treated with the compound, such as conditions associated with impaired  
XX CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
XX CC liver and bowel may also be treated using the compound. The compound is  
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to  
XX CC learn, and to stimulate the memory of a subject.  
XX SQ Sequence 11 AA:  
Query Match 100.0%; Score 11; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8 5e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
QY 1 ARKSRDMTA1K 11  
| | | | | | | | | | | |  
Db 1 ARKSRDMTA1K 11  
RESULT 2  
ABG69350

RESULT 3  
 ABB74692  
 ID ABB74692 standard; Peptide: 8 AA.  
 XX AC ABB74692:  
 XX D7 18-APR-2002 (first entry)  
 XX DE Transcription factor nuclear localisation signal peptide SEQ ID NO:454.  
 XX KW Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 XX KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX OS Synthetic.  
 XX PN WO200193836-A2.  
 XX PD 13-DEC-2001.  
 XX PF 08-JUN-2001; 2001WO-US18657.  
 XX PR 09-JUN-2000; 2000US-210925P.  
 XX PA (BOUL/) BOULIKAS T.  
 XX PI Boulikas T.  
 XX DR WPI; 2002-164295/21.  
 XX PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with  
 PT nuclear localization signal/lipogenic peptide conjugates into liposome;  
 PT liposome complexes.  
 XX PS Claim 14; Page 79; 107pp; English.  
 CC The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 40-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74245 to ABB74255 are used in the exemplification of the present  
 CC invention.  
 XX SQ Sequence 8 AA:  
 Query Match 45.5%; Score 5; DS 26; Length 80  
 Best Local Similarity 100.0%; Pred. No 5; Act 5;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Diffs 0  
 QY 2 RKSRD 6  
 DB 2 RKSRD 6  
 RESULT 4  
 ABB74740

ABB74740: Sequence 4; Length 4; AA  
 ABB74740:  
 DE ABB74740: (first entry)  
 DE Transcription factor nuclear localisation signal peptide SEQ ID NO:454.  
 KW Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX OS Synthetic.  
 XX PN WO200193836-A2.  
 XX PD 13-DEC-2001.  
 XX PF 08-JUN-2001; 2001WO-US18657.  
 XX PR 09-JUN-2000; 2000US-210925P.  
 XX PA (BOUL/) BOULIKAS T.  
 XX PI Boulikas T.  
 XX DR WPI; 2002-164295/21.  
 XX PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with  
 PT nuclear localization signal/lipogenic peptide conjugates into liposome;  
 PT liposome complexes.  
 XX PS Claim 14; Page 79; 107pp; English.  
 CC The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 40-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74245 to ABB74255 are used in the exemplification of the present  
 CC invention.  
 XX SQ Sequence 8 AA:  
 Query Match 45.5%; Score 5; DS 26; Length 80  
 Best Local Similarity 100.0%; Pred. No 5; Act 5;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Diffs 0  
 QY 2 RKSRD 6  
 DB 2 RKSRD 6  
 RESULT 5  
 ABB74741  
 ID ABB74741: Sequence 4; Length 4; AA  
 XX AC ABB74741:  
 XX D7 18-APR-2002 (first entry)  
 XX DE Transcription factor nuclear localisation signal peptide SEQ ID NO:454.  
 XX KW Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 XX KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX OS Synthetic.  
 XX PN WO200193836-A2.  
 XX PD 13-DEC-2001.  
 XX PF 08-JUN-2001; 2001WO-US18657.  
 XX PR 09-JUN-2000; 2000US-210925P.  
 XX PA (BOUL/) BOULIKAS T.  
 XX PI Boulikas T.  
 XX DR WPI; 2002-164295/21.  
 XX PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with  
 PT nuclear localization signal/lipogenic peptide conjugates into liposome;  
 PT liposome complexes.  
 XX PS Claim 14; Page 79; 107pp; English.  
 CC The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 40-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74245 to ABB74255 are used in the exemplification of the present  
 CC invention.  
 XX SQ Sequence 8 AA:  
 Query Match 45.5%; Score 5; DS 26; Length 80  
 Best Local Similarity 100.0%; Pred. No 5; Act 5;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Diffs 0  
 QY 2 RKSRD 6  
 DB 2 RKSRD 6



XX 18-APR-2002 (first entry)  
XX  
DE Transcription factor nuclear localisation signal peptide SEQ ID NO:507  
XX  
XX Fusogetic: nuclear localisation signal; NLS; encapsulation; liposome;  
KW liposome; micelle; karyophilic; cytosolic; antitumour; solid tumour;  
KW peptide-lipid-poly-nucleotide complex; neoplastic disease; gene therapy;  
KW breast carcinoma; prostate carcinoma.  
XX  
OS Rattus sp.  
XX  
XX W0200193836-A2.  
PN  
XX  
XX 13-DEC-2001.  
PD  
XX  
XX 08-JUN-2001; 2001WO-US18657.  
PF  
XX  
XX 09-JUN-2000; 2000US-210925P.  
PR  
XX  
XX (BOUL/) BOULIKAS T.  
PA  
XX  
XX Boulikas T.  
PI  
XX  
XX WPI: 2002-164295/21.  
DR  
XX  
XX Encapsulation of plasmid DNA (Lipogenus) and therapeutic agents with  
PT nuclear localisation signal/fusogenic peptide conjugates into targeted  
PT liposome complexes -  
XX  
XX Claim 14; Page 81; 107pp; English.  
XX  
CC The present invention describes a method for producing micelles with  
CC entrapped therapeutic agents. The method comprises: (1) combining  
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
CC of the negatively charged atoms are neutralised by positive charges on  
CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
CC ethanol; and (2) combining the micelle complex of (1) with fusogenic  
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
CC micelles with entrapped therapeutic agents. Also described is a method  
CC for delivering a therapeutic agent in vivo, comprising the administration  
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
CC nuclear localisation signal (NLS) peptides for use in the method as the  
CC fusogetic-karyophilic peptides. The micelles produced can have cytostatic  
CC and antitumour activities. The peptide-lipid-poly-nucleotide complexes  
CC produced are useful for inhibiting the progression of neoplastic  
CC diseases. The invention relates to the field of gene therapy and is  
CC directed toward methods for producing peptide-lipid-poly-nucleotide  
CC complexes suitable for delivery of polynucleotides. The encapsulated  
CC molecules display therapeutic efficacy in eradicating solid tumors  
CC including but not limited to breast carcinoma or prostate carcinoma.  
CC ABB74235 to ABB74255 are used in the exemplification of the present  
CC invention.  
XX  
XX  
SQ Sequence 8 AA;  
Query Match 45.5%; Score 5; DB 23; Length 8;  
Best Local Similarity 100.0%; Prod. No. 9,464,55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 2 RKSRD 6  
Db 2 RKSRD 6  
RESULT 6  
ABB74756  
ID ABB74756 standard; Peptide: 8 AA.  
XX  
AC ABB74756;  
XX  
DT 18-APR-2002 (first entry)  
XX

DE Transcription factor nuclear localisation signal peptide SEQ ID NO: 507  
XX  
XX Fusogetic: nuclear localisation signal; NLS; encapsulation; liposome;  
KW liposome; micelle; karyophilic; cytosolic; antitumour; solid tumour;  
KW peptide-lipid-poly-nucleotide complex; neoplastic disease; gene therapy;  
KW breast carcinoma; prostate carcinoma.  
XX  
OS Rattus sp.  
XX  
XX W 200193836-A2.  
PN  
XX  
XX 13-DEC-2001.  
PD  
XX  
XX 08-JUN-2001; 2001WO-US18657.  
PF  
XX  
XX 09-JUN-2000; 2000US-210925P.  
PR  
XX  
XX (BOUL/) BOULIKAS T.  
PA  
XX  
XX Boulikas T.  
PI  
XX  
XX WPI: 2002-164295/21.  
DR  
XX  
XX Encapsulation of plasmid DNA (Lipogenus) and therapeutic agents with  
PT nuclear localisation signal/fusogenic peptide conjugates into targeted  
PT liposome complexes -  
XX  
XX Claim 14; Page 81; 107pp; English.  
XX  
CC The present invention describes a method for producing micelles with  
CC entrapped therapeutic agents. The method comprises: (1) combining  
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
CC of the negatively charged atoms are neutralised by positive charges on  
CC lipid molecules; (2) forming an electrostatic micelle complex in 20-80 %  
CC ethanol; and (3) combining the micelle complex of (2) with fusogenic  
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
CC micelles with entrapped therapeutic agents. Also described is a method  
CC for delivering a therapeutic agent in vivo, comprising the administration  
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
CC nuclear localisation signal (NLS) peptides for use in the method as the  
CC fusogetic-karyophilic peptides. The micelles produced can have cytostatic  
CC and antitumour activities. The peptide-lipid-poly-nucleotide complexes  
CC produced are useful for inhibiting the progression of neoplastic  
CC diseases. The invention relates to the field of gene therapy and is  
CC directed toward methods for producing peptide-lipid-poly-nucleotide  
CC complexes suitable for delivery of polynucleotides. The encapsulated  
CC molecules display therapeutic efficacy in eradicating solid tumors  
CC including but not limited to breast carcinoma or prostate carcinoma.  
CC ABB74235 to ABB74255 are used in the exemplification of the present  
CC invention.  
XX  
XX  
SQ Sequence 8 AA;  
Query Match 45.5%; Score 5; DB 23; Length 8;  
Best Local Similarity 100.0%; Prod. No. 9,464,55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 2 RKSRD 6  
Db 2 RKSRD 6  
RESULT 7  
ABB74756  
ID ABB74756 standard; Peptide: 8 AA.  
XX  
AC ABB74756;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human peptide #708 encoded by a SSB oligonucleotide.  
XX  
KW Immunosuppressive; immunostimulatory; anti-inflammatory; cytostatic

KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; adherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
XX nervous system disease.  
OS  
XX Homo sapiens.  
XX WO200147944-A2.  
XX 05-JUL-2001.  
XX 28-DEC-2000; 2000WO-US35498.  
XX 28-DEC-1999; 99US-0173419.  
XX 27-DEC-2000; 2000US-0173419.  
XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach M;  
XX WPI; 2001-465210/50.  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polykerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -  
XX  
XX Disclosure; Page 3823; 4143pp; English.  
XX The present invention relates to oligonucleotides (see AA:26753-AAL44655)  
XX encoding polymorphic variants of proteins related to amylases, amyloid  
XX proteins, angiotensin, apoptosis related proteins, adherin, cyclin,  
XX complement, oncogenes, histones, kinases, colony stimulating factors,  
XX complement related proteins, cytochromes, kinesins, cytokines,  
XX interferons, interleukins, G-protein coupled receptors and thioesterases.  
XX The present sequence is a peptide encoded by one such oligonucleotide.  
XX The oligonucleotides and the peptides encoded by them may be used in the  
XX prevention, diagnosis and treatment of diseases associated with  
XX inappropriate expression of the proteins listed above. Disorders that may  
XX be prevented, diagnosed and/or treated include multifactorial diseases  
XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus,  
XX CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
XX brain, breast, colon and kidney, leukaemia), diseases of the nervous  
XX system and an infection of pathogenic organisms.  
XX  
XX Sequence 14 AA:  
Query Match 45.5%; Score 5; LH 22; Length 14;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 RKSRD 6  
DB IIIII  
5 RKSRD 9  
RESULT 8  
AAR72176  
ID AAR72176 standard; peptide; 8 AA.  
XX  
XX AAR72176;  
XX  
XX 25-MAR-2003 (updated)  
XX 28-JUN-1995 (first entry)  
XX  
XX Hepatitis C Virus NS5a octapeptide for epitope mapping.  
XX  
XX Hepatitis C Virus; HCV; non-structural protein; NS5a;  
XX dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.  
XX

US Synthetic  
XX EP424547-A1  
XX 17-NOV-1994.  
XX PD  
XX 02 MAY-1994; 94EP 4593-A  
XX 12-MAY-1994; 94EP 4593-A  
XX (S-81) S-81 IN POLYMERASE S-81  
XX Bonelli F, Guretti E, Guretti S, Rosa G;  
XX WPI; 1994-45745/44.  
XX New peptides (S-81) related to hepatitis C virus dominant epitopes of non-  
XX structural proteins, for some time and selected for detection of  
XX antibodies in body fluid.  
XX Example 1: F-4 (S-81) 1-4 (S-81).  
XX 12 overlapped octapeptides (AAR72176-22222) were synthesised to  
XX cover the more hydrophobic domain of the hepatitis C virus NS5a  
XX non-structural protein (1-4 between poly amino acids 2256-  
XX 2307). The peptides were analysed in an ELISA in order to map the  
XX immunodominant epitope of NS5a based on the assay results and  
XX highly immunoreactive peptide was synthesised (AAR72176) which is  
XX useful for in vitro detection of HCV.  
XX (Updated on 25-MAR-2003 to remove PW field.)  
XX (Updated on 25-MAR-2003 to remove PW field.)  
XX Sequence 8 AA:  
Query Match 45.4%; Score 4; LH 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 RKSR 6  
DB IIIII  
5 RKSR 6  
RESULT 9  
AAR72177  
ID AAR72177 standard; peptide; 8 AA.  
XX  
XX AAR72177;  
XX  
XX 25-MAR-2003 (updated)  
XX 28-JUN-1995 (first entry)  
XX  
XX Hepatitis C Virus NS5a octapeptide for epitope mapping.  
XX  
XX Hepatitis C Virus; HCV; non-structural protein; NS5a;  
XX dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.  
XX  
XX Synthetic.  
XX EP424547-A1  
XX 17-NOV-1994.  
XX PD  
XX 02 MAY-1994; 94EP 4593-A  
XX 12-MAY-1994; 94EP 4593-A  
XX (S-81) S-81 IN POLYMERASE S-81  
XX Bonelli F, Guretti E, Guretti S, Rosa G;  
XX WPI; 1994-45745/44.  
XX

PT New peptide(s) contg hepatitis C virus dominant epitopes - of non-  
PT structural proteins, for sensitive and selective detection of  
PT antibodies in body fluids

PS Example 1; Fig 3; 39pp; English.

XX 52 overlapping octapeptides (AAR72158-R72209) were synthesised to  
CC cover the more hydrophobic domain of the hepatitis C virus NS5a  
CC non-structural polypeptide (i.e. between HCV amino acids 2256-  
CC 2307). The peptides were analysed in an ELISA in order to map the  
CC immunodominant epitope of NS5a. Based on the assay results, a  
CC highly immunoreactive peptide was synthesised (AAR72156) which is  
CC useful for in vitro detection of HCV.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 3e-05;  
Matches 4; Conservative 0; Mismatches 0; Index 0;

QY 2 RKSR 5  
DB 111  
2 RKSR 5

RESULT 10

AAR72178  
ID AAR72178 standard; peptide: 8 AA.

XX AC AAR72178;

XX 25-MAR-2003 (updated)  
DT 28-JUN-1995 (first entry)

XX Hepatitis C Virus NS5a octapeptide for epitope mapping.

XX Hepatitis C Virus; HCV; non-structural protein; NS5a;  
KW dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.

XX Synthetic.

XX EP624597-A1.

XX 17-NOV-1994.

XX 02-MAY-1994; 94EP-0830208.

XX 12-MAY-1993; 93IT-RM00309.

XX (SORI-) SORIN BIOMEDICA SPA.

XX Bonelli F, Garetto F, Griva S, Osborne SJ, Rosa C.

XX WPI; 1994-350745/44.

XX New peptide(s) contg hepatitis C virus dominant epitopes - of non-  
PT structural proteins, for sensitive and selective detection of  
PT antibodies in body fluids

PS Example 1; Fig 3; 39pp; English.

XX 52 overlapping octapeptides (AAR72158-R72209) were synthesised to  
CC cover the more hydrophobic domain of the hepatitis C virus NS5a  
CC non-structural polypeptide (i.e. between HCV amino acids 2256-  
CC 2307). The peptides were analysed in an ELISA in order to map the  
CC immunodominant epitope of NS5a. Based on the assay results, a  
CC highly immunoreactive peptide was synthesised (AAR72156) which is  
CC useful for in vitro detection of HCV.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 4e-05;  
Matches 4; Conservative 0; Mismatches 0; Index 0;

QY 2 RKSR 5  
DB 111  
2 RKSR 4

RESULT 11

AAR72174  
ID AAR72174 standard; peptide: 8 AA.

XX AC AAR72174;

XX 25-MAR-2003 (updated)

DT 28-JUN-1995 (first entry)

XX Hepatitis C Virus NS5a octapeptide for epitope mapping

XX Hepatitis C Virus; HCV; non-structural protein; NS5a;

KW dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.

XX Synthetic.

XX EP624597-A1.

XX 17-NOV-1994.

XX 02-MAY-1994; 94EP-0830208.

XX 12-MAY-1993; 93IT-RM00309.

XX (SORI-) SORIN BIOMEDICA SPA.

XX Bonelli F, Garetto F, Griva S, Osborne SJ, Rosa C.

XX WPI; 1994-350745/44.

XX New peptide(s) contg hepatitis C virus dominant epitopes - of non-  
PT structural proteins, for sensitive and selective detection of  
PT antibodies in body fluids

PS Example 1; Fig 3; 39pp; English.

XX 52 overlapping octapeptides (AAR72158-R72209) were synthesised to  
CC cover the more hydrophobic domain of the hepatitis C virus NS5a  
CC non-structural polypeptide (i.e. between HCV amino acids 2256-  
CC 2307). The peptides were analysed in an ELISA in order to map the  
CC immunodominant epitope of NS5a. Based on the assay results, a  
CC highly immunoreactive peptide was synthesised (AAR72156) which is  
CC useful for in vitro detection of HCV.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 4e-05;  
Matches 4; Conservative 0; Mismatches 0; Index 0;

QY 2 RKSR 5  
DB 111  
5 RKSR 4

RESULT 12

AAR72175  
ID AAR72175 standard; peptide: 8 AA.

XX AC AAR72175;



CC Substrates can be used e.g. to measure the amount of active PSA in  
 CC patient serum to diagnose, or determine the malignant potential of,  
 CC a patient's prostate disease. They are especially useful to diagnose  
 CC metastatic prostate cancer. The substrates can also be used in assays  
 CC to identify PSA inhibitors, which can be administered to treat or  
 CC prevent prostate cancer.

XX Sequence 9 AA;  
 SQ

Query Match 36.48; Score 4; LB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRDM 7  
 DQ 4 SRDM 7

RESULT 15  
 AAW83914  
 ID AAW83914 standard; peptide; 9 AA;  
 XX  
 AC AAW83914;  
 XX  
 DT 14-JAN-1999 (first entry)  
 XX  
 DE Peptide specific antigen (PSA) substrate PR2.  
 XX  
 KW Human prostate specific antigen; PSA; substrate; prostate cancer;  
 KW metastatic prostate cancer; PSA inhibitor;  
 XX  
 OS Synthetic.  
 OS  
 PN W09840738-A1.  
 XX  
 PD 17-SEP-1998.  
 XX  
 PF 09-MAR-1998; 98WO-US04557.  
 XX  
 PR 11-MAR-1997; 97US-0040174.  
 XX  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 XX  
 PI Blobel C., Roghani M., Rothman J.  
 XX  
 DR WPI: 1998-520833/44.  
 XX  
 PT Improved human prostate specific antigen substrates useful to  
 PT e.g. measure prostate specific antigen activity; identify  
 PT therapeutically useful inhibitors or diagnose metastatic prostate  
 PT cancer

XX  
 PS Example 1; Page 16; 147pp; English.

CC The presents sequence represents a substrate for human prostate specific  
 CC antigen (PSA). The PSA substrates are useful in assays which measure PSA  
 CC activity. Such assays may provide a clinical evaluation of patient's  
 CC suffering from, or at risk for, prostate cancer. Elevated levels of PSA  
 CC in serum are widely used as a marker of prostate cancer, and the  
 CC substrates can be used e.g. to measure the amount of active PSA in  
 CC patient serum to diagnose, or determine the malignant potential of,  
 CC a patient's prostate disease. They are especially useful in assays  
 CC to identify PSA inhibitors. The substrates can also be used in assays  
 CC to identify PSA inhibitors, which can be administered to treat or  
 CC prevent prostate cancer.

XX Sequence 9 AA;  
 SQ

Query Match 36.48; Score 4; LB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRDM 7

14 4 SRDM 7

RESULT 16  
 AAW4195  
 ID AAW4195 standard; peptide; 9 AA;  
 XX  
 AC AAW4195;  
 XX  
 DT 10-APR-1998 (first entry)  
 XX  
 DE Human TEF SSP substrate; peptide; 9 AA;  
 XX  
 KW Carboxyl terminal region of protein tyrosine phosphatase; human  
 KW detected in tumours; TEF SSP substrate; TEF SSP substrate;  
 KW non-enzymatic protein;  
 XX  
 OS Homo sapiens  
 XX  
 PN W09840738-A1.  
 XX  
 PD 17-SEP-1998.  
 XX  
 PF 10-APR-1998; 98WO-US04557.  
 XX  
 PR 11-MAR-1997; 97US-0040174.  
 XX  
 PA (MADE) MADE PEPID; 9 AA;  
 XX  
 PI Kowalewski S., et al. K. Kowalewski  
 XX  
 DR WPI: 1998-520833/44.  
 XX  
 PT Detection and diagnosis of cancer using specific substrates  
 PT cancer associated with TEF SSP substrate for treatment of its inhibitors  
 PT for detection

XX  
 PS Claim 1; Page 19; 147pp; English.

CC AAW4195-W1998 are synthetic peptides derived from protein tyrosine which  
 CC match fragments of the TEF SSP substrate. The TEF SSP substrate  
 CC and are used in a method for detecting cervical cancer. The method  
 CC involves detecting the presence of a cervical cancer associated protein  
 CC (CVC) in a tissue sample. The CVC is characterized as  
 CC having a molecular weight of 44000 daltons as determined by sodium  
 CC dodecyl sulphate (SDS) PAGE techniques and an isoelectric point (pI) of  
 CC 5.1. It is determined by standard isoelectric focusing techniques that  
 CC protein is further characterized as being a non-chromatin protein which  
 CC is detectable at a higher level in a human cervical cancer cell than in  
 CC a normal human cervical cell. It is determined by 2D gel electrophoresis  
 CC The methods can be used for the early and rapid detection of cervical  
 CC cancer, for monitoring cervical cancers and for monitoring the efficacy of  
 CC cancer treatment

XX Sequence 9 AA;  
 SQ

Query Match 36.48; Score 4; LB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRDM 7  
 DQ 4 SRDM 7

RESULT 17  
 AAW4195  
 ID AAW4195 standard; peptide; 9 AA;  
 XX  
 AC AAW4195;  
 XX  
 DT 17-SEP-1998 (first entry)  
 XX

```

XX DE Human MHC class I molecule HLA-A3 binding 103p206 peptide #49
XX KW 103p206: PCR primer; DNA adaptor; prostate; testis; foetal tissue
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cystostatic
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder
XX KW single chain monoclonal antibody; cervix; human
XX OS Homo sapiens.
XX PN WO200162925-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001: 2001WO-US05996.
XX PR 24-FEB-2000: 2000US-0184558.
XX PR 13-JUL-2000: 2000US-0218856.
XX PA (UROS-) UROGENESYS INC.
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SM, Bulcroft AS,
XX PI Challita-old PM, Paris M, Jakobovits A.
XX DR WPI: 2001-557705/62.
XX PT New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103p206 gene which encodes for 103p206 related proteins.
XX PS Example 15: Page 87; 132pp: English.
XX CC Sequences AAU23815-AAU24515 represent the 103p206 related protein and
XX CC peptide fragments of the polypeptide. 103p206 is not expressed in normal
XX CC adult tissue but is aberrantly expressed in some foetal tissues and many
XX CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX CC ovary, breast, pancreas, colon and lung. The 103p206 polynucleotide, its
XX CC related protein and also peptide fragments of the protein are therefore
XX CC useful for diagnosing and treating cancer. A vector comprising a
XX CC polynucleotide which encodes a single chain monoclonal antibody, that
XX CC immunospecifically binds to an 103p206 related protein, and a ribozyme
XX CC capable of cleaving a polynucleotide having the 103p206 coding sequence
XX CC are both useful in the preparation of a composition for treating a
XX CC patient with a cancer that expresses 103p206. The sequences can be used
XX CC in diagnostic methods to monitor the level of 103p206 gene products in
XX CC serum, blood, urine and tissue and to thereby detect the presence of
XX CC cancerous cells.
XX SQ Sequence 9 AA:
    Query Match 36.4% Score 4: 106 226 Length 90
    Best Local Similarity 100.0% Prod. No. 9, 3e+05
    Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
OY 2 RKS 5
DB 111
6 RKS 9
RESULT 18
AAU24130
ID AAU24130 standard; Peptide: 9 AA.
XX AC AAU24130:
XX DT 17-DEC-2001 (first entry)
XX DE Human MHC molecule HLA-A11 binding 103p206 peptide #15.
XX KW 103p206: PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cystostatic
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.

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XX H 8054 000
XX IN WO200162925-A2.
XX PF 30-AUG-2001
XX XX 26-FEB-2001: 2001WO-US05996
XX XX 24-FEB-2000: 2000US-0184558
XX XX 13-JUL-2000: 2000US-0218856
XX PA (UROS-) UROGENESYS INC.
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SM, Bulcroft AS,
XX PI Challita-old PM, Paris M, Jakobovits A.
XX DR WPI: 2001-557705/62
XX PT New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103p206 gene which encodes for 103p206 related proteins
XX PS Example 15: Page 87; 132pp: English.
XX CC Sequences AAU23815-AAU24515 represent the 103p206 related protein and
XX CC peptide fragments of the polypeptide. 103p206 is not expressed in normal
XX CC adult tissue but is aberrantly expressed in some foetal tissues and many
XX CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX CC ovary, breast, pancreas, colon and lung. The 103p206 polynucleotide, its
XX CC related protein and also peptide fragments of the protein are therefore
XX CC useful for diagnosing and treating cancer. A vector comprising a
XX CC polynucleotide which encodes a single chain monoclonal antibody, that
XX CC immunospecifically binds to an 103p206 related protein, and a ribozyme
XX CC capable of cleaving a polynucleotide having the 103p206 coding sequence
XX CC are both useful in the preparation of a composition for treating a
XX CC patient with a cancer that expresses 103p206. The sequences can be used
XX CC in diagnostic methods to monitor the level of 103p206 gene products in
XX CC serum, blood, urine and tissue and to thereby detect the presence of
XX CC cancerous cells.
XX SQ Sequence 9 AA:
    Query Match 36.4% Score 4: 106 226 Length 90
    Best Local Similarity 100.0% Prod. No. 9, 3e+05
    Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
OY 2 RKS 5
DB 111
6 RKS 9
RESULT 18
AAU24224
ID AAU24224 standard; Peptide: 9 AA.
XX AC AAU24224:
XX DT 17-DEC-2001 (first entry)
XX DE Human MHC class I molecule HLA-A23 binding 103p206 peptide #1.
XX KW 103p206: PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cystostatic
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.
XX OS Homo sapiens.
XX PN WO200162925-A2.
XX PD 30-AUG-2001
XX PF 26-FEB-2001: 2001WO-US05996

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PR 24-FEB-2000; 2000US-0184558.  
 PR 13-JUL-2000; 2000US-0218856.  
 PA (UROG-) UROGENESYS INC.  
 PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-eid PM, Faris M, Jakobovits A;  
 DR WP1: 2001-557705/62.  
 XX  
 XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -  
 XX  
 XX Example 15; Page 92; 132pp; English.  
 XX  
 XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 36.4%; Score 4; DR 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RKSR 5  
 DB 1111  
 3 RKSR 6

RESULT 20  
 AAU24329  
 ID AAU24329 standard; Peptide: 9 AA.  
 AC AAU24329;  
 XX  
 XX 17-DEC-2001 (first entry)  
 DT  
 XX Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #14.  
 DE  
 XX  
 XX 103P2D6: PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200162925-A2.  
 PN  
 XX  
 XX 30-AUG-2001.  
 PD  
 XX  
 XX 26-FEB-2001; 2001WO-US05996.  
 PF  
 XX  
 XX 24-FEB-2000; 2000US-0184558.  
 PR  
 XX 13-JUL-2000; 2000US-0218856.  
 PR  
 XX (UROG-) UROGENESYS INC.  
 PA  
 XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-eid PM, Faris M, Jakobovits A;  
 PI  
 XX

WP1: 2001-557705/62.

XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins

Example 15; Page 92; 132pp; English.

XX Sequences AAU24415-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 36.4%; Score 4; DR 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RKSR 5

DB 1111

3 RKSR 6

RESULT 20

AAU24329

ID

AAU24329 standard; Peptide: 9 AA.

AC

AAU24329;

XX

XX 17-DEC-2001 (first entry)

DT

XX

XX Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #14.

DE

XX

XX 103P2D6: PCR primer; DNA adaptor; prostate; testis; foetal tissue;

KW

KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;

KW

KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;

KW

KW single chain monoclonal antibody; cervix; human.

XX

XX Homo sapiens.

OS

XX

XX WO200162925-A2.

PN

XX

XX 30-AUG-2001.

PD

XX

XX 26-FEB-2001; 2001WO-US05996.

PF

XX

XX 24-FEB-2000; 2000US-0184558.

PR

XX 13-JUL-2000; 2000US-0218856.

PR

XX (UROG-) UROGENESYS INC.

PA

XX

XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;

PI

PI Challita-eid PM, Faris M, Jakobovits A;

PI

XX

DR WPI: 2002-329578/36.  
 XX Detecting enzyme activity in immunoassay involves incubating  
 PT protein/peptide/derivative comprising sequence motif with enzyme to  
 PT modify protein/peptide/derivative, adding antibody, and detecting  
 PT enzyme activity.  
 XX  
 PS Example 11: Page 33; 61pp; English.  
 XX  
 CC The invention describes a method of detecting enzyme activity in an  
 CC immunoassay comprising incubating a protein/peptide or its derivative  
 CC (1) as a substrate for an enzyme with the enzyme that modifies (1). An  
 CC antibody is added to discriminate a modified position from the unmodified  
 CC position of (1), where the discrimination is mediated by the presence of  
 CC an enhancer. The method is useful for detecting enzyme activity such as  
 CC kinase, carboxylase, decarboxylase, acylase, deacetylase, hydroxylase,  
 CC dehydroxylase, amylase, and deamylase, in particular phosphatase,  
 CC acetylase or deacetylase activity in an immunoassay. In addition, the  
 CC method is useful for screening compound libraries in order to locate  
 CC molecules which inhibit or activate phosphatases, and these molecules are  
 CC promising candidates for designing drugs for the treatment of e.g.,  
 CC Parkinson's disease, Alzheimer's disease, cancer, diabetes mellitus and  
 CC other metabolic disorders. The method is highly reliable and simple  
 CC to perform. When used for detecting phosphatase activity, the method does  
 CC not require the need to develop specific high affinity  
 CC anti-phospho-serine/-phospho-threonine antibodies. This sequence  
 CC represents a synthetic peptide that can be used as a substrate to  
 CC identify acetyltransferase or deacetylase activity in an immunoassay.  
 XX  
 SQ Sequence 9 AA:  
 Query Match 36.4%; Score 4; DB 21; Length 9;  
 Best local Similarity 100.0%; Pred. No. 9, 100%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKKS 4  
 DB IIII  
 1 AKKS 4  
 RESULT 22  
 AAU78978  
 ID AAU78978 standard; Peptide; 9 AA.  
 AC  
 AC AAU78978;  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Histone H3 antigenic fragment #2.  
 XX  
 KW Histone; antibody; antigen; methyllysine; gene activation;  
 KW gene repression; heterochromatin; euchromatin; histone methylation;  
 KW genetic imprinting; gene silencing; Prader-Willi syndrome;  
 KW Angelman syndrome.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 5 /note- \*lys is methylated\*  
 FT  
 FT  
 XX  
 XX WO200218418-A1.  
 PN  
 XX  
 XX 07-MAR-2002.  
 PD  
 XX  
 XX 23-AUG-2001; 2001WO-US26283.  
 PF  
 XX  
 XX 25-AUG-2000; 2000US-227767P.  
 PR  
 XX 03-JUL-2001; 2001US-302747P.  
 PR  
 XX (UYVI-) UNIV VIRGINIA PATENT FOUND.  
 PA  
 XX Allis CD, Strahl BD;  
 PI

XX WPI: 2002-415647/6  
 XX New methyllysine specific antibody useful for as diagnostic tool  
 PT screening tools, as well as in identifying regions of heterochromatin  
 PT or euchromatin  
 XX  
 PS Claim 1: Page 6; 61pp; English  
 XX  
 CC This invention relates to novel methyllysine histone antibodies which  
 CC specifically bind to histones H3 and H4. The present invention is  
 CC directed to fast, reliable and specific methods of histones, in particular  
 CC the methylation of lysine residues. Methylation of histones has been  
 CC shown to be important for gene activation and repression. The antibodies  
 CC are useful in identifying the regions of heterochromatin or euchromatin. The  
 CC antibodies are also useful as diagnostic or screening tools. The  
 CC antibodies may also be used to analyse chromosomes for regions of  
 CC transcriptional activity according to differential methylation and also  
 CC to studies of gene expression and gene silencing. The antibodies may  
 CC also be useful for identifying disease linked to imprinting such as Prader  
 CC Willi Syndrome or Angelman syndrome. The present sequence represents the  
 CC histone antibodies of histone H3 specific and the N-terminal histone H4  
 CC used to generate novel screening antibodies of the invention  
 XX  
 SQ Sequence 9 AA:  
 Query Match 36.4%; Score 4; DB 21; Length 9;  
 Best local Similarity 100.0%; Pred. No. 9, 100%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKKS 4  
 DB IIII  
 1 AKKS 4  
 RESULT 22  
 AAU78978  
 ID AAU78978 standard; Peptide; 9 AA.  
 AC  
 AC AAU78978;  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Histone H3 antigenic fragment #2.  
 XX  
 KW Histone; antibody; antigen; methyllysine; gene activation;  
 KW gene repression; heterochromatin; euchromatin; histone methylation;  
 KW genetic imprinting; gene silencing; Prader-Willi syndrome;  
 KW Angelman syndrome.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 5 /note- \*lys is methylated\*  
 FT  
 FT  
 XX  
 XX WO200218418-A1  
 PN  
 XX  
 XX 07-MAR-2002  
 PD  
 XX  
 XX 23-AUG-2001; 2001WO-US26283  
 PF  
 XX  
 XX 25-AUG-2000; 2000US-227767P  
 PR  
 XX 03-JUL-2001; 2001US-302747P  
 PR  
 XX (UYVI-) UNIV VIRGINIA PATENT FOUND  
 PA  
 XX Allis CD, Strahl BD;  
 PI



XX Claim 1; Page 8; 60pp; English.

XX This invention relates to novel methyllysine histone antibodies which

XX specifically bind to histones H3 and H4. The present invention is

CC directed to post translational modifications of histones, in particular

CC the methylation of lysine residues. Methylation of histones has been

CC shown to be important for gene activation and repression. The antibodies

CC are useful in identifying regions of heterochromatin or euchromatin. The

CC antibodies are also useful as diagnostic or screening tools. The

CC antibodies may also be used to analyse chromosomes for regions of

CC transcriptional activity according to differential methylation and also

CC in studies of genetic imprinting and gene silencing. The antibodies may

CC also be useful for studying diseases linked to imprinting such as Prader-

CC Willi syndrome or Angelman syndrome. The present sequence represents the

CC histone antigenic fragment #3 specific for the N terminal of histone H3

XX used to generate anti histone antibodies of the invention.

XX Sequence 9 AA:

Query Match 36.48; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Prod. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4

DB 3 ARKS 6

RESULT 24

ABR04917

ID ABR04917 standard; Peptide: 9 AA

AC ABR04917;

XX 19 MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 HIA peptide #252.

DE Human; cytostatic; vaccine; cancer; immune response; HIA;

KW human leukocyte antigen.

XX Homo sapiens.

OS WO20020283921-A2.

PN 24-OCT-2002.

PD 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Eid PM, Faris M, Go W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI: 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prophylactic and

PT diagnostic reagents for eliciting cellular or humoral immune response

PT in cancer patients.

XX Claim 13; Page 161; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or treatment, cancer, as coding sequences responsible for

CC directing the expression of the proteins as tools for modulation of

CC inhibiting the expression of the proteins and peptides are useful as

CC therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prophylactic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX from the invention.

SQ Sequence 9 AA:

Query Match 36.48; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Prod. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4

DB 4 ARKS 7

RESULT 25

ABR04917

ID ABR04917 standard; Peptide: 9 AA

AC ABR04917;

XX 19 MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 HIA peptide #294

DE Human; cytostatic; vaccine; cancer; immune response; HIA;

KW human leukocyte antigen

XX Homo sapiens

OS WO20020283921-A2;

PN 24-OCT-2002

PD 10-APR-2002; 2002WO-US11654

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Eid PM, Faris M, Go W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI: 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prophylactic and

PT diagnostic reagents for eliciting cellular or humoral immune response

PT in cancer patients.

XX Claim 13; Page 161; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or treatment of cancer, as coding sequences responsible for

CC directing the expression of the proteins as tools for modulation of

CC inhibiting the expression of genes and/or translation of translated genes and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prophylactic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX from the invention.

SQ Sequence 9 AA:

Query Match: 35.4%; Score: 4; Dis. 24; Length: 64  
Best Local Similarity: 100.0%; Pred. No.: 1,000,000  
Matches: 4; Conservative: 0; Mismatches: 0; Labels:

QY 1 ARKS 4  
|||  
DB 5 ARKS 8

92 J. INGSER

AAV01246  
ID AAV01246 standard; peptide; 10 AA.

XX  
AC

27-MAY 1999 (first entry)

Internalising peptide ligand FRS

Internalising ligand; bacteriophage; fibroblast; gene therapy; histiocytosis; hyperproliferative disorder; smooth muscle cell; disseminated cutaneous tumour; melanoma; neuroblastoma; pituitary secretory cell; meningioma; angiofibroma; arteriovenous malformation; arthritis; bone healing; atherosclerotic plaque; corneal graft; cerebrovascularisation; tumour; hemangioma; hemophilic joint; hypertrophic scar; nevus; glabrous fracture; Oster-Weber syndrome; fibrosis; pyoderma gangrenosum; scleroderma; retroviral fibroplasia; vascular adhesion

OS Mäntmäki Ltd.

XX  
PN  
W094104BS-A1[illegible]

XX  
DF: 09-01-86 08:00

XX  
XX

XXXX

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

XX  
'03 FEB 20 1971

DR 80 WPI: 1999 190616/16.

PT Selection method for internalizing ligands using barbiturate

PS Claim 20: Page 30: 45pp: English

The invention relates to new selection methods for internalising ligands. The method comprises (a) connecting a library of bacteriophage-expressing peptides with a cell, where the bacteriophage carries a gene encoding a detectable product; and (b) detecting the product thereby identifying a bacteriophage expressing a heterologous peptide that binds to a cell surface receptor and internalises. The methods can be used to select cDNAs, fabs, SVF, or random peptides, for the discovery of new ligands. They can also be used to detect mutated and gene-shuttled versions of known ligands for targeting ability. The ligands identified by the methods may be used as targeting agents for delivering therapeutic agents to cells or tissues. The bacteriophages provided are useful for treating and preventing various diseases, syndromes, hyperproliferative disorders, such as metastasis, other smooth muscle cell diseases, tumours, such as melanomas, ovarian cancers, neuroblastomas, pterygia, or secondary lens dislocation, and idiopathic, arteriovenous malformations, arthritis, atherosclerotic plaques, cerebral neovascularisation, delayed wound healing, diabetic neuropathy, granulations due to burns, hemangiomas, desmoplastic trypsin, hypertrophic scars, neovascular glaucoma, nonunion fractures, osteoarthrodynia, psoriasis, pyogenic granuloma, nonunion fractures, osteoarthrodynia, solid tumors, trachoma or vascular adhesions. Sequences AAV6.44-48 represent internalising ligands identified by the method of the invention.

```

QY      2 RKSR 5
Db      7 RKSR 10

RESULT 28
AAU24177
1D  AAU24177 standard; Peptide; 10 AA.
AC  AAU24177;
XX
XX
DT  17-DEC-2001 (first entry)
DE  Human MHC molecule HLA-A*11:01 binding 103P206 peptide #62.
XX
XX  103P206; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
KW  tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
KW  gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
KW  single chain monoclonal antibody; cervix; human.
XX
OS  Homo sapiens.
PN  WO200162925-A2.
XX
XX  30-AUG-2001.
XX
XX  26-FEB-2001; 2001WO-US05996.
XX
XX  24-FEB-2000; 2000US-0184558.
PR  13-JUL-2000; 2000US-0218856.
XX
XX  (UROC-) UROGENESYS INC.
XX
XX  Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
PI  Challita-eid PM, Faris M, Jakobovits A;
XX
XX  WPI; 2001-557705/62.
XX
XX  New polynucleotide for treating and diagnosing prostate cancer is the
PT  103P206 gene which encodes for 103P206-related proteins.
XX
XX  Example 15; Page 90; 132pp; English.
XX
XX  Sequences AAU23815-AAU24515 represent the 103P206 related protein and
CC  peptide fragments of the polypeptide. 103P206 is not expressed in normal
CC  adult tissue but is aberrantly expressed in some foetal tissues and many
CC  cancers including tumours of the prostate, testis, bladder, bone, ovary,
CC  ovary, breast, pancreas, colon and lung. The 103P206 polynucleotide, its
CC  related protein and also peptide fragments of the protein are therefore
CC  useful for diagnosing and treating cancer. A vector comprising a
CC  polynucleotide which encodes a single chain monoclonal antibody, that
CC  immunospecifically binds to an 103P206-related protein, and a ribozyme
CC  capable of cleaving a polynucleotide having the 103P206 coding sequence,
CC  are both useful in the preparation of a composition for treating a
CC  patient with a cancer that expresses 103P206. The sequences can be used
CC  in diagnostic methods to monitor the level of 103P206 gene products in
CC  serum, blood, urine and tissue and to thereby detect the presence of
CC  cancerous cells.
XX
SQ  Sequence 10 AA;
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Prod. No. 4062;
Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY      2 RKSR 5
Db      6 RKSR 9

RESULT 29
AAU24202

```

```

1D  AAU24202 standard; Peptide; 10 AA.
AC  AAU24202;
XX
XX  17-DEC-2001 (first entry)
XX
XX  Human MHC molecule HLA-A*11:01 binding 103P206 peptide #62.
XX
XX  103P206; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
KW  tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
KW  gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
KW  single chain monoclonal antibody; cervix; human.
XX
OS  Homo sapiens.
PN  WO200162925-A2.
XX
XX  30-AUG-2001.
XX
XX  26-FEB-2001; 2001WO-US05996.
XX
XX  24-FEB-2000; 2000US-0184558.
PR  13-JUL-2000; 2000US-0218856.
XX
XX  (UROC-) UROGENESYS INC.
XX
XX  Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
PI  Challita-eid PM, Faris M, Jakobovits A;
XX
XX  WPI; 2001-557705/62.
XX
XX  New polynucleotide for treating and diagnosing prostate cancer is the
PT  103P206 gene which encodes for 103P206-related proteins.
XX
XX  Example 15; Page 90; 132pp; English.
XX
XX  Sequences AAU23815-AAU24515 represent the 103P206 related protein and
CC  peptide fragments of the polypeptide. 103P206 is not expressed in normal
CC  adult tissue but is aberrantly expressed in some foetal tissues and many
CC  cancers including tumours of the prostate, testis, bladder, bone, ovary,
CC  ovary, breast, pancreas, colon and lung. The 103P206 polynucleotide, its
CC  related protein and also peptide fragments of the protein are therefore
CC  useful for diagnosing and treating cancer. A vector comprising a
CC  polynucleotide which encodes a single chain monoclonal antibody, that
CC  immunospecifically binds to an 103P206-related protein, and a ribozyme
CC  capable of cleaving a polynucleotide having the 103P206 coding sequence,
CC  are both useful in the preparation of a composition for treating a
CC  patient with a cancer that expresses 103P206. The sequences can be used
CC  in diagnostic methods to monitor the level of 103P206 gene products in
CC  serum, blood, urine and tissue and to thereby detect the presence of
CC  cancerous cells.
XX
SQ  Sequence 10 AA;
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Prod. No. 4062;
Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY      2 RKSR 5
Db      6 RKSR 9

RESULT 30
AAU24274
1D  AAU24274 standard; Peptide; 10 AA.
AC  AAU24274;
XX
XX  17-DEC-2001 (first entry)
XX
XX  Human MHC molecule HLA-A*23 binding 103P206 peptide #64.
XX

```

KW 103P2D6: PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200162925-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 26-FEB-2001: 2001WO-US05996.  
 XX  
 PR 24-FEB-2000: 2000US-0184558.  
 PR 13-JUL-2000: 2000US-0218856.  
 XX  
 PA (UROC-) UROGENESYS INC.  
 XX  
 PI Rattano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-eid PM, Paris M, Jakobovits A;  
 XX  
 DR WPI: 2001-557705/62.  
 XX  
 XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins.  
 XX  
 PS Example 15; page 93; 132pp; English.  
 XX  
 CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, lung, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.  
 XX  
 SQ Sequence: 10 AA:  
 QY Query Match: 36.4%; Score 4; E=22; Length 10;  
 DB Best Local Similarity: 100.0%; Pred. No. 40-02;  
 Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 RKSR 5  
 DB IIII  
 4 RKSR 7  
 RESULT 31  
 AAU24369  
 ID AAU24369 standard; Peptide: 10 AA.  
 XX  
 AC AAU24369;  
 XX  
 DT 17-DEC-2001 (first entry)  
 XX  
 DE Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #54.  
 KW 103P2D6: PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200162925-A2.

XX  
 IL 30-AUG-2001.  
 XX  
 PF 26-FEB-2001: 2001WO-US05996.  
 XX  
 PR 24-FEB-2000: 2000US-0184558.  
 PR 13-JUL-2000: 2000US-0218856.  
 XX  
 PA (UROC-) UROGENESYS INC.  
 XX  
 PI Rattano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-eid PM, Paris M, Jakobovits A;  
 XX  
 DR WPI: 2001-557705/62.  
 XX  
 XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins.  
 XX  
 PS Example 15; page 93; 132pp; English.  
 XX  
 CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, lung, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody that  
 CC immunospecifically binds to a 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.  
 XX  
 SQ Sequence: 10 AA:  
 QY Query Match: 36.4%; Score 4; E=22; Length 10;  
 DB Best Local Similarity: 100.0%; Pred. No. 40-02;  
 Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 RKSR 5  
 DB IIII  
 4 RKSR 7  
 RESULT 32  
 AAU24515  
 ID AAU24515 standard; Peptide: 10 AA.  
 XX  
 AC AAU24515;  
 XX  
 DT 17-FEB-2001 (first entry)  
 XX  
 DE Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #4.  
 KW 103P2D6: PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W020162925-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 26-FEB-2001: 2001WO-US05996.  
 XX  
 PR 24-FEB-2000: 2000US-0184558.  
 PR 13-JUL-2000: 2000US-0218856.  
 XX

PA (UOOG-) UKOGENESYS INC.  
 PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-eid PM, Paris M, Jakobovits A;  
 XX WPI: 2001-557705/62.  
 XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins .  
 XX  
 XX Example 15; Page 100; 132pp; English.  
 XX  
 XX Sequences AAU23015-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody, that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.  
 XX  
 XX SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSR 5  
 IIII  
 Db 4 RKSR 7

RESULT 33  
 AAU43146  
 ID AAU43146 standard; Peptide: 10 AA.  
 XX  
 AC AAU43146:  
 XX  
 XX 22-OCT-2001 (first entry)  
 XX  
 DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 453.  
 XX  
 KW Mycoplasma genitalium; complementary peptide; ligand;  
 KW protein-protein interaction; drug design; intermolecular;  
 KW intramolecular.  
 XX

XX  
 OS Mycoplasma genitalium.  
 XX  
 XX WO200142278-A2.  
 XX  
 XX 14-JUN-2001.  
 XX  
 PF 13-DEC-2000; 2000WO-GB04778.  
 XX  
 PR 13-DEC-1999; 99GB-0029456.  
 XX  
 PA (PROT-) PROTEOM LTD.  
 XX  
 PI Roberts GW, Heal JR;  
 XX  
 XX WPI: 2001-514238/56.  
 XX  
 DR Complementary peptide ligands as reagents and drugs for drug discovery  
 XX  
 PT Programs and as lead ligands to facilitate drug design and development,  
 PT are generated from microbial genome sequences .

XX  
 PS Example 2; Page 112; 214p; English.  
 XX  
 XX The present sequence is one of a large number of complementary peptide  
 CC ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or assisting specific interaction of a protein with  
 CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of both transceptor screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming  
 CC sampling problems. The set of complementary peptides includes both  
 CC intermolecular (between proteins) and intramolecular (within a  
 CC protein) sequences.  
 XX  
 XX Sequence 10 AA.

Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKRS 4  
 IIII  
 Db 2 AKRS 5

RESULT 34  
 AAU43147  
 ID AAU43147 standard; Peptide: 10 AA.

XX  
 AC AAU43147:  
 XX  
 XX 22-OCT-2001 (first entry)  
 XX

DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 454.  
 XX  
 KW Mycoplasma genitalium; complementary peptide; ligand;  
 KW protein-protein interaction; drug design; intermolecular;  
 KW intramolecular.  
 XX

XX  
 OS Mycoplasma genitalium.  
 XX  
 XX WO200142278-A2.  
 XX  
 XX 14-JUN-2001.  
 XX  
 PF 13-DEC-2000; 2000WO-GB04778.  
 XX  
 PR 13-DEC-1999; 99GB-0029456.  
 XX  
 XX (PROT-) PROTEOM LTD.  
 XX  
 XX Roberts GW, Heal JR;  
 XX  
 XX WPI: 2001-514238/56.  
 XX  
 PT Complementary peptide ligands as reagents and drugs for drug discovery  
 PT programs and as lead ligands to facilitate drug design and development,  
 PT are generated from microbial genome sequences .

XX Example 2; Page 112; 214p; English.

XX  
 XX The present sequence is one of a large number of complementary peptide  
 CC ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or assisting specific interaction of a protein with

CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of high-throughput screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming  
 CC sampling problems. The set of complementary peptides includes both  
 CC intramolecular (between proteins) and intermolecular (within a  
 CC protein) sequences.  
 XX  
 SQ Sequence 10 AA:

Query Match 36.4% Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4062;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 IIII  
 DB 2 ARKS 5

RESULT 35  
 AAM43468  
 ID AAM43468 standard; Peptide: 10 AA.

XX  
 AC AAM43468;

XX 22-OCT-2001 (first entry)

XX Mycoplasma genitalium intramolecular complementary peptide, SEQ ID 777.

XX Mycoplasma genitalium; complementary peptide; ligand;

KW protein-protein interaction; drug design; intermolecular;

KW intramolecular.

XX  
 XX Mycoplasma genitalium.

XX WO200142278-A2.

XX 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04778.

XX 13-DEC-1999; 99GB-0029466.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-514238/56.

XX Complementary peptide ligands as reagents and drugs for drug discovery  
 PT programs and as lead ligands to facilitate drug design and development,  
 PT are generated from intermolecular genome sequences.

PS Example 4; Page 157; 161pp; English.

XX The present sequence is one of a large number of complementary peptide  
 CC ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or agonising specific interaction of a protein with  
 CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of high-throughput screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming

CC same problems. The set of complementary peptides includes both  
 CC intramolecular (between proteins) and intermolecular (within a  
 CC protein) sequences.

SQ Sequence 10 AA:

Query Match 36.4% Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 4062;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 I  
 DB 2 ARKS 5

RESULT 36

AAM43469

ID AAM43469 standard; Peptide: 10 AA.

XX  
 AC AAM43469;

XX 22-OCT-2001 (first entry)

XX Mycoplasma genitalium intramolecular complementary peptide, SEQ ID 778.

XX Mycoplasma genitalium; complementary peptide; ligand;

KW protein-protein interaction; drug design; intermolecular;

KW intramolecular.

XX  
 XX Mycoplasma genitalium.

XX WO200142278-A2.

XX 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04778.

XX 13-DEC-1999; 99GB-0029466.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-514238/56.

PT Complementary peptide ligands as reagents and drugs for drug discovery  
 PT programs and as lead ligands to facilitate drug design and development,  
 PT are generated from intermolecular genome sequences.

PS Example 4; Page 157; 161pp; English.

XX The present sequence is one of a large number of complementary peptide  
 CC ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or agonising specific interaction of a protein with  
 CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of high-throughput screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming  
 CC sampling problems. The set of complementary peptides includes both  
 CC intramolecular (between proteins) and intermolecular (within a  
 CC protein) sequences.

SQ Sequence 10 AA.

Query Match 36.4% Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 4062;

```
Matches 4; Conservative 0; Mismatches 0; Gaps 0
QY 1 ARKS 4
DB 1111
2 ARKS 5

RESULT 17
AAG94948
ID AAG94948 standard; Peptide; 10 AA.
XX AC AAG94948;
XX DT 18-SEP-2001 (first entry)
XX DE Human complementary peptide, SEQ ID NO: 1142.
XX KW Human; complementary peptide; ligand; drug discovery; drug design
XX OS Homo sapiens.
XX PN WO200142277 A2.
XX PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB04776.
XX PR 13-DEC-1999; 99GB-0029464.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX WP1: 2001-408419/43.
XX PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs.
XX Example 4; Page 203; 646pp; English.
XX CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as novel
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX SQ Sequence 10 AA;
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0
QY 1 ARKS 4
DB 1111
3 ARKS 6

RESULT 18
AAG94950
ID AAG94950 standard; Peptide; 10 AA.
XX AC AAG94950;
XX DT 18-SEP-2001 (first entry)
XX DE Human complementary peptide, SEQ ID NO: 1144.
XX KW Human; complementary peptide; ligand; drug discovery; drug design.
XX OS Homo sapiens.
```

```
XX W200142277 A2.
XX 14 JUN 2001
XX 13 DEC 2000; 2000WO-GB04776
XX 13 DEC 1999; 99GB-0029464
XX (PROT-) PROTEOM LTD.
XX Roberts GW, Heal JR;
XX WP1: 2001-408419/43
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs.
XX Example 4; Page 203; 646pp; English.
XX The invention relates to a set of complementary peptide ligands
XX generated from the human genome. The complementary peptides
XX interact with their relevant target proteins encoded in the human
XX genome. They can be used as reagents in drug discovery and as novel
XX ligands to facilitate drug design and development. The present
XX sequence is a complementary peptide provided in the specification.
XX SQ Sequence 10 AA;
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0
QY 1 ARKS 4
DB 1111
4 ARKS 7

RESULT 19
AAG94949
ID AAG94949 standard; Peptide; 10 AA.
XX AC AAG94949;
XX DT 18-SEP-2001 (first entry)
XX DE Human complementary peptide, SEQ ID NO: 2944
XX KW Human; complementary peptide; ligand; drug discovery; drug design.
XX OS Homo sapiens.
XX W200142277 A2
XX 14 JUN 2001
XX 13 DEC 2000; 2000WO-GB04776
XX 13 DEC 1999; 99GB-0029464
XX (PROT-) PROTEOM LTD.
XX Roberts GW, Heal JR;
XX WP1: 2001-408419/43
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs.
```

PS Example 4: Page 472; 646pp; English.

CC The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 2 RKSR 5  
DB 1111  
2 RKSR 5

RESULT 40

AAG97695

ID AAG97695 standard; Peptide; 10 AA;

XX AAG97695;

XX 18-SEP-2001 (first entry)

XX Human complementary peptide; SEQ ID NO: 4899;

DE Human: complementary peptide; ligand; drug discovery; drug design

KW Human: complementary peptide; ligand; drug discovery; drug design

XX Homo sapiens.

OS Homo sapiens.

XX WQ200142277-A2.

PN WQ200142277-A2.

XX 14-JUN-2001.

PD 14-JUN-2001.

PF 13-DEC-2000; 2000WO-GB04776.

XX 13-DEC-1999; 99GB-0029464.

PR 13-DEC-1999; 99GB-0029464.

XX (PROT-) PROTEUM LTD.

PA Roberts GW, Heai JR;

PI WPI: 2001-438419/43.

DR WPI: 2001-438419/43.

XX A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.

XX Example 6: Page 591; 646pp; English.

PS The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 1 ARKS 4  
DB 1111  
1 ARKS 4

RESULT 41

AAG97695

ID AAG97695 standard; Peptide; 10 AA;

XX AAG97695;

XX 18-SEP-2001 (first entry)

XX Human complementary peptide; SEQ ID NO: 4899;

DE Human: complementary peptide; ligand; drug discovery; drug design

KW Human: complementary peptide; ligand; drug discovery; drug design

XX Homo sapiens.

OS Homo sapiens.

XX WQ200142277-A2.

PN WQ200142277-A2.

XX 14-JUN-2001.

PD 14-JUN-2001.

PF 13-DEC-2000; 2000WO-GB04776.

XX 13-DEC-1999; 99GB-0029464.

PR 13-DEC-1999; 99GB-0029464.

XX (PROT-) PROTEUM LTD.

PA Roberts GW, Heai JR;

PI WPI: 2001-438419/43.

DR WPI: 2001-438419/43.

XX A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.

XX Example 6: Page 591; 646pp; English.

PS The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 1 ARKS 4  
DB 1111  
1 ARKS 4



PK 13-DEC-1999; 99GB-0029464.  
 XX (PROT-) PROTEOM LTD.  
 PA  
 XX Robert's GW, Heal JR;  
 PI  
 XX WPI; 2001-408419/43.  
 DR  
 XX  
 XX A set of peptide ligands consisting of specific complementary peptides  
 PT to proteins encoded by genes of the human genome, useful in an assay  
 PT for screening and identifying of one or more novel peptides which are  
 PT drug candidates or pro-drugs -  
 XX  
 XX Example 6; Page 591; 646pp; English.  
 PS  
 XX The invention relates to a set of complementary peptide ligands  
 CC generated from the human genome. The complementary peptides  
 CC interact with their relevant target proteins encoded in the human  
 CC genome. They can be used as reagents in drug discovery and as lead  
 CC ligands to facilitate drug design and development. The present  
 CC sequence is a complementary peptide provided in the Specification.  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 4002;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 1 ARKS 4  
 DB IIII  
 2 ARKS 5  
 RESULT 43  
 ID AAG97700 standard; Peptide: 10 AA.  
 AC  
 AC AAG97700;  
 XX  
 XX 18-SEP-2001 (first entry)  
 DT  
 XX Human complementary peptide, SEQ ID NO: 3895.  
 DE  
 XX Human; complementary peptide; ligand; drug discovery; drug design.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200142277-A2.  
 PN  
 XX 14-JUN-2001.  
 PD  
 XX 13-DEC-2000; 2000WO-GB04776.  
 PF  
 XX 13-DEC-1999; 99GB-0029464.  
 PR  
 XX (PROT-) PROTEOM LTD.  
 PA  
 XX Robert's GW, Heal JR;  
 PI  
 XX WPI; 2001-408419/43.  
 DR  
 XX  
 XX A set of peptide ligands consisting of specific complementary peptides  
 PT to proteins encoded by genes of the human genome, useful in an assay  
 PT for screening and identifying of one or more novel peptides which are  
 PT drug candidates or pro-drugs -  
 XX  
 XX Example 6; Page 592; 646pp; English.  
 PS  
 XX The invention relates to a set of complementary peptide ligands  
 CC generated from the human genome. The complementary peptides  
 CC interact with their relevant target proteins encoded in the human  
 CC genome. They can be used as reagents in drug discovery and as lead  
 CC ligands to facilitate drug design and development. The present

CC sequence is a complementary peptide provided in the Specification  
 XX  
 XX Sequence 10 AA  
 SQ  
 Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 4002;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 1 ARKS 4  
 DB IIII  
 2 ARKS 5  
 RESULT 44  
 ID AAG97946 standard; Peptide: 10 AA.  
 AC  
 AC AAG97946;  
 XX  
 XX 18-SEP-2001 (first entry)  
 DT  
 XX Human complementary peptide, SEQ ID NO: 3896.  
 DE  
 XX Human; complementary peptide; ligand; drug discovery; drug design.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200142277-A2.  
 PN  
 XX 14-JUN-2001.  
 PD  
 XX 13-DEC-2000; 2000WO-GB04776.  
 PF  
 XX 13-DEC-1999; 99GB-0029464.  
 PR  
 XX (PROT-) PROTEOM LTD.  
 PA  
 XX Robert's GW, Heal JR;  
 PI  
 XX WPI; 2001-408419/43.  
 DR  
 XX  
 XX A set of peptide ligands consisting of specific complementary peptides  
 PT to proteins encoded by genes of the human genome, useful in an assay  
 PT for screening and identifying of one or more novel peptides which are  
 PT drug candidates or pro-drugs -  
 XX  
 XX Example 6; Page 592; 646pp; English.  
 PS  
 XX The invention relates to a set of complementary peptide ligands  
 CC generated from the human genome. The complementary peptides  
 CC interact with their relevant target proteins encoded in the human  
 CC genome. They can be used as reagents in drug discovery and as lead  
 CC ligands to facilitate drug design and development. The present  
 CC sequence is a complementary peptide provided in the Specification.  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 4002;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 1 ARKS 4  
 DB IIII  
 2 ARKS 5  
 RESULT 45  
 ID AAG97946 standard; Peptide: 10 AA.  
 AC  
 AC AAG97946;  
 XX  
 XX 18-SEP-2001 (first entry)  
 DT

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XX DE Human complementary peptide, SEQ ID NO: 431.
XX DE Human: complementary peptide: ligand; drug discovery; drug design.
XX OS Homo sapiens.
XX PN WO200142277-A2.
XX PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB04776.
XX PR 13-DEC-1999; 99GB-0029464.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX WP1: 2001-408419/43.
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, used in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs.
XX Example 6; Page 625; 646pp; English.
XX The invention relates to a set of complementary peptide ligands
XX generated from the human genome. The complementary peptides
XX interact with their relevant target proteins encoded in the human
XX genome. They can be used as reagents in drug discovery and as lead
XX ligands to facilitate drug design and development. The present
XX sequence is a complementary peptide provided in the specification.
XX Sequence 10 AA;
XX
XX Query Match 36.4%; Score 4; Db 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 4e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARKS 4
XX DB 1111
XX 6 ARKS 9
XX
XX RESULT 46
XX AAG84101
XX ID AAG84101 standard; Peptide: 10 AA.
XX AC AAG84101;
XX DT 11-SEP-2001 (first entry)
XX DE Arabidopsis thaliana peptide ligand #741.
XX KW Plant: peptide pesticide; peptide herbicide; agricultural research.
XX OS Arabidopsis thaliana.
XX PN WO200142279-A2.
XX PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB04781.
XX PR 13-DEC-1999; 99GB-0029469.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX WP1: 2001-381629/40.

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XX A set of peptide ligands for agricultural research and development of
XX therapeutic agents comprising specific complementary peptides to proteins
XX encoded by genes of plant genomes.
XX Example 4; Page 134; 211pp; English.
XX The present invention relates to a set of peptide ligands consisting of
XX specific complementary peptides to proteins encoded by genes of plant
XX genomes. The present sequence is a complementary peptide from Arabidopsis
XX thaliana. The peptide of the present invention are useful in an assay to
XX identify a peptide, especially a peptide pesticide or herbicide. The
XX peptides are also useful for tools for agricultural research and
XX development.
XX Sequence 10 AA;
XX
XX Query Match 36.4%; Score 4; Db 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 4e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARKS 4
XX DB 1111
XX 1 ARKS 4
XX
XX RESULT 47
XX AAG84105
XX ID AAG84105 standard; Peptide: 1 AA.
XX AC AAG84105.
XX DT 11-SEP-2001 (first entry)
XX DE Arabidopsis thaliana peptide ligand #745.
XX KW Plant: peptide pesticide; peptide herbicide; agricultural research.
XX OS Arabidopsis thaliana.
XX PN WO200142279-A2.
XX PD 14-JUN-2001.
XX PF 13-SEP-2000; 2000WO-GB04781.
XX PR 13-SEP-1999; 99GB-0029479.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX WP1: 2001-381629/40.
XX
XX A set of peptide ligands for agricultural research and development of
XX therapeutic agents comprising specific complementary peptides to proteins
XX encoded by genes of plant genomes.
XX Example 4; Page 134; 211pp; English.
XX The present invention relates to a set of peptide ligands consisting of
XX specific complementary peptides to proteins encoded by genes of plant
XX genomes. The present sequence is a complementary peptide from Arabidopsis
XX thaliana. The peptide of the present invention are useful in an assay to
XX identify a peptide, especially a peptide pesticide or herbicide. The
XX peptides are also useful for tools for agricultural research and
XX development.
XX Sequence 10 AA;
XX
XX Query Match 36.4%; Score 4; Db 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 4e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



OS Homo sapiens.  
XX WO200283921-A2.  
XX 24-OCT-2002.  
XX 10-APR-2002; 2002WO-US11654.  
XX 10-APR-2001; 2001US-282739P.  
XX 10-APR-2001; 2001US-283112P.  
XX 25-APR-2001; 2001US-286630P.  
XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Challita-Eid PM, Faris M, Go W, Roberts RS;  
XX Morrison K, Morrison RK, Raitano AH;  
XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients.  
XX Claim 13: Page 160; 1021pp; English.  
XX The present invention relates to novel human cancer related genes and  
XX proteins (AB278120-AB278168 and AB278189-AB278186), the genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.  
XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulation of  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.  
XX Sequence 10 AA;  
SQ  
Query Match 36.4%; Score 4; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 40+32;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ARKS 4  
DB 4 ARKS 7  
Search completed: September 30, 2003, 10:25:45  
Job time : 46.1667 secs

GenCore version 6.1.1  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 11:3335 seconds  
(without alignments)  
93,340 Million cell updates/sec

Title: US-09-787-443-22

Perfect score: 11

Sequence: 1 AKSRDMTAK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2062

Minimum DB seq length: 8  
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : PIR76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	8	1	LF5AME
2	3	27.3	10	2	H28027
3	3	27.3	10	2	PN0165
4	3	27.3	11	2	PH0919
5	3	27.3	12	2	A44874
6	3	27.3	12	2	S43013
7	3	27.3	13	2	A53608
8	3	27.3	13	2	PN0122
9	3	27.3	13	2	PC4055
10	3	27.3	13	2	S61798
11	3	27.3	14	2	A49018
12	3	27.3	14	2	A35377
13	3	27.3	14	2	B34135
14	3	27.3	14	2	PH1471
15	3	27.3	15	2	PA0053
16	3	27.3	15	2	A41338
17	3	27.3	15	2	PA0075
18	3	27.3	15	2	PA0102
19	3	27.3	15	2	A47628
20	3	27.3	15	2	G49255
21	3	27.3	15	2	PH1590
22	2	18.2	8	2	PH1407
23	2	18.2	8	2	A31570
24	2	18.2	8	2	S43971
25	2	18.2	8	2	S43972
26	2	18.2	8	2	T10077
27	2	18.2	8	2	PC4131
28	2	18.2	8	2	S37141
29	2	18.2	8	2	S21273

31	2	18.2	8	2	hypothetical protein
32	2	18.2	8	2	paramyosin-like protein
33	2	18.2	8	2	serpin family A member 1
34	2	18.2	8	2	serpin family A member 1
35	2	18.2	8	2	serpin family A member 1
36	2	18.2	8	2	serpin family A member 1
37	2	18.2	8	2	serpin family A member 1
38	2	18.2	8	2	serpin family A member 1
39	2	18.2	8	2	serpin family A member 1
40	2	18.2	8	2	serpin family A member 1
41	2	18.2	8	2	serpin family A member 1
42	2	18.2	8	2	serpin family A member 1
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44	2	18.2	8	2	serpin family A member 1
45	2	18.2	8	2	serpin family A member 1
46	2	18.2	8	2	serpin family A member 1
47	2	18.2	8	2	serpin family A member 1
48	2	18.2	8	2	serpin family A member 1
49	2	18.2	8	2	serpin family A member 1
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73	2	18.2	8	2	serpin family A member 1
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78	2	18.2	8	2	serpin family A member 1
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84	2	18.2	8	2	serpin family A member 1
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86	2	18.2	8	2	serpin family A member 1
87	2	18.2	8	2	serpin family A member 1
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89	2	18.2	8	2	serpin family A member 1
90	2	18.2	8	2	serpin family A member 1
91	2	18.2	8	2	serpin family A member 1
92	2	18.2	8	2	serpin family A member 1
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95	2	18.2	8	2	serpin family A member 1
96	2	18.2	8	2	serpin family A member 1
97	2	18.2	8	2	serpin family A member 1
98	2	18.2	8	2	serpin family A member 1
99	2	18.2	8	2	serpin family A member 1
100	2	18.2	8	2	serpin family A member 1
101	2	18.2	8	2	serpin family A member 1
102	2	18.2	8	2	serpin family A member 1



249	2	18.2	13	2	S23638	Ig kappa chain J s	322	2	18.2	14	2	S23639	Ig kappa chain J s
250	2	18.2	13	2	S23640	Ig kappa chain J s	323	2	18.2	14	2	PA1667	T cell receptor alpha
251	2	18.2	13	2	B61458	Ig kappa chain V-I	324	2	18.2	14	2	S23638	T cell receptor alpha
252	2	18.2	13	2	B61458	Ig kappa chain V-I	325	2	18.2	14	2	PA1667	T cell receptor alpha
253	2	18.2	13	2	PL0157	Ig kappa chain V-I	326	2	18.2	14	2	S23638	T cell receptor alpha
254	2	18.2	13	2	B61458	Ig kappa chain V-I	327	2	18.2	14	2	S23639	T cell receptor alpha
255	2	18.2	13	2	B61458	Ig kappa chain V-I	328	2	18.2	14	2	PA1667	T cell receptor alpha
256	2	18.2	13	2	S47359	Ig kappa chain V-I	329	2	18.2	14	2	PA1667	T cell receptor alpha
257	2	18.2	13	2	S47377	T-cell antigen rec	330	2	18.2	14	2	PA1667	T cell receptor alpha
258	2	18.2	13	2	S47384	T-cell antigen rec	331	2	18.2	14	2	PA1667	T cell receptor alpha
259	2	18.2	13	2	S47388	T-cell antigen rec	332	2	18.2	14	2	PA1667	T cell receptor alpha
260	2	18.2	13	2	S23372	T-cell receptor alpha	333	2	18.2	14	2	PA1667	T cell receptor alpha
261	2	18.2	13	2	S56046	urinary tract ston	334	2	18.2	14	2	PA1667	T cell receptor alpha
262	2	18.2	13	2	S10562	zona pellucida-bi	335	2	18.2	14	2	PA1667	T cell receptor alpha
263	2	18.2	13	2	A39836	aggreccan - bovine	336	2	18.2	14	2	PA1667	T cell receptor alpha
264	2	18.2	13	2	C53275	Ig kappa-1 chain J	337	2	18.2	14	2	PA1667	T cell receptor alpha
265	2	18.2	13	2	E53275	Ig kappa-1 chain J	338	2	18.2	14	2	PA1667	T cell receptor alpha
266	2	18.2	13	2	H25448	Ig kappa-1 chain J	339	2	18.2	14	2	PA1667	T cell receptor alpha
267	2	18.2	13	2	PC2240	heat shock protein	340	2	18.2	14	2	PA1667	T cell receptor alpha
268	2	18.2	13	2	PH1636	Ig H chain V-D-J	341	2	18.2	14	2	PA1667	T cell receptor alpha
269	2	18.2	13	2	PH1620	Ig H chain V-D-J	342	2	18.2	14	2	PA1667	T cell receptor alpha
270	2	18.2	13	2	PH1593	Ig H chain V-D-J	343	2	18.2	14	2	PA1667	T cell receptor alpha
271	2	18.2	13	2	PH1593	Ig H chain V-D-J	344	2	18.2	14	2	PA1667	T cell receptor alpha
272	2	18.2	13	2	PH1596	Ig H chain V-D-J	345	2	18.2	14	2	PA1667	T cell receptor alpha
273	2	18.2	13	2	PH1585	Ig H chain V-D-J	346	2	18.2	14	2	PA1667	T cell receptor alpha
274	2	18.2	13	2	D37267	Ig heavy chain C	347	2	18.2	14	2	PA1667	T cell receptor alpha
275	2	18.2	13	2	A33933	Ig kappa chain J	348	2	18.2	14	2	PA1667	T cell receptor alpha
276	2	18.2	13	2	B26406	Ig kappa chain J	349	2	18.2	14	2	PA1667	T cell receptor alpha
277	2	18.2	13	2	PH0799	T-cell receptor alpha	350	2	18.2	14	2	PA1667	T cell receptor alpha
278	2	18.2	13	2	PH0805	T-cell receptor alpha	351	2	18.2	14	2	PA1667	T cell receptor alpha
279	2	18.2	13	2	D47630	Ig kappa chain J	352	2	18.2	14	2	PA1667	T cell receptor alpha
280	2	18.2	13	2	H85575	hypothetrical prote	353	2	18.2	14	2	PA1667	T cell receptor alpha
281	2	18.2	13	2	S01043	glutamate-ammonia	354	2	18.2	14	2	PA1667	T cell receptor alpha
282	2	18.2	13	2	S54344	glyoxaldehyde-3-P	355	2	18.2	14	2	PA1667	T cell receptor alpha
283	2	18.2	13	2	AB0764	his operon leader	356	2	18.2	14	2	PA1667	T cell receptor alpha
284	2	18.2	13	4	I70075	glycophorin B (mis	357	2	18.2	14	2	PA1667	T cell receptor alpha
285	2	18.2	14	1	NYR614	hypothetrical tetra	358	2	18.2	14	2	PA1667	T cell receptor alpha
286	2	18.2	14	1	QWVHM	mastoparan M - hor	359	2	18.2	14	2	PA1667	T cell receptor alpha
287	2	18.2	14	1	LFECW	trp operon leader	360	2	18.2	14	2	PA1667	T cell receptor alpha
288	2	18.2	14	1	LFECFS	trp operon leader	361	2	18.2	14	2	PA1667	T cell receptor alpha
289	2	18.2	14	2	A60622	somatostatin - spu	362	2	18.2	14	2	PA1667	T cell receptor alpha
290	2	18.2	14	2	B61309	lutropin beta chain	363	2	18.2	14	2	PA1667	T cell receptor alpha
291	2	18.2	14	2	JN0389	histamine-releasin	364	2	18.2	14	2	PA1667	T cell receptor alpha
292	2	18.2	14	2	PH1677	Ig heavy chain V	365	2	18.2	14	2	PA1667	T cell receptor alpha
293	2	18.2	14	2	PH1705	Ig heavy chain V	366	2	18.2	14	2	PA1667	T cell receptor alpha
294	2	18.2	14	2	S51430	hemoglobin beta ch	367	2	18.2	14	2	PA1667	T cell receptor alpha
295	2	18.2	14	2	S50900	calorophyll a/b-hi	368	2	18.2	14	2	PA1667	T cell receptor alpha
296	2	18.2	14	2	A42473	crk leader peptide	369	2	18.2	14	2	PA1667	T cell receptor alpha
297	2	18.2	14	2	A44515	trp EG leader pept	370	2	18.2	14	2	PA1667	T cell receptor alpha
298	2	18.2	14	2	JH0328	prolactin tetradec	371	2	18.2	14	2	PA1667	T cell receptor alpha
299	2	18.2	14	2	E90858	trp operon leader	372	2	18.2	14	2	PA1667	T cell receptor alpha
300	2	18.2	14	2	B38222	excinuclease ABC c	373	2	18.2	14	2	PA1667	T cell receptor alpha
301	2	18.2	14	2	I54388	Km(r) protein - Es	374	2	18.2	14	2	PA1667	T cell receptor alpha
302	2	18.2	14	2	B44854	disaggregatase - M	375	2	18.2	14	2	PA1667	T cell receptor alpha
303	2	18.2	14	2	A60158	protein QAL0054 -	376	2	18.2	14	2	PA1667	T cell receptor alpha
304	2	18.2	14	2	PA0111	omega-allylamine 1 a	377	2	18.2	14	2	PA1667	T cell receptor alpha
305	2	18.2	14	2	PN0147	omega-allylamine 2	378	2	18.2	14	2	PA1667	T cell receptor alpha
306	2	18.2	14	2	PN0151	20K protein 5503 -	379	2	18.2	14	2	PA1667	T cell receptor alpha
307	2	18.2	14	2	PS0255	perin rics (stra	380	2	18.2	14	2	PA1667	T cell receptor alpha
308	2	18.2	14	2	PS0249	unidentified 6.9/5	381	2	18.2	14	2	PA1667	T cell receptor alpha
309	2	18.2	14	2	PQ0698	acetyl-CoA carboxy	382	2	18.2	14	2	PA1667	T cell receptor alpha
310	2	18.2	14	2	S35267	actin B - slime mo	383	2	18.2	14	2	PA1667	T cell receptor alpha
311	2	18.2	14	2	A39239	mastoparan B - hor	384	2	18.2	14	2	PA1667	T cell receptor alpha
312	2	18.2	14	2	S14336	Ig heavy chain V r	385	2	18.2	14	2	PA1667	T cell receptor alpha
313	2	18.2	14	2	B39111	Ig heavy chain CDR	386	2	18.2	14	2	PA1667	T cell receptor alpha
314	2	18.2	14	2	PT0223	Ig heavy chain CDR	387	2	18.2	14	2	PA1667	T cell receptor alpha
315	2	18.2	14	2	PT0294	Ig heavy chain D2	388	2	18.2	14	2	PA1667	T cell receptor alpha
316	2	18.2	14	2	PH1347	Ig heavy chain D2	389	2	18.2	14	2	PA1667	T cell receptor alpha
317	2	18.2	14	2	PH1327	Ig heavy chain DJ	390	2	18.2	14	2	PA1667	T cell receptor alpha
318	2	18.2	14	2	PH1311	Ig heavy chain DJ	391	2	18.2	14	2	PA1667	T cell receptor alpha
319	2	18.2	14	2	PH1321	Ig heavy chain DJ	392	2	18.2	14	2	PA1667	T cell receptor alpha
320	2	18.2	14	2	PH1305	Ig heavy chain DJ	393	2	18.2	14	2	PA1667	T cell receptor alpha
321	2	18.2	14	2	PH1306	Ig heavy chain DJ	394	2	18.2	14	2	PA1667	T cell receptor alpha





A:Accession: H28027  
A:Molecule type: protein  
A:Residues: 1-10 <BAU>  
A>Note: 4-Val was also found

Query Match 27.3%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AIK 11  
|||  
DB 1 AIK 3

RESULT 3  
PN0165  
C:Species: Fusarium sporotrichioides (fragment)  
C:Date: 05-Aug-1994 #sequence\_revision 06-Jan-1995 #text\_change 23 Mar 1995  
C:Accession: PN0165  
R: Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsudita, A.; Ueno, Y.; Tabuchi, K.  
Submitted to JIPID, May 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
A:Reference number: PN0160  
A:Accession: PN0165  
A:Molecule type: protein  
A:Residues: 1-10 <PUK>  
A:Experimental source: strain M-1-1  
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 27.3%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3  
|||  
DB 1 ARK 3

RESULT 4  
PH0919  
T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0919  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandemark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0919  
A:Molecule type: mRNA  
A:Residues: 1-11 <GOL>  
A:Experimental source: concanavalin A-activated lymphoblast  
A>Note: the authors translated the codon CAG for residue 11 as Gln  
C:Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6  
|||  
DB 3 SRD 5

RESULT 5  
A44874  
proboscipedia - fruit fly (Drosophila pseudoobscura) (fragment)  
C:Species: Drosophila pseudoobscura  
C:Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Oct-1999  
C:Accession: A44874  
R:Randazzo, F.M.; Gribbs, D.L.; Kaufman, T.C.  
Development 113, 257-271, 1991

```

Db          6 KSK 8

RESULT 8
PN0122
Oll protein - vaccinia virus (strain 1.1Vb) (fragment)
C:Species: vaccinia virus
C:Date: 15-Jan-1994 #sequence_revision 15 Jan 1994 #ext_change 25 Jan 1994
C:Accession: PN0122
R:Rajankina, O.I.; Shchelkunov, S.N.; Muravlev, A.I.; Novosol, N.A.; Mikhajkov, N.N.
Mol. Biol. (Mosk.) 24, 968-976, 1990
A:Title: The molecular biological study of vaccinia virus genome in reactivation and
A:Reference number: PN0119; MUID:91066899; PMID:245685
A:Accession: PN0122
A:Molecule type: DNA
A:Residues: 1-13 <RCA>
C:Superfamily: variola major virus hypothetical protein Q12.

Query Match          27.3% Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 8 AKK 10

RESULT 9
PC4055
Hypothetical 13 protein - Frankia sp. (fragment)
C:Species: Frankia sp.
C:Date: 10-Sep-1995 #sequence_revision 27 Sep 1995 #ext_change 27 Sep 1995
R:Riario, O.T.; Hosted, T.J.; Benson, D.K.
Gene 161, 64-67, 1995
A:Title: Sequences of nifX, nifW, nifZ, nifB and two other nif-like Frankia nif genes.
A:Reference number: JC4203; MUID:95369744; PMID:7642148
A:Accession: PC4055
A:Molecule type: DNA
A:Residues: 1-13 <HAR>
A:CROSS-references: GB:L29299

Query Match          27.3% Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MTA 9
DB 1 MTA 3

RESULT 10
S61798
T-cell-specific transcription factor 1 splice form 3 - human (fragment)
N:Alternate names: transcription factor TCF-1C
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 18 Jul 1997 #ext_change 24 Jul 1998
R:Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, K.G.
Biochim. Biophys. Acta 1263, 169-172, 1995
A:Title: The human high mobility group (HMG) box transcription factor 17.1 is novel isoform
A:Reference number: S61796; MUID:95367594; PMID:7649179
A:Accession: S61798
A:Molecule type: mRNA
A:Residues: 1-13 <MAY>
A:CROSS-references: EMBL:247364
A:Note: DNA was also sequenced
C:Keywords: alternative splicing; DNA binding; transcription factor

Query Match          27.3% Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          6 KSK 8
14 1 AKK 10

RESULT 11
A05049
Cytochrome b5H2, liver, rat (fragment) (Tramont)
C:Species: Rattus norvegicus (Wistar-Kyoto) (Tramont)
C:Date: 10-May-1994 #sequence_revision 10 May 1994 #ext_change 25 Jan 1995
C:Accession: A05049
R:Randel, S.; Ashworth, S.; Wainwright, S.; Johnston, I.; Vellody, M.; Buchanan, R.; Zella,
J. Biol. Chem. 269, 9245-9251, 1994
A:Title: Type 2A cytochrome b5H2 is a member of the cytochrome b5 family and does
A:Reference number: A05049; MUID:95367594; PMID:7649179
A:Accession: A05049
A:Molecule type: mRNA
A:Residues: 1-14 <MAY>
A:CROSS-references: GB:L29299
R:Randel, S.; Ashworth, S.; Wainwright, S.; Johnston, I.; Vellody, M.; Buchanan, R.; Zella,
J. Biol. Chem. 269, 9245-9251, 1994
A:Title: Type 2A cytochrome b5H2 is a member of the cytochrome b5 family and does
A:Reference number: A05049; MUID:95367594; PMID:7649179
A:Accession: A05049
A:Molecule type: mRNA
A:Residues: 1-14 <MAY>
A:CROSS-references: GB:L29299
C:Keywords: skeletal muscle

Query Match          27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KSK 5
DB 2 KSK 4

RESULT 12
A05047
Cytochrome b5H2, liver, rat (fragment) (Tramont)
C:Species: Rattus norvegicus (Wistar-Kyoto) (Tramont)
C:Date: 27 Aug 1994 #sequence_revision 27 Aug 1994 #ext_change 24 Jul 1997
C:Accession: A05047
R:Randel, S.; Ashworth, S.; Wainwright, S.; Johnston, I.; Vellody, M.; Buchanan, R.; Zella,
J. Biol. Chem. 269, 9245-9251, 1994
A:Title: Type 2A cytochrome b5H2 is a member of the cytochrome b5 family and does
A:Reference number: A05047; MUID:95367594; PMID:7649179
A:Accession: A05047
A:Molecule type: mRNA
A:Residues: 1-14 <MAY>
A:CROSS-references: GB:L29299
C:Keywords: skeletal muscle

Query Match          27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MTA 9
DB 1 MTA 3

RESULT 13
B34145
DNA binding protein 1 - human (fragment) (Tramont)
C:Species: Homo sapiens (man) (Tramont)
C:Date: 05-Sep-1994 #sequence_revision 6 Sep 1994 #ext_change 27 Jan 1995
C:Accession: B34145
R:Randel, S.; Ashworth, S.; Wainwright, S.; Johnston, I.; Vellody, M.; Buchanan, R.; Zella,
J. Biol. Chem. 269, 9245-9251, 1994
A:Title: Type 2A cytochrome b5H2 is a member of the cytochrome b5 family and does
A:Reference number: B34145; MUID:95367594; PMID:7649179
A:Accession: B34145
A:Molecule type: mRNA
A:Residues: 1-13 <MAY>
A:CROSS-references: EMBL:247364
A:Note: DNA was also sequenced
C:Keywords: alternative splicing; DNA binding; transcription factor

```

FEBS Lett. 260, 57-61, 1990  
 A:Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan *Crithidia fascicularis*  
 A:Reference number: A34135  
 A:Accession: B34135  
 A:Molecule type: protein  
 A:Residues: 1-14 <IT>  
 C:Genetics:  
 C:Genome: mitochondrion  
 A:Genetic code: SGC6  
 C:Keywords: mitochondrion

Query Match 27.3%, Score 3, DB 2, Length 14

Best Local Similarity 100.0%, Pred. No. 2, Gap 0

Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKS 4

DB 11 RKS 13

#### RESULT 14

PHI471  
 T-cell receptor beta chain (clone A24/PEF4) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11 Apr-1995  
 C:Accession: PHI471  
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Baria, C.; Pannetier, C.; Roman, A.; K...  
 J. Exp. Med. 177, 811-820, 1993  
 A:Title: T cell receptor selection by and recognition of two classes of major histocompatibility complex peptides  
 A:Reference number: PHI430; MUID:93171621; PMID:841691  
 A:Accession: PHI471  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <CAS>  
 A:Experimental source: cytolytic T-lymphocyte  
 C:Superfamily: immunoglobulin homology  
 C:Keywords: receptor; T-cell

Query Match 27.3%, Score 3, DB 2, Length 14

Best Local Similarity 100.0%, Pred. No. 2, Gap 0

Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 SRD 6

DB 4 SRD 6

#### RESULT 15

PA0003  
 nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 18-Nov-1994 #sequence\_revision 06-Jan-1995 #text\_change 15-Mar-1996  
 C:Accession: PA0003  
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JPIB, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
 A:Reference number: PA0001  
 A:Accession: PA0003  
 A:Molecule type: protein  
 A:Residues: 1-15 <KAM>  
 A:Experimental source: leaf and callus  
 C:Superfamily: nucleoside-diphosphate kinase  
 C:Keywords: phosphotransferase

Query Match 27.3%, Score 3, DB 2, Length 15

Best Local Similarity 100.0%, Pred. No. 2, Gap 0

Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 9 AIK 11

DB 9 AIK 11

#### RESULT 16

AD144  
 Spectrinase (EC 3.1.1.1) - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 28-May-1992 #sequence\_revision 28-May-1992 #text\_change 24-Jun-1994  
 C:Accession: A1144  
 R:Boyd, J.C.; Belleson, S.; Bressan, M.  
 J. Biochem. J. 294, 1-10, 1993  
 A:Title: Purification and characterization of Arabidopsis spectrinase  
 A:Reference number: A1144; MUID:91010101; PMID:1518865  
 A:Accession: A1144  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 H Y  
 C:Keywords: spectrinase; spectrinase; spectrinase

Query Match 27.3%, Score 3, DB 2, Length 15

Best Local Similarity 100.0%, Pred. No. 2, Gap 0

Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 SRD 6

DB 4 SRD 6

#### RESULT 17

PA0075  
 Fructose-bisphosphate phosphatase (EC 3.1.3.2) - human (fragment)  
 A:Title: Human fructose-bisphosphate phosphatase (Fru-Pase)  
 C:Species: HOMO SAPIENS (human)  
 C:Date: 20-Jul-1995 #sequence\_revision 20-Jul-1995 #text\_change 20-Jul-2001  
 C:Accession: I1A\_76; PA0075  
 R:Gibson, J.P.; Fagan, M.; Stanton, V.; Goss, V.; Labadie, K.; Johnston, A.  
 submitted to JPIB, Oct-1994  
 A:Description: Purification and electrophoretic analysis of human fructose-bisphosphate phosphatase (Fru-Pase)  
 A:Reference number: PA0075  
 A:Accession: PA0075  
 A:Molecule type: protein  
 A:Residues: 1-15 H Y  
 A:Notes: The form (1) had a pI of 4.6 and an isoelectric point of 4.6  
 A:Keywords: fructose-bisphosphate phosphatase; Fru-Pase

Query Match 27.3%, Score 3, DB 2, Length 15

Best Local Similarity 100.0%, Pred. No. 2, Gap 0

Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 SRD 6

DB 4 SRD 6

#### RESULT 18

PA0142  
 Fructose-bisphosphate phosphatase (EC 3.1.3.2) - human (fragment)  
 C:Species: HOMO SAPIENS (human)  
 C:Date: 20-Jul-1995 #sequence\_revision 20-Jul-1995 #text\_change 20-Jul-2001  
 C:Accession: PA0142  
 R:Gibson, J.P.; Fagan, M.; Stanton, V.; Goss, V.; Labadie, K.; Johnston, A.  
 submitted to JPIB, Oct-1994  
 A:Description: Purification and electrophoretic analysis of human fructose-bisphosphate phosphatase (Fru-Pase)  
 A:Reference number: PA0142  
 A:Accession: PA0142  
 A:Molecule type: protein  
 A:Residues: 1-15 H Y  
 C:Keywords: fructose-bisphosphate phosphatase; Fru-Pase

Query Match 27.3%, Score 3, DB 2, Length 15

Best Local Similarity 100.0%, Pred. No. 2, Gap 0

Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKS 4  
III  
DB 8 RKS 10

## RESULT 19

A47628

Fc gamma receptor II (CD32) - human (fragments)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07 May 1994

C:Accession: A47628

R:Warmerdam, P.A.M.; van de Winkel, J.G.J.; Gosselin, E.J.; Copel, P.L.A.

J. Exp. Med. 172, 19-25, 1990

A:Title: Molecular basis for a polymorphism of human Fc gamma receptor II (CD32).

A:Reference number: A47628; PMID:90293679; PMID:2141627

A:Accession: A47628

A&gt;Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-15 &lt;WAR&gt;

C:Keywords: immunoglobulin receptor

Query Match 27.3% Score 3; LB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2; Re-0.0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 MTA 9

III

DB 1 MTA 3

## RESULT 20

G49255

T-cell receptor beta chain V-D-J-C region (V beta 24, J beta 2.1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30 May 1997

C:Accession: G49255

R:Rosenberg, W.M.; Moss, P.A.; Bell, J.L.

Eur. J. Immunol. 22, 541-549, 1992

A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A:Reference number: A49039; PMID:92164737; PMID:1311263

A:Accession: G49255

A&gt;Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-15 &lt;ROS&gt;

A:Note: sequence extracted from NCBI backbone (NCBI:90728)

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2; Re-0.0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 SRD 6

III

DB 4 SRD 6

## RESULT 21

PH1590

19 H chain V-D-J region (wild-type clone 141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1994

C:Accession: PH1590

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-28 mice

A:Reference number: PH1580; PMID:93301609; PMID:8115367

A:Accession: PH1590

A:Molecule type: DNA

A:Residues: 1-15 &lt;LEV&gt;

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2; Re-0.0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 SRD 7

III

DB 4 SRD 6

## RESULT 22

PH1499

19 Heavy chain V region (clone 141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 01-Dec-1993 #sequence\_revision 01-Dec-1993 #text\_change 07-Mar-1994

C:Accession: PH1499

R:Shirasaka, T.; Miyazaki, H.; Kikuchi, S.; Kimoto, H.; Shimotoh, K.; Yoshimura, M.

J. Exp. Med. 176, 209-214, 1992

A:Title: Heavy chain (H chain) of the B cell receptor generated by V(D)J recombination

A:Accession: PH1499

A:Molecule type: DNA

A:Residues: 1-15 &lt;SHI&gt;

A:Note: sequence extracted from NCBI backbone (NCBI:90728)

C:Keywords: immunoglobulin receptor

Query Match 27.3% Score 3; LB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2; Re-0.0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 SRD 4

III

DB 4 SRD 4

## RESULT 23

A41576

androgen-inhibited androgen-dependent cell line (L6E9)

C:Species: Thymus albuminosus (yellow rat)

C:Date: 31-Mar-1990 #sequence\_revision 01-Mar-1990 #text\_change 16-Aug-2000

C:Accession: A41576

R:Kobama, Y.; Matsushima, S.; Kato, H.; Teramoto, T.; Sakabe, M.; Mizuno, Y.

J. Biol. Chem. 265, 447-452, 1990

A:Title: Isolation of androgen-inhibited androgen-dependent cell line (L6E9)

A:Reference number: A41576; PMID:215668

A:Accession: A41576

A:Molecule type: protein

A:Residues: 1-16 &lt;KOB&gt;

A:Note: the sequence is described as 16 thymus monocytes

C:Keywords: androgens; androgen-inhibited androgen-inhibition

Query Match 27.3% Score 3; LB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2; Re-0.0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 SRD 6

III

DB 4 SRD 6



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Tl0952
hypothetical protein 1 - spring vetch
C:Species: Vicia sativa (spring vetch, tare)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: Tl0952
R:Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgaard, N.; Larsen, K.; Yang, W.; Hiss,
submitted to the EMBL Data Library, December 1995
A:Description: A novel type of DNA binding protein interacts with a conserved sequence
A:Reference number: 217228
A:Accession: Tl0952
A>Status: preliminary; translated from GB/EMBL/DDRJ
A:Molecule type: mRNA
A:Residues: 1-8 <CHR>
A:Cross-references: EMBL:X95995; NID:g1360633; PIR:025824

Query Match      18.2%  Score 2: DB 2: Length 8;
Best Local Similarity 100.0%: Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MT 8
DB 3 MT 4

RESULT 31
S22428
chitin-binding protein - potato (fragment)
C:Species: Solanum tuberosum (potato)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Nov-1996
C:Accession: S22428
R:Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, G.; Slabas, A.P.; Redwood, G.F.
Biochem. J. 283, 813-821, 1992
A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A:Reference number: S21288; MUID:92272683; PML:01530771
A:Accession: S22428
A:Molecule type: protein
A:Residues: 1-8 <ML>
C:Function:
A:Description: may be involved in plant defence
C:Keywords: glycoprotein; hydroxyproline

Query Match      18.2%  Score 2: DB 2: Length 8;
Best Local Similarity 100.0%: Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DM 7
DB 3 DM 4

RESULT 32
PL0162
paramyosin - northern quahog (fragment)
C:Species: Mercenaria mercenaria (northern quahog)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 11-May-2000
C:Accession: PL0162
R:Watabe, S.; Tsuchiya, T.; Hartshorne, D.J.
Comp. Biochem. Physiol. B 94, 813-821, 1989
A:Title: Phosphorylation of paramyosin.
A:Reference number: PL0162; MUID:90107385; PML:0254591
A:Accession: PL0162
A:Molecule type: protein
A:Residues: 1-8 <WAT>
A:Experimental source: white adductor muscle
A:Note: The sequence is the phosphorylated tryptic peptide
C:Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-par
om the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated by
C:Keywords: muscle; phosphoprotein
F:5/Binding site: phosphate (ser) (covalent) #status experimental

Query Match      18.2%  Score 2: DB 2: Length 8;
Best Local Similarity 100.0%: Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 SA 5
DB 1 SA 2

RESULT 33
PL0800
serum albumin - boar (fragment)
C:Species: Capra hircus (mountain goat)
C:Date: 03-Jul-1993 #sequence_revision 03-Jul-1993 #text_change 31-Dec-1993
C:Accession: PL0800
R:Parraway, R.; Gotschall, P.; Bower, W.; Mitra, S.P.
J. Immunol. 153, 176-180, 1994
A:Title: Structures of histidine residues in boar albumin peptides formed by the action of acid pr
A:Reference number: A45800; MUID:92441111; PML:02474609
A:Accession: PL0800
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <WAT>

Query Match      18.2%  Score 2: DB 2: Length 8;
Best Local Similarity 100.0%: Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 2 AG 3

RESULT 34
PL0618
beta chain V-D J region (C1H10A) mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Mar-1994 #sequence_revision 2-Mar-1994 #text_change 17-May-1999
C:Accession: PL0618
R:Levinson, D.A.; Cohn, S.; Leber, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of T cell receptor induced immunodominant C1H10A
A:Reference number: PL0618; MUID:92770019; PML:0155447
A:Accession: PL0618
A:Molecule type: DNA
A:Residues: 1-8 <LEV>
A:Experimental source: bone marrow from lymphocyte
C:Keywords: immunoglobulin

Query Match      18.2%  Score 2: DB 2: Length 8;
Best Local Similarity 100.0%: Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 2 AG 3

RESULT 35
PL0619
T cell receptor beta chain V-D J region (C1H10A) mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Mar-1994 #sequence_revision 2-Mar-1994 #text_change 06-May-1999
C:Accession: PL0619
R:Penney, A.J.
J. Exp. Med. 174, 115-125, 1991
A:Title: Functional sequences of T cell receptor beta chains have two N regions
A:Reference number: PL0619; MUID:92770019; PML:0155447
A:Accession: PL0619
A>Status: translation not available
A:Molecule type: mRNA
A:Residues: 1-8 <PEN>
A:Experimental source: spleen lymphocytes strain BALB/c
C:Keywords: T cell receptor

Query Match      18.2%  Score 2: DB 2: Length 8;

```

Best Local Similarity 100.0%; Pred. No. 2; Length 8;  
Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

QY 1 AR 2  
DB 7 AR 8

# RESULT 36

A47618  
beta-galactosidase (EC 3.2.1.23) lacZ - Streptococcus bovis (Trappett)  
C:Species: Streptococcus bovis  
C>Date: 01-Feb-1994 #sequence\_revision 03 Feb 1994 #text\_change 05 Nov 1994  
C:Accession: A47618  
R:Gilbert, H.J.; Hall, J.  
J. Gen. Microbiol. 133, 2285-2293, 1987  
A:Title: Molecular cloning of Streptococcus bovis lactose catabolic genes.  
A:Reference number: A47618  
A:Accession: A47618  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 18 <GIL>  
A:Cross-references: GB:M35285; NID:q154682; PDB:AAA7412; EMBL:2000  
C:Keywords: glycosidase; hydrolase

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Length 8;  
Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

QY 9 AI 10  
DB 7 AI 8

# RESULT 37

T13818  
cytochrome oxidase subunit 1 - Atlantic hagfish mitochondrion (Trappett)  
C:Species: mitochondrion Myxine glutinosa (Atlantic hagfish)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Jul-2000  
C:Accession: T13818  
R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Bachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the NID and the CIL  
A:Reference number: 217775; M010:97398704; PMID:9254918  
A:Accession: T13818  
A:Status: preliminary; translated from GB/EMBL/0081  
A:Molecule type: DNA  
A:Residues: 18 <DEB>  
A:Cross-references: EMBL:Y09527; NID:q2345619; PDB:CAA7071R; PDB:22445822  
C:Genetics:  
A:Genome: mitochondrion  
A:Note: COI  
C:Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Length 8;  
Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

QY 4 SR 5  
DB 4 SR 5

# RESULT 38

S66296  
Na<sup>+</sup>-transporting ATP synthase (EC 3.6.1.3) chain c - Acetobacterium woodii (Trappett)  
N:Alternate names: ATPase chain c  
C:Species: Acetobacterium woodii  
C>Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07 May 1999  
C:Accession: S66296  
R:Reidlinger, J.; Mueller, V.  
Eur. J. Biochem. 223, 275-283, 1994  
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a

A:Accession: S66296  
A:Molecule type: Protein  
A:Postscript: 18 <GIL>  
A:Experiment: 18 <GIL>  
C:Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Length 8;  
Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

QY 9 AI 10  
DB 7 AI 8

# RESULT 39

A47618  
beta-galactosidase (EC 3.2.1.23) lacZ - Streptococcus bovis (Trappett)  
C:Species: Streptococcus bovis  
C>Date: 01-Feb-1994 #sequence\_revision 03 Feb 1994 #text\_change 05 Nov 1994  
C:Accession: A47618  
R:Gilbert, H.J.; Hall, J.  
J. Gen. Microbiol. 133, 2285-2293, 1987  
A:Title: Molecular cloning of Streptococcus bovis lactose catabolic genes.  
A:Reference number: A47618  
A:Accession: A47618  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 18 <GIL>  
A:Cross-references: GB:M35285; NID:q154682; PDB:AAA7412; EMBL:2000  
C:Keywords: glycosidase; hydrolase

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Length 8;  
Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

# RESULT 40

T13818  
cytochrome oxidase subunit 1 - Atlantic hagfish mitochondrion (Trappett)  
C:Species: mitochondrion Myxine glutinosa (Atlantic hagfish)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Jul-2000  
C:Accession: T13818  
R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Bachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the NID and the CIL  
A:Reference number: 217775; M010:97398704; PMID:9254918  
A:Accession: T13818  
A:Status: preliminary; translated from GB/EMBL/0081  
A:Molecule type: DNA  
A:Residues: 18 <DEB>  
A:Cross-references: EMBL:Y09527; NID:q2345619; PDB:CAA7071R; PDB:22445822  
C:Genetics:  
A:Genome: mitochondrion  
A:Note: COI  
C:Keywords: mitochondrion

# RESULT 41

T13818  
cytochrome oxidase subunit 1 - Atlantic hagfish mitochondrion (Trappett)  
C:Species: mitochondrion Myxine glutinosa (Atlantic hagfish)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Jul-2000  
C:Accession: T13818  
R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Bachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the NID and the CIL  
A:Reference number: 217775; M010:97398704; PMID:9254918  
A:Accession: T13818  
A:Status: preliminary; translated from GB/EMBL/0081  
A:Molecule type: DNA  
A:Residues: 18 <DEB>  
A:Cross-references: EMBL:Y09527; NID:q2345619; PDB:CAA7071R; PDB:22445822  
C:Genetics:  
A:Genome: mitochondrion  
A:Note: COI  
C:Keywords: mitochondrion

QY 9 AI 10  
DB 7 AI 8

# RESULT 42

T13818  
cytochrome oxidase subunit 1 - Atlantic hagfish mitochondrion (Trappett)  
C:Species: mitochondrion Myxine glutinosa (Atlantic hagfish)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Jul-2000  
C:Accession: T13818  
R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Bachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the NID and the CIL  
A:Reference number: 217775; M010:97398704; PMID:9254918  
A:Accession: T13818  
A:Status: preliminary; translated from GB/EMBL/0081  
A:Molecule type: DNA  
A:Residues: 18 <DEB>  
A:Cross-references: EMBL:Y09527; NID:q2345619; PDB:CAA7071R; PDB:22445822  
C:Genetics:  
A:Genome: mitochondrion  
A:Note: COI  
C:Keywords: mitochondrion

QY 9 AI 10  
DB 7 AI 8

# RESULT 43

T13818  
cytochrome oxidase subunit 1 - Atlantic hagfish mitochondrion (Trappett)  
C:Species: mitochondrion Myxine glutinosa (Atlantic hagfish)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Jul-2000  
C:Accession: T13818  
R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Bachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the NID and the CIL  
A:Reference number: 217775; M010:97398704; PMID:9254918  
A:Accession: T13818  
A:Status: preliminary; translated from GB/EMBL/0081  
A:Molecule type: DNA  
A:Residues: 18 <DEB>  
A:Cross-references: EMBL:Y09527; NID:q2345619; PDB:CAA7071R; PDB:22445822  
C:Genetics:  
A:Genome: mitochondrion  
A:Note: COI  
C:Keywords: mitochondrion





R:Ernstroem, U.; Gafvelin, G.; Rud'ja, J.M.  
 Biosci. Rep. 10: 403-412, 1990  
 A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship of  
 A:Reference number: A60957; MUID:91064427; PMID:224504  
 A:Accession: A60957  
 A:Molecule type: protein  
 A:Residues: 1-9 <ERN>  
 C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral  
 in a variety of immunoassays  
 C:Comment: This peptide was isolated in two forms. One form contained the pyroglutamate  
 r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a  
 C:Superfamily: thymic factor  
 C:Keywords: blocked amino end; pyroglutamic acid  
 F:/Modified site: pyroglutamate carboxylic acid (Glx) (in FTS) \*status experimental  
 F:/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) \*status experim

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 KS 4  
 DB 1  
 1 KS 4

RESULT 47  
 S3538  
 ribosomal protein S7 - Mycobacterium intracellulare (fragment)  
 C:Species: Mycobacterium intracellulare  
 C:Date: 09-Dec-1993 #sequence\_revision 14 NID:1497 #text\_change 13-Aug-1994  
 C:Accession: S3538  
 R:Hair, J.; Kouse, D.; Morris, S.  
 Nucleic Acids Res. 21: 1039, 1993  
 A:Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intracellulare  
 A:Reference number: S3537; MUID:9197130; PMID:845117  
 A:Accession: S3538  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-9 <NA>  
 A:Cross-references: EMBL:108171; NID:q149994; PIDN:AAA5476.1; PID:551901  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994  
 C:Superfamily: Escherichia coli ribosomal protein S7  
 C:Keywords: protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RK 3  
 DB 1  
 3 RK 4

RESULT 48  
 S30494  
 cat gene leader peptide - Streptococcus agalactiae plasmid pIP501  
 C:Species: Streptococcus agalactiae  
 C:Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 24-Sep-1999  
 C:Accession: S30494  
 R:Tricu-Cuot, P.; de Cespedes, G.; Haraud, T.  
 Plasmid 28, 272-276, 1992  
 A:Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Streptococcus agalactiae plasmid pIP501  
 A:Reference number: JQ1950; MUID:93096867; PMID:346142  
 A:Accession: S30494  
 A:Molecule type: DNA  
 A:Residues: 1-9 <TRI>  
 A:Cross-references: EMBL:X65462; NID:q49071; PIDN:CAA464.1; PID:q51554  
 C:Genetics:  
 A:Genome: plasmid pIP501  
 C:Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RK 3  
 DB 1  
 3 RK 4

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 KS 4  
 DB 1  
 1 KS 4

RESULT 49  
 B24362  
 chloramphenicol acetyl transferase leader peptide - Staphylococcus aureus (strain of)  
 C:Species: Staphylococcus aureus  
 C:Date: 07-Apr-1984 #sequence\_revision 10-Apr-1994 #text\_change 11-May-2000  
 C:Accession: B24362  
 R:Bruckner, R.; Walther, J.  
 EMBL J. 4: 2245-2247, 1986  
 A:Title: purification of the nucleotide sequence of the chloramphenicol acetyl transferase gene from Staphylococcus aureus  
 A:Reference number: A60957; MUID:91064427; PMID:224504  
 A:Accession: B24362  
 A:Molecule type: DNA  
 A:Residues: 1-9 <NA>  
 A:Cross-references: EMBL:108171; NID:q149994; PIDN:AAA5476.1; PID:551901  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994  
 C:Superfamily: Escherichia coli ribosomal protein S7  
 C:Keywords: protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 KS 4  
 DB 1  
 1 KS 4

RESULT 50  
 S30496  
 ribosomal protein S7 - Mycobacterium intracellulare (fragment)  
 C:Species: Mycobacterium intracellulare  
 C:Date: 10-Feb-1993 #sequence\_revision 13-Feb-1993 #text\_change 13-Feb-1993  
 C:Accession: S30496  
 R:Hair, J.; Kouse, D.; Morris, S.  
 Nucleic Acids Res. 21: 1039, 1993  
 A:Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intracellulare  
 A:Reference number: S3537; MUID:9197130; PMID:845117  
 A:Accession: S3538  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-9 <NA>  
 A:Cross-references: EMBL:108171; NID:q149994; PIDN:AAA5476.1; PID:551901  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994  
 C:Superfamily: Escherichia coli ribosomal protein S7  
 C:Keywords: protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 RK 4  
 DB 1  
 4 RK 5

Search and Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

GenCore version: 5.1.5  
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# OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 6.25 seconds  
(without alignments)  
82.767 Million cell updates/sec

Title: US-09-787-443-22

Perfect score: 11

Sequence: 1 AKSRDWTAK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7.7

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	3	27.3	8	1	LPMS-STAPP	P21211 staphylococ
2	3	27.3	10	1	ARKH-LOCMI	P81626 locusta miq
3	3	27.3	10	1	GS09-BACSU	P80243 bacillus su
4	3	27.3	11	1	UYB2-YEAST	P99313 saccharomyc
5	3	27.3	13	1	NEUT_CAVPO	P12560 cavia porce
6	3	27.3	13	1	RS19-ASHYP	Q44592 ash yellow
7	3	27.3	13	1	YPE2-LACLC	P42021 lactococcus
8	3	27.3	14	1	HGYA-MEGCR	Q10583 megathura c
9	3	27.3	15	1	ACEA-ACICA	P24467 acinetobact
10	3	27.3	15	1	RS20-BACST	P59681 bacillus st
11	3	27.3	15	1	TAL-TREBR	P46070 tremella br
12	2	18.2	8	1	ACT_THUAL	P18691 thannus alb
13	2	18.2	8	1	ACT_CARMA	P60709 carcinus ma
14	2	18.2	8	1	AL12-CARMA	P61915 carcinus ma
15	2	18.2	8	1	AL18-CARMA	P61821 carcinus ma
16	2	18.2	8	1	ALL3-CYDPO	P62154 cydia pomon
17	2	18.2	8	1	ALL4-CYDPO	P62155 cydia pomon
18	2	18.2	8	1	ALL5-CYDPO	P62156 cydia pomon
19	2	18.2	8	1	RS1-FRWCH	P37895 erwinia chi
20	2	18.2	8	1	RS7-MYCI1	P34564 mycobacteri
21	2	18.2	8	1	UC26-MAI2E	P60632 zea mays (m
22	2	18.2	9	1	FARA-CALVO	P41865 calliphora
23	2	18.2	9	1	IPYR-RHOVI	P62992 rhodospiride
24	2	18.2	9	1	LPAC-STAAU	P16984 staphylococ
25	2	18.2	9	1	NEF-HV12B	P12481 human immun
26	2	18.2	9	1	NEUX-HUMAN	P64277 homo sapien
27	2	18.2	9	1	PPK1-PERAM	P82693 periphaneta
28	2	18.2	9	1	SAMP-MUSCA	P15095 mustelus ca
29	2	18.2	9	1	THYF-PIG	P31255 sus scrofa
30	2	18.2	9	1	TKCL-CALVO	P41517 calliphora
31	2	18.2	9	1	ULAK-MOUSE	P96031 mus muscu
32	2	18.2	10	1	AL19-CARMA	P81822 carcinus ma
33	2	18.2	10	1	CATB-SHEEP	P83205 ovnis aries

34	2	18.2	10	1	OXK2-KAKLI	P60396 ovis aries
35	2	18.2	10	1	OXK2-SHEEP	P60397 ovis aries
36	2	18.2	10	1	ETBA-PRST1	P14577 ceratopithec
37	2	18.2	10	1	MALE-KLEPN	Q65514 kladosiphon
38	2	18.2	10	1	NE40-TRBAT	P55962 nicotiana gl
39	2	18.2	10	1	SYK2-BEVIN	P82923 bos taurus
40	2	18.2	10	1	SYK2-TAMJP	Q46454 caprylobact
41	2	18.2	10	1	ETMK-RANLE	P56923 rana tempor
42	2	18.2	10	1	ETMK-RANPA	P22689 rana tempor
43	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
44	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
45	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
46	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
47	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
48	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
49	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
50	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
51	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
52	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
53	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
54	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
55	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
56	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
57	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
58	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
59	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
60	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
61	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
62	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
63	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
64	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
65	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
66	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
67	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
68	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
69	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
70	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
71	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
72	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
73	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
74	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
75	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
76	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
77	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
78	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
79	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
80	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
81	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
82	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
83	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
84	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
85	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
86	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
87	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
88	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
89	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
90	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
91	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
92	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
93	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
94	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
95	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
96	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
97	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
98	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
99	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
100	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
101	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
102	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
103	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
104	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
105	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa
106	2	18.2	10	1	ETMK-ETG	P02122 sus scrofa







Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9  
111  
Db 1 MTA 3

## RESULT 2

ID AKHX\_LOCM1 STANDARD: PRT: 10 AA.  
AC P81626;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Peptide hormone.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN 11;  
RP SEQUENCE.  
RC Tissue-Corpora cardiaca;  
RA Siebert K.J.;  
RL Submitted (DEC-1998) to the SWISS-PRCT data bank.  
CC -!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LIGAND  
INTERMEDIARY METABOLISM; BEHAVIOR AND/OR DEVELOPMENT.  
CC -!- SIMILARITY: BELONGS TO THE AKH / RHCH / RHCH FAMILY.  
DR InterPro: IPR002047; AKH.  
KW PROSITE: PS00256; AKH; 1.  
DR Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION  
SQ SEQUENCE 10 AA; 1222 MW; 81BFF67A8415B9D1 CRC64;

Query Match 27.38; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
111  
Db 5 SRD 7

## RESULT 3

ID GS09\_BACSU STANDARD: PRT: 10 AA.  
AC P80243;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE General stress protein 9 (GSP9) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN 11;  
RP SEQUENCE.  
RC STRAIN=168 / 1S58;  
RX MEDLINE=94282319; PubMed=8012595;  
RA Voelker U., Engelmann S., Maul B., Riechdorf S., Voelker A.,  
RA Schmid R., Mech H., Hecker M.;  
RT \*Analysis of the induction of general stress proteins of Bacillus subtilis.\*;  
RL Microbiology 140:741-752(1994).  
CC -!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE  
LIMITATION AND OXYGEN LIMITATION.  
CC -!- CAUTION: Could not be found in the genome of B. subtilis 168.  
KW Heat shock.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1168 MW; 99766442D5A2C05A CRC64;

Query Match 27.38; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 4  
111  
Db 1 SRD 4

## RESULT 4

ID UXP2\_YEAST STANDARD: PRT: 11 AA.  
AC P99013;  
DT 01-NOV-1996 (Rel. 37, Created)  
DT 01-NOV-1996 (Rel. 37, Last sequence update)  
DT 01-NOV-1996 (Rel. 37, Last annotation update)  
DE Unknown protein from yeast (baker's yeast).  
OS Saccharomyces cerevisiae (baker's yeast).  
OC Eukaryota; Eumycota; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycotina; Saccharomycetes; Saccharomycotina; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN 11;  
RP SEQUENCE.  
RC STRAIN X218-1A;  
RA Siebert K.J.;  
RL Submitted (AUG-1996) to the SWISS-PRCT data bank.  
CC -!- MISCELLANEOUS: IN THE 3D-STRUCTURE DETERMINED BY X-RAY  
CRYSTALLOGRAPHY, PROTEIN HAS 6.3 Å RES. MW 12.4 KDa  
DR SWISS-PROT: P99013; YEAST.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1428 MW; 10460210EDF421A CRC64;

Query Match 27.38; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APR 3  
111  
Db 7 APR 4

## RESULT 5

ID NEUT\_GAVPO STANDARD: PRT: 15 AA.  
AC P42566;  
DT 01-NOV-1994 (Rel. 27, Created)  
DT 01-NOV-1994 (Rel. 27, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neurotensin (NT).  
GN NT.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Muridae; Caviidae; Cavia.  
OX NCBI\_TaxID=10143;  
RN 11;  
RP SEQUENCE.  
RC TISSUE: Small intestine.  
RX MEDLINE=86244785; PubMed=387996;  
RA Shaw C., Thompson C., Campbell M.;  
RT \*Isolation and characterization of the human pro-neurotensin gene.  
RL FEBS Lett 222:187-192(1988).  
CC -!- FUNCTION: Small intestine secreted and peptide.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: NEUT-RES IN THE NEUROTENSIN FAMILY.  
DR PIR: A53606; A44408  
KW Vasopressin; Peptide hormone; Neuropeptide.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 15 AA; 1740 MW; 4983434404115B5 CRC64;

Query Match 27.38; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 5

```

DB      6 KSR 8
RESULT 6
RS19_ASHYP STANDARD; PRT: 13 AA.
AC Q44592;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RPS19
OS Ash yellows phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=35780;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis K.F., Kingsbury D.T.;
RT Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.*;
RL J. Bacteriol. 176:5244-5254(1994).
CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announcements/
CC or send an email to license@sib-sib.ch).
CC
DR HAMAP: MF_00531; ; 1.
DR InterPro: IPR002222; Ribosomal_S19.
DR PROSITE: PS00423; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1433 MW; CCAU10B84605D CRQ4;

Query Match 27.3%; Score 3; DH 1; Length 13;
Best local Similarity 100.0%; Pred. No. 9,4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AIK 11
DB 6 AIK 8

RESULT 7
YPE2_LACLC STANDARD; PRT: 13 AA.
AC P42021;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PEPT 5' region (ORF2) (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245610; PubMed=8188586;
RA Hlerau I., Haandrikman A.J., Veltrop O., Tan P.S.T., Leenhouts K.L.,
RA Konings W.N., Venema G., Kok J.;
RT "Tripeptidase gene (pept) of Lactococcus lactis: molecular cloning
RT and nucleotide sequencing of pept and construction of a chromosomal
RT deletion mutant.*;
RL J. Bacteriol. 176:2854-2861(1994).

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CC or send an email to license@sib-sib.ch).
CC
DR EMBL: L2599; AAAZ; ; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1662 MW; 214592 CRQ64;

Query Match 27.3%; Score 3; DH 1; Length 14;
Best local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAI 4
DB 2 TAI 4

RESULT 8
RYA_MMRK STANDARD; PRT: 14 AA.
AC Q3584;
FT 01-OCT-1995 (Rel. 41, Created)
IT 01-OCT-1995 (Rel. 41, Last sequence update)
IT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemovanin A chain (R1A) (Fragment).
DE Medial heme chain of a hemoerythrin subunit.
DE F. karysti; Medial heme chain of a hemoerythrin subunit.
DE Venkatesh Reddy, S. and Reddy, P. J. J. Biochem. Biophys. Res. Commun.
DE 214:104-109(1995).
CX NBL_TaxID=54429;
PX [1]
RP SEQUENCE.
RX MEDLINE=9623070; PubMed=84708;
RA Swedlow P.L., Huet B.F., Lee P.; Reddy P. J. J. Mol. Cell. Biochem.
RA "Keyhole limpet hemocyanin: structural and functional
RA characterization of a hemoerythrin subunit and multimers.*;
RA Characterization of a hemoerythrin subunit and multimers.*;
RA Comp. Biochem. Physiol. 114:525-531(1996).
CC -!- FUNCTION: HEMOVANIN A CHAIN IS A HEMOPHYRIN-CONTAINING OXYGEN CARRIERS
CC -!- CARRIERS BELONGS TO THE HEMOPHYRIN-CONTAINING OXYGEN CARRIERS AND
CC -!- CARRIERS ARE HEMOPHYRINS.
CC -!- SOURCE: F. KARISTI; TISSUE: HEMOCYTES.
CC -!- SUBCELLULAR LOCATION: Cytoplasm, Lysol.
CC -!- TISSUE SPECIFICITY: Hemocytoblasts.
CC -!- RATIONALE: This is a hemoerythrin subunit used classically as a control
CC protein for hemoerythrin and hemoerythrin in human erythrocytes and for
CC immunotherapy of thalassaemia.
CC -!- SIMILARITY: BELONGS TO THE HEMOPHYRIN-CONTAINING OXYGEN CARRIERS
CC -!- SUBFAMILY.
DR InterPro: IPR000960; Hemovanin.
DR PROSITE: PS00202; HEMOVANIN_A; PARTIAL.
DR PROSITE: PS00212; HEMOVANIN_A; PARTIAL.
KW Oxygen transport; hemoerythrin; hemoerythrin subunit.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1662 MW; 214592 CRQ64;

Query Match 27.3%; Score 3; DH 1; Length 14;
Best local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLS 4
DB 5 PLS 7

RESULT 9
RYA_A10CA STANDARD; PRT: 15 AA.
TX AKA_A10CA

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ACT_CARMA          STANDARD:          PRT:          8 AA.
ID ACT_CARMA
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinidae.
OX NCBI_TaxID:6759;
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjean P., Wolsten S.,
RA Baghdassarian D.:
RT "A transaldolase. An enzyme implicated in crab stress response".
RL Endocrine 5:23-32(1996).
CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UNIQUELY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DIFFERENTIAL IS 4 TIMES MORE IN L2
CC 6.8, ITS MW IS: 46 kDa.
CC -1- SIMILARITY: Belongs to the actin family.
CC InterPro: IPR004001; Actin.
DR InterPro: IPR004000; Actin-like.
DR PROSITE: PS00406; ACTINS.1; PARTIAL.
DR PROSITE: PS00442; ACTINS.2; PARTIAL.
DR PROSITE: PS01192; ACTINS-ACT-LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA: 976 MW: 14240058320AAENA CKEGA.

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1; Gap 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RK 3
   1
DB 7 RK 8
   1
   1

RESULT 14
ID AL12_CARMA          STANDARD:          PRT:          8 AA.
AC P81815;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinastatin 12.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinidae.
OX NCBI_TaxID:6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=9812119; PubMed=9461295;
RA Devo H., Johnsen A.H., Maestro J. L., Scott A.V., Jones P.J.,
RA Thorpe A.:
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas".
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 8 AA: 913 MW: 672879QDCR569AH7 CPEV4;

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1; Gap 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

ACT_CARMA          STANDARD:          PRT:          8 AA.
ID ACT_CARMA
AC P82154;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydlistatin 3.
OS Cydia pomonella (Hummel) (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Eulophoptera; Lepidoptera; Glossata; Ditystia;
OC Tortricidae; Tortricinae; Tortricini; Cydia.
OX NCBI_TaxID:6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Intestine;
RA Devo H., Johnsen A.H., Maestro J. L., Scott A.V., Winstanley J.,
RA Thorpe A.:
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas".
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 8 AA: 913 MW: 672879QDCR569AH7 CPEV4;

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1; Gap 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RK 3
   1
DB 7 RK 8
   1
   1

RESULT 14
ID AL12_CARMA          STANDARD:          PRT:          8 AA.
AC P82154;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydlistatin 3.
OS Cydia pomonella (Hummel) (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Eulophoptera; Lepidoptera; Glossata; Ditystia;
OC Tortricidae; Tortricinae; Tortricini; Cydia.
OX NCBI_TaxID:6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Intestine;
RA Devo H., Johnsen A.H., Maestro J. L., Scott A.V., Winstanley J.,
RA Thorpe A.:
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas".
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 8 AA: 913 MW: 672879QDCR569AH7 CPEV4;

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1; Gap 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 4 SR 5  
 DB 1 SR 2

## RESULT 17

ALL4\_CYPDO  
 ID ALL4\_CYPDO STANDARD: PRT: 8 AA  
 AC P82155:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 4.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia.  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Kinstinely D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RC "Lepidopteran peptides of the allatostatin superfamily."  
 CC Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 910 MW: 922879D5AB47749D C6064;

Query Match 18.2%; Score 2; 55 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

OY 1 AR 2  
 DB 1 AR 2

## RESULT 18

ALL5\_CYPDO  
 ID ALL5\_CYPDO STANDARD: PRT: 8 AA  
 AC P82156:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 5.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia.  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Kinstinely D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RC "Lepidopteran peptides of the allatostatin superfamily."  
 CC Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 898 MW: 922879CAB858649D C6064;

Query Match 18.2%; Score 2; 54 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

OY 1 AR 2  
 DB 1

OY 1 SR 2

## RESULT 19

RS7\_EFWCH  
 ID RS7\_EFWCH STANDARD: PRT: 8 AA  
 AC P47065:  
 DT 31-DEC-1994 (Rel. 39, Created)  
 DT 31-DEC-1994 (Rel. 39, Last sequence update)  
 DT 31-DEC-1994 (Rel. 39, Last annotation update)  
 DE RS7\_EFWCH.  
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae.  
 OC Enterobacteriaceae; Enterobacteriaceae; Enterobacteriaceae.  
 OX NCBI\_TaxID=1225;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Whole Cell;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Kinstinely D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RC "Lepidopteran peptides of the allatostatin superfamily."  
 CC Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 857 MW: 922879D5AB47749D C6064;

Query Match 18.2%; Score 2; 55 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

OY 1 SR 2  
 DB 1

## RESULT 20

RS7\_MWCH  
 ID RS7\_MWCH STANDARD: PRT: 8 AA  
 AC P47066:  
 DT 31-DEC-1994 (Rel. 39, Created)  
 DT 31-DEC-1994 (Rel. 39, Last sequence update)  
 DT 31-DEC-1994 (Rel. 39, Last annotation update)  
 DE RS7\_MWCH.  
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae.  
 OC Enterobacteriaceae; Enterobacteriaceae; Enterobacteriaceae.  
 OX NCBI\_TaxID=1225;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Whole Cell;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Kinstinely D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RC "Lepidopteran peptides of the allatostatin superfamily."  
 CC Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 857 MW: 922879D5AB47749D C6064;

OY 1 SR 2  
 DB 1



Db 5 AI 6

## RESULT 24

```

ID LPCA-STAAU STANDARD; PRT; 9 AA.
AC P36884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
DE Staphylococcus aureus, and
OS Streptococcus agalactiae.
OG Plasmid pSCS6, Plasmid pSCS7, plasmid pUB112, and plasmid pIP501.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus; STRAIN-436; PLASMID-pSCS7;
RX MEDLINE-92027652; PubMed-1929326;
RA Schwarz S., Cardoso M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
aureus."
RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus; PLASMID-pUB112;
RX MEDLINE-86081739; PubMed-3865770;
RA Brueckner R., Matura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
of the Staphylococcus aureus plasmid pUB112."
RL EMBO J. 4:2295-2300(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-S.agalactiae; PLASMID-pIP501;
RX MEDLINE-93096867; PubMed-1461942;
RA Trieu-Chot P., de Cespedes G., Horiad T.;
RT the streptococcal plasmid pIP501."
RL Plasmid 28:272-276(1992).
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CC -----
DR EMBL: M58515; AAA26612.1;
DR EMBL: M58516; AAA16528.1;
DR EMBL: X02872; CAA26630.1;
DR EMBL: X60827; CAA43217.1;
DR EMBL: X65462; CAA46454.1;
DR PIR: B24362; B24362;
DR PIR: S30494; S30494;
KW Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 9 AA: 1074 MW: 509CAB5AAB05B333 CRC64;

```

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4  
 11  
 DE 3 KS 4

## RESULT 25

```

NEF_HV128 STANDARD; PRT; 9 AA.
ID P12441;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 43, Last annotation update)
DE Negative factor (p12441) (27 kDa protein) (short) (fragment)
GN NEF
OS Human immunodeficiency virus type 1 (Z 84 isolate) (HIV 1);
OC VIRUSES; Retrovira; Retroviridae; Lentivirinae;
OX NCBI_TaxID=11681;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-86287241; PubMed-373737;
RA Young J., Gajdosik R., Bock R., Zlatos E., Ward S.H.H.;
RA Gajdosik R.;
RT "Nucleotide sequence and phylogeny of a new Zlatos E.
isolate HIV 1."
RL AIDS Res. Hum. Retroviruses 4:155-158(1988).
CC "The HIV-1 NEF has tyrosine GTP binding and autophosphorylation
activities. It seems to down-regulate the CD4(14) antigen."
CX 1 MISCELLANEOUS THE Z 84 ISOLATE WAS TAKEN FROM A 54 YEAR OLD
ZALREAN MALE.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J04663; AAA44663.1;
DR EMBL: J03653; NEFSV1;
KW AIDS; Myristic GTP binding
FT Lipid 2 9
FT N-TER 2 9
SQ SEQUENCE 9 AA: 967 MW: 107622AA02A02802CRC64.

```

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4  
 11  
 DE 3 KS 4

## RESULT 26

```

NEEX_HUMAN STANDARD; PRT; 9 AA.
ID P04277;
DT 21-MAR-1987 (Rel. 11, Created)
DT 21-MAR-1987 (Rel. 11, Last sequence update)
DT 29-FEB-2003 (Rel. 43, Last annotation update)
DE Neurotensin-related peptide (NRP) (kinetins)
OS Homo sapiens (Human);
OS Eus taurus (Bovine);
OS Cytotrichus canaliculus (Rabbit);
OC Metazoa; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleostomi; Homiinae; Homiidae; B270;
OX NCBI_TaxID=9606, 9606, 9606;
RN [1]
RP SEQUENCE
RC SPECIES-Human;
RX MEDLINE-86242180; PubMed-602452;
RA Moyard M.H., Kobayashi K., Chen S.F., Lee T.D., Reeve L.R.;

```



KW Pyroglutamate carboxylic acid, pyroglutamate carboxylic acid  
 FT MOD\_RES 1 1  
 SQ SEQUENCE 9 AA: 876 MW: 65008878665640 (65008878665640)

Query Match 18.2% Score 2: 18.2% Length 42  
 Best Local Similarity 100.0% Pred. No. 1, 40-05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 KS 4  
 II  
 Db 3 KS 4

## RESULT 0)

TRC1\_CALVO  
 ID TRC1\_CALVO STANDARD: PRT: 9 AA  
 AC P41517  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Callitachykinin I.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Proctoptera.  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscivora; Muscidae; Calliphoridae; Calliphora  
 CC NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;  
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nardone P.,  
 RA Naessle D.R.  
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
 RT the blowfly Calliphora vomitoria, that have resemblances to  
 RT tachykinins."  
 RL Peptides 15:761-768(1994).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA: 981 MW: 24170868590017 (24170868590017)

Query Match 18.2% Score 2: 18.2% Length 9;  
 Best Local Similarity 100.0% Pred. No. 1, 40-05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 TA 9  
 II  
 Db 3 TA 4

## RESULT 31

ULAK\_MOUSE  
 ID ULAK\_MOUSE STANDARD: PRT: 9 AA  
 AC P99031;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Unknown protein from 20-page of liver tissue (Spot 21, 01410)  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Van Dijk  
 RA Hoogland C., Appel R.D., Binz P.A., Hochstrasser G.F.,  
 RA Coathorne M.;  
 RL Submitted (AUG-1998) TO THE SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.

KW Pyroglutamate carboxylic acid, pyroglutamate carboxylic acid  
 FT MOD\_RES 1 1  
 SQ SEQUENCE 9 AA: 876 MW: 65008878665640 (65008878665640)

Query Match 18.2% Score 2: 18.2% Length 42  
 Best Local Similarity 100.0% Pred. No. 1, 40-05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 KS 4  
 II  
 Db 3 KS 4

## RESULT 0)

TRC1\_CALVO  
 ID TRC1\_CALVO STANDARD: PRT: 9 AA  
 AC P41517  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Callitachykinin I.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Proctoptera.  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscivora; Muscidae; Calliphoridae; Calliphora  
 CC NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;  
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nardone P.,  
 RA Naessle D.R.  
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
 RT the blowfly Calliphora vomitoria, that have resemblances to  
 RT tachykinins."  
 RL Peptides 15:761-768(1994).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA: 981 MW: 24170868590017 (24170868590017)

Query Match 18.2% Score 2: 18.2% Length 9;  
 Best Local Similarity 100.0% Pred. No. 1, 40-05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 TA 9  
 II  
 Db 3 TA 4

## RESULT 31

ULAK\_MOUSE  
 ID ULAK\_MOUSE STANDARD: PRT: 9 AA  
 AC P99031;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Unknown protein from 20-page of liver tissue (Spot 21, 01410)  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Van Dijk  
 RA Hoogland C., Appel R.D., Binz P.A., Hochstrasser G.F.,  
 RA Coathorne M.;  
 RL Submitted (AUG-1998) TO THE SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.

CC -1- FUNCTION: Thiol protease which is believed to participate in  
 CC intracellular degradation and turnover of proteins. Has also been  
 CC implicated in tumor invasion and metastasis.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds. Preferentially cleaves -Ar-Arg-Xaa bonds in  
 CC small molecule substrates (thus differing from cathepsin B). In  
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase  
 CC activity, liberating C-terminal dipeptides.  
 CC -1- SUBUNIT: Dimer of a heavy chain and a light chain cross linked  
 CC by a disulfide bond (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 DR InterPro: IPR000169; SHprot\_arcite.  
 DR PROSITE: PS00640; THIOL\_PROTEASE\_ASN; PARTIAL.  
 DR PROSITE: PS00139; THIOL\_PROTEASE\_CYS; PARTIAL.  
 DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON\_TER 10  
 FT 10  
 SQ SEQUENCE 10 AA; 1177 MW; 87957800AA05PA (RefSeq).

Query Match 18.2% Score 24.18 (11 Length 10)  
 Best Local Similarity 100.0% Pred. No. 9.76 (10)  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 1 AR 2  
 II  
 Db 7 AR 8

RESULT 34  
 COXQ\_RABIT  
 ID COXQ\_RABIT STANDARD: PRT; 10 AA.  
 AC P80316;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Viii-liver/heart (E01945.1)  
 DE (Fragment).  
 GN COX8H.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RA Freund R., Kadenbach B.;  
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED CYTOCHROME  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) + 4 H(2)O ->  
 CC c + 2 H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON\_TER 10  
 FT 10  
 SQ SEQUENCE 10 AA; 1027 MW; 20325C3401874336 (RefSeq).

Query Match 18.2% Score 24.18 (11 Length 10)  
 Best Local Similarity 100.0% Pred. No. 9.76 (10)  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 1 AR 2  
 II  
 Db 6 AR 7

RESULT 35  
 COXQ\_SHEEP  
 ID COXQ\_SHEEP STANDARD: PRT; 10 AA.  
 AC P80317;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

II 26-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Viii-liver/heart (E01945.1)  
 DE (Fragment).  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds. Preferentially cleaves -Ar-Arg-Xaa bonds in  
 CC small molecule substrates (thus differing from cathepsin B). In  
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase  
 CC activity, liberating C-terminal dipeptides.  
 CC -1- SUBUNIT: Dimer of a heavy chain and a light chain cross linked  
 CC by a disulfide bond (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 DR InterPro: IPR000169; SHprot\_arcite.  
 DR PROSITE: PS00640; THIOL\_PROTEASE\_ASN; PARTIAL.  
 DR PROSITE: PS00139; THIOL\_PROTEASE\_CYS; PARTIAL.  
 DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON\_TER 10  
 FT 10  
 SQ SEQUENCE 10 AA; 1177 MW; 87957800AA05PA (RefSeq).

Query Match 18.2% Score 24.18 (11 Length 10)  
 Best Local Similarity 100.0% Pred. No. 9.76 (10)  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 1 AR 2  
 II  
 Db 7 AR 8

RESULT 36  
 COXQ\_RABIT  
 ID COXQ\_RABIT STANDARD: PRT; 10 AA.  
 AC P80316;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Viii-liver/heart (E01945.1)  
 DE (Fragment).  
 GN COX8H.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RA Freund R., Kadenbach B.;  
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED CYTOCHROME  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) + 4 H(2)O ->  
 CC c + 2 H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON\_TER 10  
 FT 10  
 SQ SEQUENCE 10 AA; 1027 MW; 20325C3401874336 (RefSeq).

Query Match 18.2% Score 24.18 (11 Length 10)  
 Best Local Similarity 100.0% Pred. No. 9.76 (10)  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 1 AR 2  
 II  
 Db 6 AR 7







TRNK\_PIG  
ID TRNK\_PIG STANDARD: PRT: 10 AA.  
AC P01292;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Neurokinin B (NKB) (Neuromedin K)  
GN TAC3 OR NKNB.  
OS Sus scrofa (Pig), and  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823, 8406;  
RN [1]  
RN [2]  
RP SEQUENCE.  
RC SPECIES-Pig; TISSUE-Spinal cord;  
RX MEDLINE=83282812; PubMed=6576785;  
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;  
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine  
spinal cord.";  
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).  
RN [2]  
RP SEQUENCE.  
RC SPECIES-R. ridibunda; TISSUE=Brain;  
RX MEDLINE=92044543; PubMed=1658233;  
RA O'Harte F., Purcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;  
RT "Ranakinin: a novel NKT tachykinin receptor agonist isolated with  
neurokinin B from the brain of the frog Rana ridibunda.";  
RL J. Neurochem. 57:2086-2091(1991).  
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS.  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR: A01560; SPPOGN.  
DR InterPro: IPR002040; Tachykinin.  
DR PROSITE: PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
FT SEQUENCE 10 AA: 1211 MW: 41676.649 CAAI CR064;  
SQ SEQUENCE 10 AA: 1211 MW: 41676.649 CAAI CR064;

Query Match 18.2% Score 2; DB 1; Length 10  
Best Local Similarity 100.0%; Pred. No. 9.7e-03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 DM 7  
DB 1 DM 2

RESULT 44  
TKUL\_UREUN  
ID TKUL\_UREUN STANDARD: PRT: 10 AA.  
AC P40751;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Urechis tachykinin 1.  
OS Urechis unicinctus.  
OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechididae; Urechis.  
OX NCBI\_TaxID=6432;  
RN [1]  
RN [2]  
RP SEQUENCE AND SYNTHESIS.  
RC TISSUE-Ventral nerve cord;  
RX MEDLINE=93236558; PubMed=8476410;  
RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
RT "Two novel tachykinin-related neuropeptides in the echinoid worm,  
Urechis unicinctus.";  
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL  
CC MUSCLE OF THE ANIMAL.  
CC -!- SUBCELLULAR LOCATION: Secreted.

QY 1 SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
FT SEQUENCE 10 AA: 1173 MW: 41676.649 CAAI CR064;  
SQ SEQUENCE 10 AA: 1173 MW: 41676.649 CAAI CR064;  
Query Match 18.2% Score 2; DB 1; Length 10  
Best Local Similarity 100.0%; Pred. No. 9.7e-03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 SP 5  
DB 1  
DB 9 SP 10  
RESULT 45  
TKU2\_UREUN  
ID TKU2\_UREUN STANDARD: PRT: 10 AA.  
AC P40752;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Urechis tachykinin 1.  
OS Urechis unicinctus.  
OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechididae; Urechis.  
OX NCBI\_TaxID=6432;  
RN [1]  
RN [2]  
RP SEQUENCE AND SYNTHESIS.  
RC TISSUE-Ventral nerve cord;  
RX MEDLINE=93236558; PubMed=8476410;  
RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
RT "Two novel tachykinin-related neuropeptides in the echinoid worm,  
Urechis unicinctus.";  
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL  
CC MUSCLE OF THE ANIMAL.  
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
FT SEQUENCE 10 AA: 1174 MW: 41676.649 CAAI CR064;  
SQ SEQUENCE 10 AA: 1174 MW: 41676.649 CAAI CR064;  
Query Match 18.2% Score 2; DB 1; Length 10  
Best Local Similarity 100.0%; Pred. No. 9.7e-03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AP 2  
DB 1  
DB 9 AP 10  
RESULT 46  
UEAF\_HUMAN  
ID UEAF\_HUMAN STANDARD: PRT: 10 AA.  
AC P40945;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein in the plasma (Spec. 45) (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Hominidae; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092343; PubMed=140069;  
RA Hughes G., Fritschy S., Fritschy N., Rayner F., Pasquini C.,  
RA Sacher J., James R., Tissot J. L., Bjellqvist B.,  
RA Hochstrasser S.;  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 20 GEI THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 7.2, ILS MW IS: 15 kDa.



RA Graumann P.L., Schmid R., Marahiel M.A.:  
 RL Submitted (Oct-1997) to the SWISS-PROT data bank.  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN-168 / JH642;  
 RX MEDLINE:96345629; PubMed:8755892;  
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.:  
 RT "Cold shock stress-induced proteins in *Bacillus subtilis*."  
 RL J. Bacteriol. 178:4611-4619(1996).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- INDUCTION: In response to low temperature.  
 CC -!- CAUTION: Could not be found in the genome of *B. subtilis* 168.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1360 MW; 15F6GCEE61227330 CR:64;

Query Match: 18.2%; Score 2; DB L: length 11;  
 Best local Similarity 100.0%; Pred. No. 10:04;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0

QY 10 IK 11  
 Db 4 IK 5

Search completed: September 30, 2003, 10:26:11  
 Job time : 7.25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 41.6667 seconds  
(without alignments) 89.639 Million cell updates/sec

Title: US-09-787-443-22

Perfect score: 11

Sequence: 1 ARKSRDMTAK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :

SPRMBL23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_ordanelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	12	8	P82164
2	3	27.3	9	2	P81363
3	3	27.3	9	4	Q9UKJ6
4	3	27.3	9	8	Q9UKJ6
5	3	27.3	9	13	Q9IA14
6	3	27.3	10	10	P82434
7	3	27.3	10	15	Q8UT83
8	3	27.3	11	2	Q47602
9	3	27.3	12	2	Q46039
10	3	27.3	12	2	Q93208
11	3	27.3	12	2	Q52112
12	3	27.3	12	2	Q8GMV1
13	3	27.3	12	2	Q8GMV8
14	3	27.3	12	2	Q8GMV2
15	3	27.3	12	5	Q8T0Y6
16	3	27.3	12	5	Q26429

17	3	27.3	12	1	P82245
18	3	27.3	12	1	P82245
19	3	27.3	12	1	Q8UKJ6
20	3	27.3	12	1	Q8UKJ6
21	3	27.3	12	1	Q8UKJ6
22	3	27.3	12	1	Q8UKJ6
23	3	27.3	12	1	Q8UKJ6
24	3	27.3	12	1	Q8UKJ6
25	3	27.3	12	1	Q8UKJ6
26	3	27.3	12	1	Q8UKJ6
27	3	27.3	12	1	Q8UKJ6
28	3	27.3	12	1	Q8UKJ6
29	3	27.3	12	1	Q8UKJ6
30	3	27.3	12	1	Q8UKJ6
31	3	27.3	12	1	Q8UKJ6
32	3	27.3	12	1	Q8UKJ6
33	3	27.3	12	1	Q8UKJ6
34	3	27.3	12	1	Q8UKJ6
35	3	27.3	12	1	Q8UKJ6
36	3	27.3	12	1	Q8UKJ6
37	3	27.3	12	1	Q8UKJ6
38	3	27.3	12	1	Q8UKJ6
39	3	27.3	12	1	Q8UKJ6
40	3	27.3	12	1	Q8UKJ6
41	3	27.3	12	1	Q8UKJ6
42	3	27.3	12	1	Q8UKJ6
43	3	27.3	12	1	Q8UKJ6
44	3	27.3	12	1	Q8UKJ6
45	3	27.3	12	1	Q8UKJ6
46	3	27.3	12	1	Q8UKJ6
47	3	27.3	12	1	Q8UKJ6
48	3	27.3	12	1	Q8UKJ6
49	3	27.3	12	1	Q8UKJ6
50	3	27.3	12	1	Q8UKJ6
51	3	27.3	12	1	Q8UKJ6
52	3	27.3	12	1	Q8UKJ6
53	3	27.3	12	1	Q8UKJ6
54	3	27.3	12	1	Q8UKJ6
55	3	27.3	12	1	Q8UKJ6
56	3	27.3	12	1	Q8UKJ6
57	3	27.3	12	1	Q8UKJ6
58	3	27.3	12	1	Q8UKJ6
59	3	27.3	12	1	Q8UKJ6
60	3	27.3	12	1	Q8UKJ6
61	3	27.3	12	1	Q8UKJ6
62	3	27.3	12	1	Q8UKJ6
63	3	27.3	12	1	Q8UKJ6
64	3	27.3	12	1	Q8UKJ6
65	3	27.3	12	1	Q8UKJ6
66	3	27.3	12	1	Q8UKJ6
67	3	27.3	12	1	Q8UKJ6
68	3	27.3	12	1	Q8UKJ6
69	3	27.3	12	1	Q8UKJ6
70	3	27.3	12	1	Q8UKJ6
71	3	27.3	12	1	Q8UKJ6
72	3	27.3	12	1	Q8UKJ6
73	3	27.3	12	1	Q8UKJ6
74	3	27.3	12	1	Q8UKJ6
75	3	27.3	12	1	Q8UKJ6
76	3	27.3	12	1	Q8UKJ6
77	3	27.3	12	1	Q8UKJ6
78	3	27.3	12	1	Q8UKJ6
79	3	27.3	12	1	Q8UKJ6
80	3	27.3	12	1	Q8UKJ6
81	3	27.3	12	1	Q8UKJ6
82	3	27.3	12	1	Q8UKJ6
83	3	27.3	12	1	Q8UKJ6
84	3	27.3	12	1	Q8UKJ6
85	3	27.3	12	1	Q8UKJ6
86	3	27.3	12	1	Q8UKJ6
87	3	27.3	12	1	Q8UKJ6
88	3	27.3	12	1	Q8UKJ6
89	3	27.3	12	1	Q8UKJ6

90	2	18.2	8	8	P92211	P92411: areqpyron c	164	2	18.2	1	8	18.2	Q8437 callosossa
91	2	18.2	8	8	P92428	P92428: peridictyon	164	2	18.2	1	8	18.2	Q84211: spirintha cl
92	2	18.2	8	8	P92386	P92386: hordeum mar	165	2	18.2	1	8	18.2	Q8437: bostrychia
93	2	18.2	8	8	P93959	P93959: hordeum ere	166	2	18.2	1	8	18.2	Q8437: varians 4a
94	2	18.2	8	8	P93985	P93985: aequilops ere	167	2	18.2	1	8	18.2	Q84211: spirintha cl
95	2	18.2	8	8	Q84V91	Q84V91: varians tim	168	2	18.2	1	8	18.2	Q84211: callosossa
96	2	18.2	8	8	Q84V99	Q84V99: locusta f 2	169	2	18.2	1	8	18.2	Q84V99: varians ncl
97	2	18.2	8	8	Q84V47	Q84V47: hydrastella	170	2	18.2	1	8	18.2	Q8437: bostrychia
98	2	18.2	8	8	Q84VE4	Q84VE4: varians mel	171	2	18.2	1	8	18.2	Q8437: asteromys
99	2	18.2	8	8	P92443	P92443: taeniatheru	172	2	18.2	1	8	18.2	Q84V18: varians ere
100	2	18.2	8	8	Q84VB2	Q84VB2: varians sal	174	2	18.2	1	8	18.2	Q84V12: libosipha x
101	2	18.2	8	8	P92391	P92391: heterantel	174	2	18.2	1	8	18.2	Q84V19: varians 4a
102	2	18.2	8	8	P93981	P93981: erithodum	176	2	18.2	1	8	18.2	Q84V6: bostrychia
103	2	18.2	8	8	Q84VF9	Q84VF9: varians ind	177	2	18.2	1	8	18.2	Q84V6: postpyra cl
104	2	18.2	8	8	P93992	P93992: australopyr	177	2	18.2	1	8	18.2	Q84V11: varians 4a
105	2	18.2	8	8	P92426	P92426: pseudoroegn	178	2	18.2	1	8	18.2	Q84V11: bostrychia
106	2	18.2	8	8	P92431	P92431: aequilops fa	179	2	18.2	1	8	18.2	Q84V6: callosossa
107	2	18.2	8	8	Q84VF3	Q84VF3: varians kel	181	2	18.2	1	8	18.2	Q84V6: varians 4a
108	2	18.2	8	8	Q84VA7	Q84VA7: varians sal	181	2	18.2	1	8	18.2	Q84V6: callosossa
109	2	18.2	8	8	Q84VB5	Q84VB5: varians sal	182	2	18.2	1	8	18.2	Q84V6: postpyra cl
110	2	18.2	8	8	P92422	P92422: psathyrosta	183	2	18.2	1	8	18.2	Q84V6: varians 4a
111	2	18.2	8	8	Q84VK4	Q84VK4: bacterioph	184	2	18.2	1	8	18.2	Q84V6: callosossa
112	2	18.2	8	8	Q84V19	Q84V19: bacterioph	185	2	18.2	1	8	18.2	Q84V6: hyphes sp
113	2	18.2	8	8	Q84VJ7	Q84VJ7: bacterioph	186	2	18.2	1	8	18.2	Q84V6: callosossa
114	2	18.2	8	8	Q84VJ5	Q84VJ5: bacterioph	187	2	18.2	1	8	18.2	Q84V6: postpyra cl
115	2	18.2	8	8	Q84VJ3	Q84VJ3: bacterioph	188	2	18.2	1	8	18.2	Q84V6: varians 4a
116	2	18.2	8	8	Q84VJ1	Q84VJ1: bacterioph	189	2	18.2	1	8	18.2	Q84V6: spirintha cl
117	2	18.2	8	8	Q84V19	Q84V19: bacterioph	190	2	18.2	1	8	18.2	Q84V6: spirintha cl
118	2	18.2	8	8	Q84V18	Q84V18: bacterioph	191	2	18.2	1	8	18.2	Q84V6: spirintha cl
119	2	18.2	8	8	Q84V16	Q84V16: bacterioph	192	2	18.2	1	8	18.2	Q84V6: spirintha cl
120	2	18.2	8	8	Q84V14	Q84V14: bacterioph	193	2	18.2	1	8	18.2	Q84V6: spirintha cl
121	2	18.2	8	8	Q84V13	Q84V13: bacterioph	194	2	18.2	1	8	18.2	Q84V6: spirintha cl
122	2	18.2	8	8	Q84V12	Q84V12: bacterioph	195	2	18.2	1	8	18.2	Q84V6: spirintha cl
123	2	18.2	8	8	Q84V6	Q84V6: bacterioph	196	2	18.2	1	8	18.2	Q84V6: spirintha cl
124	2	18.2	8	8	Q84V6	Q84V6: bacterioph	197	2	18.2	1	8	18.2	Q84V6: spirintha cl
125	2	18.2	8	8	Q84V6	Q84V6: bacterioph	198	2	18.2	1	8	18.2	Q84V6: spirintha cl
126	2	18.2	8	10	Q84V6	Q84V6: bacterioph	199	2	18.2	1	8	18.2	Q84V6: spirintha cl
127	2	18.2	8	10	Q84V6	Q84V6: bacterioph	200	2	18.2	1	8	18.2	Q84V6: spirintha cl
128	2	18.2	8	11	Q84V6	Q84V6: bacterioph	201	2	18.2	1	8	18.2	Q84V6: spirintha cl
129	2	18.2	8	11	Q84V6	Q84V6: bacterioph	202	2	18.2	1	8	18.2	Q84V6: spirintha cl
130	2	18.2	8	11	Q84V6	Q84V6: bacterioph	203	2	18.2	1	8	18.2	Q84V6: spirintha cl
131	2	18.2	8	12	Q84V6	Q84V6: bacterioph	204	2	18.2	1	8	18.2	Q84V6: spirintha cl
132	2	18.2	8	12	Q84V6	Q84V6: bacterioph	205	2	18.2	1	8	18.2	Q84V6: spirintha cl
133	2	18.2	8	12	Q84V6	Q84V6: bacterioph	206	2	18.2	1	8	18.2	Q84V6: spirintha cl
134	2	18.2	8	13	Q84V6	Q84V6: bacterioph	207	2	18.2	1	8	18.2	Q84V6: spirintha cl
135	2	18.2	9	1	Q50832	Q50832: metarococ	208	2	18.2	1	8	18.2	Q84V6: spirintha cl
136	2	18.2	9	2	Q84V6	Q84V6: bacterioph	209	2	18.2	1	8	18.2	Q84V6: spirintha cl
137	2	18.2	9	2	Q84V6	Q84V6: bacterioph	210	2	18.2	1	8	18.2	Q84V6: spirintha cl
138	2	18.2	9	2	Q84V6	Q84V6: bacterioph	211	2	18.2	1	8	18.2	Q84V6: spirintha cl
139	2	18.2	9	2	Q84V6	Q84V6: bacterioph	212	2	18.2	1	8	18.2	Q84V6: spirintha cl
140	2	18.2	9	2	Q84V6	Q84V6: bacterioph	213	2	18.2	1	8	18.2	Q84V6: spirintha cl
141	2	18.2	9	2	Q84V6	Q84V6: bacterioph	214	2	18.2	1	8	18.2	Q84V6: spirintha cl
142	2	18.2	9	2	Q84V6	Q84V6: bacterioph	215	2	18.2	1	8	18.2	Q84V6: spirintha cl
143	2	18.2	9	2	Q84V6	Q84V6: bacterioph	216	2	18.2	1	8	18.2	Q84V6: spirintha cl
144	2	18.2	9	2	Q84V6	Q84V6: bacterioph	217	2	18.2	1	8	18.2	Q84V6: spirintha cl
145	2	18.2	9	2	Q84V6	Q84V6: bacterioph	218	2	18.2	1	8	18.2	Q84V6: spirintha cl
146	2	18.2	9	4	Q84V6	Q84V6: bacterioph	219	2	18.2	1	8	18.2	Q84V6: spirintha cl
147	2	18.2	9	4	Q84V6	Q84V6: bacterioph	220	2	18.2	1	8	18.2	Q84V6: spirintha cl
148	2	18.2	9	4	Q84V6	Q84V6: bacterioph	221	2	18.2	1	8	18.2	Q84V6: spirintha cl
149	2	18.2	9	4	Q84V6	Q84V6: bacterioph	222	2	18.2	1	8	18.2	Q84V6: spirintha cl
150	2	18.2	9	4	Q84V6	Q84V6: bacterioph	223	2	18.2	1	8	18.2	Q84V6: spirintha cl
151	2	18.2	9	4	Q84V6	Q84V6: bacterioph	224	2	18.2	1	8	18.2	Q84V6: spirintha cl
152	2	18.2	9	4	Q84V6	Q84V6: bacterioph	225	2	18.2	1	8	18.2	Q84V6: spirintha cl
153	2	18.2	9	4	Q84V6	Q84V6: bacterioph	226	2	18.2	1	8	18.2	Q84V6: spirintha cl
154	2	18.2	9	4	Q84V6	Q84V6: bacterioph	227	2	18.2	1	8	18.2	Q84V6: spirintha cl
155	2	18.2	9	5	Q84V6	Q84V6: bacterioph	228	2	18.2	1	8	18.2	Q84V6: spirintha cl
156	2	18.2	9	6	Q84V6	Q84V6: bacterioph	229	2	18.2	1	8	18.2	Q84V6: spirintha cl
157	2	18.2	9	8	Q84V6	Q84V6: bacterioph	230	2	18.2	1	8	18.2	Q84V6: spirintha cl
158	2	18.2	9	8	Q84V6	Q84V6: bacterioph	231	2	18.2	1	8	18.2	Q84V6: spirintha cl
159	2	18.2	9	8	Q84V6	Q84V6: bacterioph	232	2	18.2	1	8	18.2	Q84V6: spirintha cl
160	2	18.2	9	8	Q84V6	Q84V6: bacterioph	233	2	18.2	1	8	18.2	Q84V6: spirintha cl
161	2	18.2	9	8	Q84V6	Q84V6: bacterioph	234	2	18.2	1	8	18.2	Q84V6: spirintha cl
162	2	18.2	9	8	Q84V6	Q84V6: bacterioph	235	2	18.2	1	8	18.2	Q84V6: spirintha cl







CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -!- MISCELLANEOUS: S14 ALPHA AND BETA FORMS DIFFER IN PL. S14 ALPHA  
 CC FORM IS THE LEAST BASIC FORM.  
 CC -!- MASS SPECTROMETRY: MW=11745.9, METHOD-ELECTROSPRAY  
 CC -!- MASS SPECTROMETRY: MW=11947, METHOD-MALDI.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 KDA.  
 CC -!- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro: IPR001209; Ribosomal\_S14.  
 DR InterPro: IPR001648; Ribosomal\_S18.  
 DR Pfam: PF00253; Ribosomal\_S14; PARTIAL.  
 DR PROSITE: PS00507; RIBOSOMAL\_S18; PARTIAL.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA: 1513 MW: 56843DF10116D057 (P0654);

Query Match 36.4%; Score 4; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5, 8, 10, 12;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARKS 4  
 DB 1 ARKS 4

RESULT 2  
 O31363  
 ID O31363 PRELIMINARY: PRT: 9 AA.  
 AC O31363;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Outer surface protein C (Fragment).  
 GN OSPC.  
 GS Borrelia garinii.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID:29519;  
 RN {1}  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PB1.  
 RA MEDLINE:97426044; PubMed:9282748;  
 RA Tilly K., Casjens S., Stevenson B., Hozo J.L., Simoes D.S., Boquet E.,  
 Rosa P.;  
 RT "The Borrelia burgdorferi circular plasmid sp24: conservation of  
 plasmid structure and targeted inactivation of the ospC gene".  
 RL Mol. Microbiol. 25:361-374(1997).  
 DR EMBL: U93699; AAC45533.1;  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1019 MW: 48640LN731A4433 (P0654);

Query Match 27.3%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8, 10, 05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 TAL 10  
 DB 7 TAL 9

RESULT 3  
 O9UKJ6  
 ID O9UKJ6 PRELIMINARY: PRT: 9 AA.  
 AC O9UKJ6;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE Androgen receptor (Fragment).  
 GN AR.  
 GS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN NCBI\_TaxID:9606;

RN SEQUENCE FROM N.A.  
 RA Trans W. (Xenopus laevis) (African clawed toad genome).  
 RT "A splice site map of the African clawed toad genome".  
 RC Submitted (JUN 1999) by EMBL/GenBank/CCDS databases.  
 DR EMBL: AF199877; AAC45533.1;  
 KW Receptor  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1118 MW: 10464 (P0654);

Query Match 27.3%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8, 10, 05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 TAL 10  
 DB 7 TAL 9

RESULT 4  
 O9UKJ6  
 ID O9UKJ6 PRELIMINARY: PRT: 9 AA.  
 AC O9UKJ6;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE Fibronectin type 1 receptor (Fragment).  
 GN FHF 2.  
 GS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN NCBI\_TaxID:9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 20112825; PubMed 10447147;

RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.  
 RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors  
 IS Generated by Alternative Promoter Usage and Differed in  
 RL Splicing."  
 RL J. Biol. Chem. 275:2589-2597(2000).  
 DR EMBL: AF199609; AAF31396.1; .  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA: 1068 MW: 148945B32407272D C8664;

Query Match: 27.3%; Score 3; DB 10; Length 9;  
 Best local Similarity 100.0%; Pred. No. 8; Gap 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RKS 4  
 DB 5 RKS 7

## RESULT 6

P82434 PRELIMINARY: PKT: 10 AA  
 AC P82434;  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE 28 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID:4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN cv. PETIT HAVANA;  
 RA Rhee K.A., Bonham V.A., Mitchell G.P., Robertson D., Stables A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture."  
 RL Planta 0:0-0(2000).  
 CC -1- SURCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA: 1054 MW: 1A4B95DDUABZ444 C8664;

Query Match: 27.3%; Score 3; DB 10; Length 10;  
 Best local Similarity 100.0%; Pred. No. 7; Gap 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARK 3  
 DB 6 ARK 10

## RESULT 7

Q8UT83 PRELIMINARY: PKT: 10 AA  
 AC Q8UT83;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Vpu protein.  
 GN VPU.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-008W1795.6;  
 RA Novitsky V.A., Smith U.R., Gilbert P., McLane M.P., Chikwendure P.,  
 RA Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thier T.,  
 RA Foley B.T., Gaolekwe S., Rybak N., Gaseitswe S., Vansberg P.,  
 RA Marlink R., Lee T.-H., Essex M.;

RA "HIV-1 Subtype 017: A New HIV-1 Subtype Sequence for an AIDS  
 RT Virus Isolated from a Patient with AIDS"  
 RL S. J. Med. J. 351: 1200-1201 (1994) PMID: 7680000  
 DR EMBL: AF144097 AA: 1000  
 SQ SEQUENCE 10 AA: 1000 MW: 11662.1032A C8664;

Query Match: 27.3%; Score 3; DB 10; Length 10;  
 Best local Similarity 100.0%; Pred. No. 7; Gap 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARK 3  
 DB 6 ARK 10

## RESULT 8

P82434 PRELIMINARY: PKT: 10 AA  
 AC P82434;  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE 28 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID:4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN cv. PETIT HAVANA;  
 RA Rhee K.A., Bonham V.A., Mitchell G.P., Robertson D., Stables A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture."  
 RL Planta 0:0-0(2000).  
 CC -1- SURCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA: 1054 MW: 1A4B95DDUABZ444 C8664;

Query Match: 27.3%; Score 3; DB 10; Length 10;  
 Best local Similarity 100.0%; Pred. No. 7; Gap 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARK 3  
 DB 6 ARK 10

## RESULT 9

Q8UT83 PRELIMINARY: PKT: 10 AA  
 AC Q8UT83;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Vpu protein.  
 GN VPU.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-008W1795.6;  
 RA Novitsky V.A., Smith U.R., Gilbert P., McLane M.P., Chikwendure P.,  
 RA Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thier T.,  
 RA Foley B.T., Gaolekwe S., Rybak N., Gaseitswe S., Vansberg P.,  
 RA Marlink R., Lee T.-H., Essex M.;

Query Match 27.3%, Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAI 10  
DB 5 TAI 7

## RESULT 10

ID Q93208 PRELIMINARY; PRT; 12 AA.  
AC Q93208;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Urf-2X protein.  
GN URF-2X.  
OS Acinetobacter sp.  
OC Plasmid pKLH205, and Plasmid pKLH254.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=472;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN:ED45-25; PLASMID-pKLH205, and pKLH204;  
RX MEDLINE=21272500; PubMed=11376944;  
RA Kholodii G.;  
RL Gene 269:121-130(2001).  
DR EMBL; AJ251707; CAC39413.1; .  
DR EMBL; AJ250851; CAC39402.1; .  
KW Plasmid.  
SQ SEQUENCE 12 AA, 1219 MR, D4B99D3E821D6776 CRG64;

Query Match 27.3%, Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MTA 9  
DB 1 MTA 3

## RESULT 11

ID Q52112 PRELIMINARY; PRT; 12 AA.  
AC Q52112; Q08093; Q08097; Q08128; Q08132; Q56909;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE URF2X protein (Fragment).  
GN URF-2X OR URF2X.  
OS Acinetobacter calcoaceticus,  
OS Pantoea agglomerans,  
OS Alcaligenes sp.,  
OS Enterobacter cloacae,  
OS Escherichia coli,  
OS Yersinia enterocolitica, and  
OS mercury resistant bacterium '96 SE13.  
OG Plasmid pKLH2, Plasmid pKLH256, Plasmid pKLH210, Plasmid pKLH17, and  
OG Plasmid pKLH201.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=471, 549, 512, 550, 562, 630, 93601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=A.calcoaceticus; PLASMID=pKLH2;  
RX MEDLINE=94134837; PubMed=8302940;  
RA Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,  
RA Yurieva O.V., Nikiforov V.G.;  
RT Molecular characterization of an aberrant mercury resistance  
transposable element from an environmental Acinetobacter strain.\*;

PL Plasmid 55000-2580000;  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Pantoea agglomerans; Strain: E.colocae, and E.colocae;  
RX MEDLINE=97404094; PubMed=94134837;  
RA Nikiforov V., Kholodii G., Mindlin S., Gorlenko Z., Kalyuzhna F.,  
RA Mindlin S., Nikiforov V.;  
RT Intercontaminant transfer of mercury resistance from strains of the moraxellaceae to Acinetobacter.  
FT In environmental bacterium.  
GN Moraxellaceae; Acinetobacter.  
OS [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Yersinia enterocolitica; Strain: Various strains;  
RX MEDLINE=94274377; PubMed=756913;  
RA Osborn S.E.V., Lomovskaya O.L., Gorlenko Z.;  
RT Nucleotide sequence with 15,926 nucleotides this as a [102] like  
transposable element and provides evidence for the origin of the moraxellaceae transfer of resistance to mercury.  
FT In environmental bacterium.  
GN Moraxellaceae; Acinetobacter.  
OS [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=A.calcoaceticus; Strain: EMBL4, PLASMID pKLH211;  
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.;  
RA Nikiforov V.G.;  
RT pKLH2-like element transposons and possible mechanisms of their dissemination.\*;  
FT Submitted (MAR 2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF213017; AAA1066.1;  
DR EMBL; Y08992; AAA70140.1;  
DR EMBL; Y08993; AAA70141.1;  
DR EMBL; Y09025; AAA70441.1;  
DR EMBL; Y10192; AAA71196.1;  
DR EMBL; X78059; AAC6479.1;  
DR EMBL; AF144211; AAC64400.1;  
DR EMBL; A251307; CAC39413.1;  
KW Plasmid.  
FT NCBI\_TaxID=472;  
SQ SEQUENCE 12 AA, 1219 MR, D4B99D3E821D6776 CRG64;

Query Match 27.3%, Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MTA 9  
DB 1 MTA 3

## RESULT 12

ID Q93208 PRELIMINARY; PRT; 12 AA.  
AC Q93208;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Urf-2X protein.  
GN URF-2X.  
OS Acinetobacter sp.  
OC Plasmid pKLH205, and Plasmid pKLH254.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=472;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN:ED45-25;  
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
RA Nikiforov V.G.;

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RT *pKLH2-like aberrant transposons and possible mechanisms of their
RL dissemination.*; 1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250245; CAC80792.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3

RESULT 13
Q8GML2
ID Q8GML2 PRELIMINARY; PRT: 12 AA.
AC Q8GML2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter junii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC13-1;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3

RESULT 14
Q8GML2
ID Q8GML2 PRELIMINARY; PRT: 12 AA.
AC Q8GML2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter sp. FD23-35.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=109250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ED23-35;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3

RESULT 15
Q8GML2
ID Q8GML2 PRELIMINARY; PRT: 12 AA.
AC Q8GML2;
DT 01-JUN-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter junii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC13-1;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3

RESULT 16
Q8GML2
ID Q8GML2 PRELIMINARY; PRT: 12 AA.
AC Q8GML2;
DT 01-JUN-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter junii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC13-1;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3

RESULT 17
Q8GML2
ID Q8GML2 PRELIMINARY; PRT: 12 AA.
AC Q8GML2;
DT 01-JUN-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter junii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC13-1;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3

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RA Radaazzo F.M., Gribbs D.B., Kaufman T.C.
RT *Rescue and regulation of proboscipodidae a homocysteine dependent dtp
RL Antennapedia Complex.
RL Development 1:3-257-271(1991).
DR EMBL: S77929; AAB20845.1;
DR Flybase; FBgn0012734; dpseXp.
FT NON_TER
SQ SEQUENCE 12 AA: 1377 MW: 4608DB:8E455A5B4 C36764

Query Match 27.38; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 8,200,000;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4
DB 4 RKS 6

RESULT 17
P82246 PRELIMINARY; PRT; 12 AA.
AC P82246;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Chloroplast 50S ribosomal protein L31 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core Eudicot;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID:3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=leaf;
RX MEDLINE-20435798; PubMed-10874046;
RA Yamauchi K., Subramanian A.R.;
RT *The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).
RL J. Biol. Chem. 275:28456-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: THERE ARE THREE FORMS, ALPHA, BETA AND GAMMA WHICH
CC DIFFER IN CHARGE.
CC -1- SIMILARITY: BELONGS TO THE L31P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002150; Ribosomal_L31.
DR Pfam; PF01197; Ribosomal_L31; PARTIAL.
DR PRINTS; PR01249; RIBOSOMAL_L31; PARTIAL.
DR PROSITE; PS01143; RIBOSOMAL_L31; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA binding.
FT NON_TER
SQ SEQUENCE 12 AA: 1529 MW: 13B983E951D761F0 C36764

Query Match 27.38; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 8,200,000;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4
DB 1 RKS 3

RESULT 18
P82247 PRELIMINARY; PRT; 12 AA.
AC P82247;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Chloroplast 50S ribosomal protein L31 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core Eudicot;

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CX C36764; P82246;
FN 1;
PP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=leaf;
RX MEDLINE-20435798; PubMed-10874046;
RA Yamauchi K., Subramanian A.R.;
RT *The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).
RL J. Biol. Chem. 275:28456-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: THERE ARE THREE FORMS, ALPHA, BETA AND GAMMA WHICH
CC DIFFER IN CHARGE.
CC -1- SIMILARITY: BELONGS TO THE L31P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002150; Ribosomal_L31.
DR Pfam; PF01197; Ribosomal_L31; PARTIAL.
DR PRINTS; PR01249; RIBOSOMAL_L31; PARTIAL.
DR PROSITE; PS01143; RIBOSOMAL_L31; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA binding.
FT NON_TER
SQ SEQUENCE 12 AA: 1529 MW: 13B983E951D761F0 C36764

Query Match 27.38; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 8,200,000;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKS 4
DB 1 RKS 3

RESULT 19
P82248 PRELIMINARY; PRT; 12 AA.
AC P82248;
DT 01-JUN-1999 (TREMBLrel. 14, Created)
DT 01-NOV-1999 (TREMBLrel. 16, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 16, Last annotation update)
DE ACP83 is protein (Fragment).
RN ACP83;
RC Eukaryotic; Mollusca;
RX MEDLINE-11174340; PubMed-10874046;
RA Yamauchi K., Subramanian A.R.;
RT *The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).
RL J. Biol. Chem. 275:28456-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: THERE ARE THREE FORMS, ALPHA, BETA AND GAMMA WHICH
CC DIFFER IN CHARGE.
CC -1- SIMILARITY: BELONGS TO THE L31P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002150; Ribosomal_L31.
DR Pfam; PF01197; Ribosomal_L31; PARTIAL.
DR PRINTS; PR01249; RIBOSOMAL_L31; PARTIAL.
DR PROSITE; PS01143; RIBOSOMAL_L31; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA binding.
FT NON_TER
SQ SEQUENCE 12 AA: 1529 MW: 13B983E951D761F0 C36764

Query Match 27.38; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 8,200,000;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKS 4
DB 1 RKS 3

RESULT 20
P83339 PRELIMINARY; PRT; 14 AA.
AC P83339;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

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DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Histone H6-like protein (Fragment)
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RA Fernandes J.M.O., Smith V.J.;
RT "Antimicrobial properties of a histone H6-like peptide from skin
RL secretions of rainbow trout, Oncorhynchus mykiss.";
RL Submitted (APR-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE AND
CC -!- GRAM-NEGATIVE BACTERIA AT SUBMICROMOLAR CONCENTRATIONS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
CC -!- MASS SPECTROMETRY: MH=6671; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE HMG-14/HMG-17 PROTEIN FAMILY.
DR InterPro: PS000079; HMG14.17.
KW Nuclear protein; DNA-binding; Antibiogenic.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1385 MW; DE408084A6121AD 76%44;

Query Match 27.3%; Score 3; 16 hits; Length 14;
Best Local Similarity 100.0%; Pred. No. 8, Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4
DB 1 1
3 RKS 5

RESULT 2;
Q53501 PRELIMINARY: PRT; 14 AA.
AC Q53501;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Orf (promoter-like sequence P80) (Fragment).
OS Lactobacillus paracasei
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95219758; PubMed=7704831;
RA Djordjevic G., Bojovic B., Barina A., Topisirovic B.;
RT "Cloning of promoter-like sequences from Lactobacillus paracasei
RT subsp. paracasei C61 and their expression in Escherichia coli.
RT Lactococcus lactis, and Lactobacillus reuteri.";
RL Can. J. Microbiol. 40:1043-1050(1994)
DR EMBL: S76787; AAR33946.2;
FT NON_TER 14
SQ SEQUENCE 14 AA; 1475 MW; CD7E795AFF1414 67%44;

Query Match 27.3%; Score 3; 16 hits; Length 14;
Best Local Similarity 100.0%; Pred. No. 8, Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3
DB 1 1
4 ARK 6

RESULT 22
Q52840 PRELIMINARY: PRT; 14 AA.
AC Q52840;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 01-MAY-2001 (TREMBLrel. 01, Last annotation update)
DE Histone H6-like protein (Fragment)
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RA Fernandes J.M.O., Smith V.J.;
RT "Antimicrobial properties of a histone H6-like peptide from skin
RL secretions of rainbow trout, Oncorhynchus mykiss.";
RL Submitted (APR-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE AND
CC -!- GRAM-NEGATIVE BACTERIA AT SUBMICROMOLAR CONCENTRATIONS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
CC -!- MASS SPECTROMETRY: MH=6671; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE HMG-14/HMG-17 PROTEIN FAMILY.
DR InterPro: PS000079; HMG14.17.
KW Nuclear protein; DNA-binding; Antibiogenic.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1385 MW; DE408084A6121AD 76%44;

Query Match 27.3%; Score 3; 16 hits; Length 14;
Best Local Similarity 100.0%; Pred. No. 8, Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4
DB 1 1
3 RKS 5

RESULT 23
Q53501 PRELIMINARY: PRT; 14 AA.
AC Q53501;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Orf (promoter-like sequence P80) (Fragment).
OS Lactobacillus paracasei
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95219758; PubMed=7704831;
RA Djordjevic G., Bojovic B., Barina A., Topisirovic B.;
RT "Cloning of promoter-like sequences from Lactobacillus paracasei
RT subsp. paracasei C61 and their expression in Escherichia coli.
RT Lactococcus lactis, and Lactobacillus reuteri.";
RL Can. J. Microbiol. 40:1043-1050(1994)
DR EMBL: S76787; AAR33946.2;
FT NON_TER 14
SQ SEQUENCE 14 AA; 1475 MW; CD7E795AFF1414 67%44;

Query Match 27.3%; Score 3; 16 hits; Length 14;
Best Local Similarity 100.0%; Pred. No. 8, Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3
DB 1 1
4 ARK 6

RESULT 24
Q52840 PRELIMINARY: PRT; 14 AA.
AC Q52840;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Orf (promoter-like sequence P80) (Fragment).
OS Lactobacillus paracasei
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95219758; PubMed=7704831;
RA Djordjevic G., Bojovic B., Barina A., Topisirovic B.;
RT "Cloning of promoter-like sequences from Lactobacillus paracasei
RT subsp. paracasei C61 and their expression in Escherichia coli.
RT Lactococcus lactis, and Lactobacillus reuteri.";
RL Can. J. Microbiol. 40:1043-1050(1994)
DR EMBL: S76787; AAR33946.2;
FT NON_TER 14
SQ SEQUENCE 14 AA; 1475 MW; CD7E795AFF1414 67%44;

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RT \*Nuclear factor Y activates the human xanthine oxidoreductase gene promoter.\*

RL FEBS Lett. 480:84-88(2000).

DR EMBL: AF203979; AAF15890.1;

FT NON\_TER 14 14

SQ SEQUENCE 14 AA: 1626 MW: D300FB701792F022 CR064;

Query Match 27.3% Score 3; DR 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 MTA 9

DB 1 MTA 3

#### RESULT 25

Q9SMV4

ID Q9SMV4 PRELIMINARY; PRT: 14 AA.

AC Q9SMV4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE Monosaccharide transporter (Fragment).

GN ATSTP1.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosidis II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI\_taxid=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RA Truernit.E.;

RL Thesis (1997), Universitaet Erlangen, Institut Botantik II.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RX MEDLINE=99406514; PubMed=10476074;

RA Stadler K., Truernit E., Gahrz M., Sauer N.;

RT \*The AtSUC1 sucrose carrier may represent the osmotic driving force

RT for anther dehiscence and pollen tube growth in Arabidopsis.\*;

RL Plant J. 19:269-278(1999).

DR EMBL: AJ001363; CAB59189.1;

FT NON\_TER 14 14

SQ SEQUENCE 14 AA: 1551 MW: 7FE37997UA0A2A24 CR064;

Query Match

Best Local Similarity 27.3% Score 3; DR 10; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARK 3

DB 6 ARK 8

#### RESULT 26

P82452

ID P82452 PRELIMINARY; PRT: 14 AA.

AC P82452;

DT 01-JUN-2000 (TrEMBLrel. 14, Created)

DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE 60S ribosomal protein L26 (Fragment).

OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta.

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

OX NCBI\_taxid=3562;

RN [1]

RP SEQUENCE.

RC STRAIN=cv. ALVARO; TISSUE=LEAF;

RA Yamaguchi K., Subramanian A.R.;

RT \*Nuclear factor Y activates the human xanthine oxidoreductase gene promoter.\*

RL Submitted (Apr 2001) to the Swiss Protein Data Bank.

DR EMBL: AF203979; AAF15890.1;

FT NON\_TER 14 14

SQ SEQUENCE 14 AA: 1626 MW: D300FB701792F022 CR064;

Query Match 27.3% Score 3; DR 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ARK 4

DB 12 ARK 11

#### RESULT 27

P04114

ID P04114 PRELIMINARY; PRT: 14 AA.

AC P04114;

DT 01-MAY-1994 (TrEMBLrel. 13, Created)

DT 01-MAY-1994 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE 2X myosin heavy chain (fragment)

OS Rattus rattus (Rat)

OC Eukaryota; Eumetazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurinae; Muridae; Muridae; Edentata;

OX NCBI\_taxid=10117;

RN [1]

RP SIOFMRP (P04114)

RC TISSUE=Brain;

EX MEDLINE=94064476; PubMed=10476074;

RA Buckdahl M., Sauer N., Gahrz M., Sauer N.;

RT \*Type 2X myosin heavy chain is encoded by a muscle fiber specific

RT and developmentally regulated gene.\*;

RL Plant J. 19:269-278(1999).

DR EMBL: X72641; CAB1089.1

FT NON\_TER 14 AA: 671 MW: 7FE37997UA0A2A24 CR064;

SQ SEQUENCE 14 AA: 671 MW: 7FE37997UA0A2A24 CR064;

Query Match

Best Local Similarity 27.3% Score 3; DR 10; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ARK 1

DB 2 ARK 1

#### RESULT 28

P04114

ID P04114 PRELIMINARY; PRT: 14 AA.

AC P04114;

DT 01-MAY-1994 (TrEMBLrel. 13, Created)

DT 01-MAY-1994 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2001 (TrEMBLrel. 19, Last annotation update)

DE 2X myosin heavy chain (fragment)

OS Rattus rattus (Rat)

OC Eukaryota; Eumetazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurinae; Muridae; Muridae; Edentata;

OX NCBI\_taxid=10117;

RN [1]

RP SIOFMRP (P04114)

RC TISSUE=Brain;

EX MEDLINE=94064476; PubMed=10476074;

RA Buckdahl M., Sauer N., Gahrz M., Sauer N.;

RT \*Type 2X myosin heavy chain is encoded by a muscle fiber specific

RT and developmentally regulated gene.\*;

RL Plant J. 19:269-278(1999).

DR EMBL: X72641; CAB1089.1

FT NON\_TER 14 AA: 671 MW: 7FE37997UA0A2A24 CR064;

SQ SEQUENCE 14 AA: 671 MW: 7FE37997UA0A2A24 CR064;

DR EMBL: X72590: CAA51188.1: 1: 27.3%  
DR EMBL: X72589: CAA51187.1: 1: 27.3%  
KW Muscle protein; Myosin.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA: 1041 MW: 410536 CYS26AFA: CRC64:

Query Match 27.3% Score 3; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSR 5  
DB 2 KSR 4

## RESULT 29

Q9R507 PRELIMINARY: PRT: 15 AA.  
ID Q9R507  
AC Q9R507  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE D-alanyl carrier protein (Fragment).  
OS Lactobacillus casei.  
OC Bacteria; Firmicutes; Lactobacilliales; Lactobacillaceae.  
OC Lactobacillus.  
OX NCBI\_TaxID:1582;  
RN [1]  
RP SKOQUENCE.  
RX MEDLINE:94131947; PubMed-8300523;  
RA Heaton M.P., Neuhaus F.C.;  
RL J. Bacteriol. 176:681-690(1994).  
SQ SEQUENCE 15 AA: 1631 MW: 422A5D0AE2368B3A: CRC64:

Query Match 27.3% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AIK 11  
DB 5 AIK 7

## RESULT 30

Q54861 PRELIMINARY: PRT: 15 AA.  
ID Q54861  
AC Q54861  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE Bm2 protein (Fragment).  
GN Bm2.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae.  
OC Streptococcus.  
OX NCBI\_TaxID:1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-M2.  
RX MEDLINE:94261050; PubMed-8202029;  
RA Podbielski A., Weber-Heynemann J., Cleary P.P.;  
RT "Immunoglobulin-binding FcR, Ecm proteins and M proteins of group A  
Streptococci, evolved independently from a common ancestral protein."  
RL Mod. Microbiol. Immunol. 18:33-42(1994).  
DR EMBL: X73159: CAA51683.2: 1: 27.3%  
FT NON\_TER 15  
SQ SEQUENCE 15 AA: 1852 MW: 4C95740B05611CEA: CRC64:

Query Match 27.3% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3

QY 2 ARK 4

## RESULT 41

Q9V25 PRELIMINARY: PRT: 15 AA.  
ID Q9V25  
AC Q9V25  
DT 01-DEC-2001 (TREMBlrel. 01, Created)  
DT 01-DEC-2001 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 01, Last annotation update)  
DE Phosphogluco-alpha (Fragment).  
GN PHOSPHOGLUCOALPHA.  
OS Streptococcus lactis.  
OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae.  
OC Streptococcus lactis.  
OX NCBI\_TaxID:43430;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN JDM-1333;  
RA MEDLINE:2343444; PubMed-1234567;  
RL J. Bacteriol. 176:1234-1235(1994).  
SQ SEQUENCE 15 AA: 1564 MW: 4A5F1C0A7C2D0C: CRC64:

Query Match 27.3% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ARK 4  
DB 2 ARK 4

## RESULT 42

Q9V25 PRELIMINARY: PRT: 15 AA.  
ID Q9V25  
AC Q9V25  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
DE Low Mr zona binding protein (Fragment).  
OS S. aureus (Pta).  
OC Eukaryota; Metazoa; Vertebrata; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontia; Simiiformes; Simiiformes; Suidae; Sus.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE:94261050; PubMed-8202029;  
RA Early B.V. Barker et al. 1994.  
RT "Characterization of low Mr zona binding proteins from boar  
Spermatozoa and associated proteins."  
RL Mol. Reprod. Dev. 38:1-10(1992).  
SQ SEQUENCE 15 AA: 1564 MW: 4A5F1C0A7C2D0C: CRC64:

Query Match 27.3% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEP 6  
DB 4 SEP 6

## RESULT 43

Q9V25 PRELIMINARY: PRT: 15 AA.  
ID Q9V25  
AC Q9V25  
DT 01-MAY-2000 (TREMBlrel. 13, Created)



DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE Alkaline phosphodiesterase I (EC 3.1.4.1) (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.

RA MEDLINE=93250579; PubMed=8387170;  
 RA Matsuyama E., Iwamatsu A., Takashima S.;  
 RL Biochem. Mol. Biol. Int. 29:579-586(1994).  
 SQ SEQUENCE 15 AA; 1678 MW; BE31498FEA8B7071 CR664;

Query Match 27.3%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 ARK 3  
 DB 13 ARK 15

## RESULT 34

Q8WK21 PRELIMINARY; PRT; 15 AA  
 AC Q8WK21;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DE 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DE putative proteolysis tag (Fragment).  
 OS Bolidomonas sp. OLI46SE.  
 OC Chloroplast.  
 CC Eukaryota; Stramenopiles; Bolidophyceae; Bolidomonas.  
 OX NCBI\_TaxID=129302;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OLI46SE;  
 RA Williams K., Guillou L., Gueneau de Novoa P.;  
 RT \*Small RNAs from non-green plastidial genomes \*;  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases  
 DR EMBL; AF169626; AAL55606.1;  
 KW Chloroplast.  
 FT NON-TER  
 SQ SEQUENCE 15 AA; 1666 MW; 0D578E9144198201 CR664;

Query Match 27.3%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 RKS 4  
 DB 9 RKS 11

## RESULT 35

P82135 PRELIMINARY; PRT; 15 AA  
 AC P82135;  
 DT 01-JUN-2000 (TREMBLrel. 14, Created)  
 DE 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
 DE Chloroplast 30S ribosomal protein S18 alpha (Fragment).  
 OS Spinacia oleracea (Spinach).  
 CC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3362;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;

RX MEDLINE=20455793; PubMed=1144074;  
 RA Yasarova K., von Klotz J., Kollmann A.R.;  
 RT The plastid ribosomal proteins: Identification of all the proteins in  
 RT the small subunit of an organelle ribosome (chloroplast).  
 RL Biol. Chem. 272:2415-2419(1997).  
 CC 1 SUBCELLULAR LOCALIZATION: CHLOROPLAST.  
 CC 1 TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC 1 MISCELLANEOUS: THE ALPHA AND BETA FORMS DIFFER IN THE SUB-UNIT  
 CC FORM 15 THE LEAST BASIC FORM.  
 CC 1 MASS SPECTROMETRY: MW 22.0 KDA, P/1: 0.4, METRIC: MALDI.  
 CC 1 MISCELLANEOUS: IN THE ALPHA AND BETA FORMS, THE MW IS 14 KDA  
 CC 1 SIMILARITY: MEMBERS OF THE SUB-FAMILY OF RIBOSOMAL PROTEIN  
 CC INTERPRO: PROTEIN-1, WITH-SUBUNIT-1.  
 DR Pfam: PF00441; Ribosomal\_S18\_ALPHA.  
 DR PROSITE: PS00477; RIBOSOMAL\_S18\_ALPHA.  
 KW Ribosomal protein, chloroplast.  
 FT NON-TER  
 SQ SEQUENCE 15 AA; 1666 MW; 0D578E9144198201 CR664;

Query Match 27.3%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 RKS 4  
 DB 10 RKS 15

## RESULT 36

Q8WK21 PRELIMINARY; PRT; 15 AA  
 AC Q8WK21;  
 DT 01-MAY-2000 (TREMBLrel. 20, Created)  
 DE 01-MAY-2000 (TREMBLrel. 20, Last sequence update)  
 DE 16 kDa alpha-lactalbumin homolog (Fragment).  
 OS Mus sp.  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=9545473; PubMed=7636241.  
 RA Suto Y., Nagasawa H., Sasakawa T., Hamada T., Inuchi T.;  
 RT "Biochemical changes during growth and regression of pregnancy  
 RT dependent mammary tumors of DEZA mice."  
 RL Proc. Soc. Exp. Biol. Med. 209:44-48(1995).  
 SQ SEQUENCE 15 AA; 1666 MW; 166A7AD707F9A4A6 CR664;

Query Match 27.3%; Score 3; DB 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 ARK 11  
 DB 11 ARK 14

## RESULT 37

Q8WK21 PRELIMINARY; PRT; 15 AA  
 AC Q8WK21;  
 DT 01-MAY-2000 (TREMBLrel. 16, Created)  
 DE 01-MAY-2000 (TREMBLrel. 16, Last sequence update)  
 DE 10 kDa MR-IMPIN SUBTENSIVE protein (Fragment).  
 OS Rattus sp.  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10114;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96195456; PubMed=8611408;

RA Goto S., Lord R., Kobayashi E., Vari F., Edwards Smith C., Kamada N.  
 RT "Novel immunosuppressive proteins purified from the spleen of liver  
 RL retransplanted rats.";  
 RL Transplantation 61:1147-1151(1996).  
 SQ SEQUENCE 15 AA: 1477 MW: 81089700000714P CRG64;

Query Match 27.3% Score 3; PH 11; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 9, 6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TA 10  
 Db 8 TA 10

## RESULT 38

Q9S605 PRELIMINARY: PRT: 8 AA.  
 ID Q9S605  
 AC Q9S605  
 DT 01-MAY-2000 (TRENBLREL, 13, Created)  
 DT 01-MAY-2000 (TRENBLREL, 13, Last sequence update)  
 DT 01-MAY-2000 (TRENBLREL, 13, Last annotation update)  
 DE Putative IS50 transposase (fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A295b;  
 RX MEDLINE=99194747; PubMed=10094716;  
 RA Rahn A., Drummelsmith J., Whitfield G.  
 RT "Conserved organization in the cps gene clusters for expression of  
 RT Escherichia coli group 1 K antigens: relationship to the enterohemolysin  
 RT biosynthesis locus and the cps genes from Klebsiella pneumoniae".  
 RL J. Bacteriol. 181:2307-2314(1999).  
 DR EMBL: AF118251; AAD30008.1;  
 FT NON\_TER 8  
 FT SEQUENCE 8 AA: 1011 MW: F21DC1A9D1B41456 CRG64;

Query Match 18.2% Score 2; PH 2; Length 27  
 Best Local Similarity 100.0%; Pred. No. 9, 6e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TA 9  
 Db 6 TA 7

## RESULT 39

Q45615 PRELIMINARY: PRT: 8 AA.  
 ID Q45615  
 AC Q45615  
 DT 01-NOV-1996 (TRENBLREL, 01, Created)  
 DT 01-NOV-1996 (TRENBLREL, 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL, 19, Last annotation update)  
 DE GcbB protein (fragment).  
 GN GUTR.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=94253000; PubMed=8195086;  
 RA Ye R., Wong S.L.;  
 RT "Transcriptional regulation of the Bacillus subtilis alcohol  
 RT dehydrogenase gene".  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL: U16626; AAA20875.1;  
 FT NON\_TER 8  
 FT SEQUENCE 8 AA: 927 MW: FD56C772D1A1F1A6 CRG64;

Query Match 18.2% Score 2; PH 2; Length 27  
 Best Local Similarity 100.0%; Pred. No. 9, 6e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TA 8  
 Db 8 TA 8

## RESULT 40

Q45615 PRELIMINARY: PRT: 8 AA.  
 ID Q45615  
 AC Q45615  
 DT 01-NOV-1996 (TRENBLREL, 01, Created)  
 DT 01-NOV-1996 (TRENBLREL, 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL, 19, Last annotation update)  
 DE GcbB protein (fragment).  
 GN GUTR.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=94253000; PubMed=8195086;  
 RA Ye R., Wong S.L.;  
 RT "Transcriptional regulation of the Bacillus subtilis alcohol  
 RT dehydrogenase gene".  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL: U16626; AAA20875.1;  
 FT NON\_TER 8  
 FT SEQUENCE 8 AA: 927 MW: FD56C772D1A1F1A6 CRG64;

Query Match 18.2% Score 2; PH 2; Length 27  
 Best Local Similarity 100.0%; Pred. No. 9, 6e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TA 10  
 Db 8 TA 10

## RESULT 41

Q45615 PRELIMINARY: PRT: 8 AA.  
 ID Q45615  
 AC Q45615  
 DT 01-NOV-1996 (TRENBLREL, 01, Created)  
 DT 01-NOV-1996 (TRENBLREL, 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL, 19, Last annotation update)  
 DE GcbB protein (fragment).  
 GN GUTR.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=94253000; PubMed=8195086;  
 RA Ye R., Wong S.L.;  
 RT "Transcriptional regulation of the Bacillus subtilis alcohol  
 RT dehydrogenase gene".  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL: U16626; AAA20875.1;  
 FT NON\_TER 8  
 FT SEQUENCE 8 AA: 927 MW: FD56C772D1A1F1A6 CRG64;

Query Match 18.2% Score 2; PH 2; Length 27  
 Best Local Similarity 100.0%; Pred. No. 9, 6e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TA 10  
 Db 6 TA 6

## RESULT 42

Q44463  
ID Q44463 PRELIMINARY: PRT: 8 AA  
AC Q44463  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
DE Agrobacterium tumefaciens Ti plasmid virB3 and virD4 genes (Fragment).  
OS Rhizobiales (rhizobacteria).  
OG Plasmid II.  
OC Bacteria; Proteobacteria; Alphaproteobacteria.  
OX NCBI\_TaxID=356;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88015611; PubMed=3658701;  
RA Portner S.G., Yanofsky M.F., Nester E.W.;  
RT "Molecular characterization of the virB operon from Agrobacterium tumefaciens".  
RT tumefaciens".  
RL Nucleic Acids Res. 15:7503-7517 (1987).  
DR EMBL: X06045; CAA29439.1; .  
KW Plasmid.  
FT NON\_TER  
SQ SEQUENCE 8 AA; 887 MW; F8F2C325B33861A6 CMC64;

## Query Match

18.2%; Score 2; 18 2; Length 4.

Best Local Similarity 100.0%; Pred. No. 8; 4005;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4

DB 4 KS 5

## RESULT 43

Q56759  
ID Q56759 PRELIMINARY: PRT: 8 AA  
AC Q56759  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Haloacid dehalogenase (Fragment).  
OS BHLB.  
GN Xanthobacter autotrophicus  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Hypomicrobiaceae; Xanthobacter.  
OX NCBI\_TaxID=280;  
[1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=GJ10, and CV. M50;  
RC MEDLINE=95173113; PubMed=7866610;  
RA Van der Ploeg J., Willemse M., van Nijl B., Janssen D.P.;  
RT "Adaptation and mobilization of the haloacid dehalogenase gene for activation and mobilization of the haloacid dehalogenase gene by RT insertion element IS1247".  
RL J. Bacteriol. 177:1348-1356 (1995).  
DR EMBL: X84038; CAA58857.1; .  
KW NON\_TER  
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D27D0A0056 CMC64;

## Query Match

18.2%; Score 2; 18 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 8; 4005;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IK 11

DB 2 IK 3

## RESULT 44

O32560  
ID O32560 PRELIMINARY: PRT: 8 AA

AC Q56759 (TRENBLrel. 01, Created)  
DT 01-JAN-2004 (TRENBLrel. 01, Last sequence update)  
DT 01-OCT-2001 (TRENBLrel. 19, Last annotation update)  
DE Haloacid dehalogenase (Fragment).  
OS BHLB.  
GN Xanthobacter autotrophicus  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Hypomicrobiaceae; Xanthobacter.  
OX NCBI\_TaxID=280;  
[1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=GJ10, and CV. M50;  
RC MEDLINE=95173113; PubMed=7866610;  
RA Van der Ploeg J., Willemse M., van Nijl B., Janssen D.P.;  
RT "Adaptation and mobilization of the haloacid dehalogenase gene for activation and mobilization of the haloacid dehalogenase gene by RT insertion element IS1247".  
RL J. Bacteriol. 177:1348-1356 (1995).  
DR EMBL: X84038; CAA58857.1; .  
KW NON\_TER  
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D27D0A0056 CMC64;

Query Match  
18.2%; Score 2; 18 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 8; 4005;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4  
DB 4 KS 5

RESULT 45  
Q56759  
ID Q56759 PRELIMINARY: PRT: 8 AA  
AC Q56759  
DT 01-MAY-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-MAY-2001 (TRENBLrel. 19, Last annotation update)  
DE Stage V sporulation protein E (fragment).  
OS BHLB.  
GN Xanthobacter autotrophicus  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OX NCBI\_TaxID=280;  
[1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=GJ10, and CV. M50;  
RC MEDLINE=95173113; PubMed=7866610;  
RA Van der Ploeg J., Willemse M., van Nijl B., Janssen D.P.;  
RT "Adaptation and mobilization of the haloacid dehalogenase gene for activation and mobilization of the haloacid dehalogenase gene by RT insertion element IS1247".  
RL J. Bacteriol. 177:1348-1356 (1995).  
DR EMBL: X84038; CAA58857.1; .  
KW NON\_TER  
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D27D0A0056 CMC64;

Query Match  
18.2%; Score 2; 18 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 8; 4005;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4  
DB 4 KS 5

RESULT 46  
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AC O47273  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Oryza sativa, cv. IR64, lines IR64, IR64-1, IR64-2, and IR64-3



Best Local Similarity 100.0%; Pred. No. B. se-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 A1 10  
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Db 4 A1 5

Search completed: September 30, 2003, 10:18:17  
Job time : 35.6667 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:05 : Search time 11.8533 Seconds  
(without alignments)  
39.331 Million cwi updates/sec

Title: US-09-787-443-22

Perfect score: 11

Sequence: 1 AKSRDWTAK 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 24459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : Issued\_Patents\_AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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## ALL MENUS

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GENERAL INFORMATION  
APPLICANT: CHUN, HUI-CHANG  
TITLE OF INVENTION: ENDOGENOUS HEPATOCYTE GROWTH FACTOR  
FILE REFERENCE: 62941-44  
CURRENT APPLICATION NUMBER: 52941-44  
PARENT APPLICATION NUMBER: 52941-44  
NUMBER OF SEQ. IN MENUS: 4  
SEQUENCE PATENT NUMBER: 52941-44  
SEQ. IN MENUS: 4  
TITLE: 4  
REMARKS: ALL INFORMATION  
FEATURES  
OTHER INFORMATION: 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426

Sequence 4, Application US/08705660  
Patent No. 5858683  
GENERAL INFORMATION:  
APPLICANT: KESSEE, SUSAN  
APPLICANT: OBAR, ROBERT  
APPLICANT: WU, YING-JYE  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
DETECTION OF CERVICAL CANCER  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/705,660  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: GREENHALGH, DUNCAN A  
REGISTRATION NUMBER: 38,678  
REFERENCE/DOCKET NUMBER: MTP-023 {#395/27}  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-705-660-4

Query Match 36.4% Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRDM 7  
Db 6 SRDM 9

## RESULT 3

US-08-146-028-402  
Sequence 402, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR HYDROLYZED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 402:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid

STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: peptide  
US-08-146-028-402

Query Match 36.4% Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KRSP 5  
Db 6 KRSP 9

## RESULT 4

US-08-146-028-404  
Sequence 404, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR HYDROLYZED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: peptide  
US-08-146-028-404

Query Match 36.4% Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRSP 5  
Db 6 KRSP 9

## RESULT 5

US-08-146-028-404  
Sequence 404, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR HYDROLYZED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 404:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-146-028-404

Query Match 36.4% Score 4: DB 2: Length 9:  
Best Local Similarity 100.0% Pred. No. 2.5e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
DB 4 RKSR 7

## RESULT 6

US-08-146-028-405  
Sequence 405, Application US/08146028  
Patent No. 5891640

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146.028  
INFORMATION FOR SEQ ID NO. 405:

SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-146-028-405

Query Match 36.4% Score 4: DB 2: Length 9:  
Best Local Similarity 100.0% Pred. No. 2.5e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
DB 3 RKSR 6

## RESULT 7

US-08-146-028-406  
Sequence 406, Application US/08146028  
Patent No. 5891640

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146.028  
INFORMATION FOR SEQ ID NO. 406:  
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-146-028-406

Query Match 36.4% Score 4: DB 2: Length 9:  
Best Local Similarity 100.0% Pred. No. 2.5e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
DB 4 RKSR 5

## RESULT 8

US-08-146-028-407  
Sequence 407, Application US/08146028  
Patent No. 5891640

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08146.028  
INFORMATION FOR SEQ ID NO. 407:

SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-146-028-407

Query Match 36.4% Score 4: DB 2: Length 9:  
Best Local Similarity 100.0% Pred. No. 2.5e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 6  
DB 3 RKSR 4

## RESULT 9

US-08-999-045 4  
Sequence 41, Application US/08146028  
Patent No. 5891640

## GENERAL INFORMATION:

APPLICANT: KESSELSMAN  
APPLICANT: GRACE BOONER  
TITLE OF INVENTION: MOLECULAR  
TITLE OF INVENTION: PEPTIDES AND COMPOSITIONS FOR THE  
TITLE OF INVENTION: TREATMENT OF CERVICAL CANCER  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: POSTAL BOX 1000  
STREET: 125 North St  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02111  
COMPUTER READABLE FORM  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Vers.08. #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/989,045  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GREENHALGH, DUNCAN A  
 REGISTRATION NUMBER: 38,674  
 REFERENCE/DOCKET NUMBER: WTP-023 (8/95/27)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 248-7000  
 TELEFAX: (617) 248-7100  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-989-045-4

Query Match 36.4% Score 4: 100.0% Seqid: 9  
 Best Local Similarity 100.0% Pred. No. 2.5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 4 SRDM 7  
 DB 6 SRDM 9

# RESULT 10

US-08-723-425A-402  
 : Sequence 402, Application US/08723425A  
 : Patent No. 6165733  
 : GENERAL INFORMATION:  
 : APPLICANT: DELEYS, ROBERT  
 : TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 : TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 : TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 : TITLE OF INVENTION: ANTIBODIES OR HINT-INITIATED PEPTIDES CORRESPONDING TO  
 : NUMBER OF SEQUENCES: 453  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: NIXON & VANDERHYE, P.C.  
 : STREET: 11100 NORTH GLEBE ROAD, 8TH FLOOR  
 : CITY: Arlington  
 : STATE: VA  
 : COUNTRY: USA  
 : ZIP: 22201  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/723,425A  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: SADOFF, B.J.  
 : REGISTRATION NUMBER: 36,663  
 : REFERENCE/DOCKET NUMBER: 1487-13  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 703-816-4000  
 : TELEFAX: 703-816-4100  
 : INFORMATION FOR SEQ ID NO: 402:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 9 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide

## US-08-723-425A-402

Query Match 36.4% Score 4: 100.0% Seqid: 9  
 Best Local Similarity 100.0% Pred. No. 2.5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 4 SRDM 7  
 DB 6 SRDM 9

## RESULT 10

US-08-723-425A-402  
 : Sequence 402, Application US/08723425A  
 : Patent No. 6165733  
 : GENERAL INFORMATION:  
 : APPLICANT: DELEYS, ROBERT  
 : TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 : TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 : TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 : NUMBER OF SEQUENCES: 453  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: NIXON & VANDERHYE, P.C.  
 : STREET: 11100 NORTH GLEBE ROAD, 8TH FLOOR  
 : CITY: Arlington  
 : STATE: VA  
 : COUNTRY: USA  
 : ZIP: 22201  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/723,425A  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: SADOFF, B.J.  
 : REGISTRATION NUMBER: 36,663  
 : REFERENCE/DOCKET NUMBER: 1487-13  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 703-816-4000  
 : TELEFAX: 703-816-4100  
 : INFORMATION FOR SEQ ID NO: 402:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 9 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-723-425A-402

Query Match 36.4% Score 4: 100.0% Seqid: 9  
 Best Local Similarity 100.0% Pred. No. 2.5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 4 SRDM 7  
 DB 6 SRDM 9

## RESULT 10

US-08-723-425A-402  
 : Sequence 402, Application US/08723425A  
 : Patent No. 6165733  
 : GENERAL INFORMATION:  
 : APPLICANT: DELEYS, ROBERT  
 : TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 : TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 : TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 : NUMBER OF SEQUENCES: 453  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: NIXON & VANDERHYE, P.C.  
 : STREET: 11100 NORTH GLEBE ROAD, 8TH FLOOR  
 : CITY: Arlington  
 : STATE: VA  
 : COUNTRY: USA  
 : ZIP: 22201  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/723,425A  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: SADOFF, B.J.  
 : REGISTRATION NUMBER: 36,663  
 : REFERENCE/DOCKET NUMBER: 1487-13  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 703-816-4000  
 : TELEFAX: 703-816-4100  
 : INFORMATION FOR SEQ ID NO: 402:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 9 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide

1 NUMBER OF SEQUENCES: 453  
 2 CORRESPONDENCE ADDRESS:  
 3 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 4 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 5 CITY: Arlington  
 6 STATE: VA  
 7 COUNTRY: USA  
 8 ZIP: 22201  
 9 COMPUTER READABLE FORM:  
 10 MEDIUM TYPE: Floppy disk  
 11 COMPUTER: IBM PC compatible  
 12 OPERATING SYSTEM: PC-DOS/MS-DOS  
 13 SOFTWARE: Patent in Release #1.0, Version #1.0  
 14 CURRENT APPLICATION DATA: US/08/723,425A  
 15 APPLICATION NUMBER: US/08/723,425A  
 16 FILING DATE:  
 17 CLASSIFICATION: 435  
 18 ATTORNEY/AGENT INFORMATION:  
 19 NAME: SADOFF, B.J.  
 20 REGISTRATION NUMBER: 36,663  
 21 REFERENCE/DOCKET NUMBER: 1487-13  
 22 TELECOMMUNICATION INFORMATION:  
 23 TELEPHONE: 703-816-4000  
 24 TELEFAX: 703-816-4100  
 25 INFORMATION FOR SEQ ID NO: 404:  
 26 SEQUENCE CHARACTERISTICS:  
 27 LENGTH: 9 amino acids  
 28 TYPE: amino acid  
 29 STRANDEDNESS: single  
 30 TOPOLOGY: linear  
 31 MOLECULE TYPE: peptide  
 32 US-08-723-425A-404

Query Match 36.48; Score 4; Db: 5; Length: 9;  
 Best Local Similarity 100.0%; Pred. No. 2; No. 5;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 HKSR 5  
 1111  
 DB 4 HKSR 7

RESULT 13  
 1 US-08-723-425A-405  
 2 Sequence 405, Application US/08723425A  
 3 Patent No. 6165730  
 4 GENERAL INFORMATION:  
 5 APPLICANT: DELAYS, ROBERT  
 6 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 7 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 8 TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 9 TITLE OF INVENTION: ANTIBODIES OR BLATTINATED PEPTIDES CORRESPONDING  
 10 NUMBER OF SEQUENCES: 453  
 11 CORRESPONDENCE ADDRESS:  
 12 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 13 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 14 CITY: Arlington  
 15 STATE: VA  
 16 COUNTRY: USA  
 17 ZIP: 22201  
 18 COMPUTER READABLE FORM:  
 19 MEDIUM TYPE: Floppy disk  
 20 COMPUTER: IBM PC compatible  
 21 OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 SOFTWARE: Patent in Release #1.0, Version #1.0  
 23 CURRENT APPLICATION DATA:  
 24 APPLICATION NUMBER: US/08/723,425A  
 25 FILING DATE:  
 26 CLASSIFICATION: 435  
 27 ATTORNEY/AGENT INFORMATION:  
 28 NAME: SADOFF, B.J.  
 29 REGISTRATION NUMBER: 36,663  
 30 REFERENCE/DOCKET NUMBER: 1487-13

1 TELECOMMUNICATION INFORMATION:  
 2 TELEPHONE: 703-816-4000  
 3 TELEFAX: 703-816-4100  
 4 INFORMATION FOR SEQ ID NO: 404:  
 5 SEQUENCE CHARACTERISTICS:  
 6 LENGTH: 9 amino acids  
 7 TYPE: amino acid  
 8 STRANDEDNESS: single  
 9 TOPOLOGY: linear  
 10 MOLECULE TYPE: peptide  
 11 US-08-723-425A-404  
 12 Query Match 36.48; Score 4; Db: 5; Length: 9;  
 13 Best Local Similarity 100.0%; Pred. No. 2; No. 5;  
 14 Matches 4; Conservative 0; Mismatches 0; Indels 0;

1 RESULT 13  
 2 US-08-723-425A-405  
 3 Sequence 405, Application US/08723425A  
 4 Patent No. 6165730  
 5 GENERAL INFORMATION:  
 6 APPLICANT: DELAYS, ROBERT  
 7 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 8 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 9 TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 10 NUMBER OF SEQUENCES: 453  
 11 CORRESPONDENCE ADDRESS:  
 12 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 13 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 14 CITY: Arlington  
 15 STATE: VA  
 16 COUNTRY: USA  
 17 ZIP: 22201  
 18 COMPUTER READABLE FORM:  
 19 MEDIUM TYPE: Floppy disk  
 20 COMPUTER: IBM PC compatible  
 21 OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 SOFTWARE: Patent in Release #1.0, Version #1.0  
 23 CURRENT APPLICATION DATA:  
 24 APPLICATION NUMBER: US/08/723,425A  
 25 FILING DATE:  
 26 CLASSIFICATION: 435  
 27 ATTORNEY/AGENT INFORMATION:  
 28 NAME: SADOFF, B.J.  
 29 REGISTRATION NUMBER: 36,663  
 30 REFERENCE/DOCKET NUMBER: 1487-13  
 31 TELECOMMUNICATION INFORMATION:  
 32 TELEPHONE: 703-816-4000  
 33 TELEFAX: 703-816-4100  
 34 INFORMATION FOR SEQ ID NO: 404:  
 35 SEQUENCE CHARACTERISTICS:  
 36 LENGTH: 9 amino acids  
 37 TYPE: amino acid  
 38 STRANDEDNESS: single  
 39 TOPOLOGY: linear  
 40 MOLECULE TYPE: peptide  
 41 US-08-723-425A-404

1 TELECOMMUNICATION INFORMATION:  
 2 TELEPHONE: 703-816-4000  
 3 TELEFAX: 703-816-4100  
 4 INFORMATION FOR SEQ ID NO: 404:  
 5 SEQUENCE CHARACTERISTICS:  
 6 LENGTH: 9 amino acids  
 7 TYPE: amino acid  
 8 STRANDEDNESS: single  
 9 TOPOLOGY: linear  
 10 MOLECULE TYPE: peptide  
 11 US-08-723-425A-404  
 12 Query Match 36.48; Score 4; Db: 5; Length: 9;  
 13 Best Local Similarity 100.0%; Pred. No. 2; No. 5;  
 14 Matches 4; Conservative 0; Mismatches 0; Indels 0;

1 RESULT 13  
 2 US-08-723-425A-405  
 3 Sequence 405, Application US/08723425A  
 4 Patent No. 6165730  
 5 GENERAL INFORMATION:  
 6 APPLICANT: DELAYS, ROBERT  
 7 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 8 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 9 TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 10 NUMBER OF SEQUENCES: 453  
 11 CORRESPONDENCE ADDRESS:  
 12 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 13 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 14 CITY: Arlington  
 15 STATE: VA  
 16 COUNTRY: USA  
 17 ZIP: 22201  
 18 COMPUTER READABLE FORM:  
 19 MEDIUM TYPE: Floppy disk  
 20 COMPUTER: IBM PC compatible  
 21 OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 SOFTWARE: Patent in Release #1.0, Version #1.0  
 23 CURRENT APPLICATION DATA:  
 24 APPLICATION NUMBER: US/08/723,425A  
 25 FILING DATE:  
 26 CLASSIFICATION: 435  
 27 ATTORNEY/AGENT INFORMATION:  
 28 NAME: SADOFF, B.J.  
 29 REGISTRATION NUMBER: 36,663  
 30 REFERENCE/DOCKET NUMBER: 1487-13  
 31 TELECOMMUNICATION INFORMATION:  
 32 TELEPHONE: 703-816-4000  
 33 TELEFAX: 703-816-4100  
 34 INFORMATION FOR SEQ ID NO: 404:  
 35 SEQUENCE CHARACTERISTICS:  
 36 LENGTH: 9 amino acids  
 37 TYPE: amino acid  
 38 STRANDEDNESS: single  
 39 TOPOLOGY: linear  
 40 MOLECULE TYPE: peptide  
 41 US-08-723-425A-404  
 42 Query Match 36.48; Score 4; Db: 5; Length: 9;  
 43 Best Local Similarity 100.0%; Pred. No. 2; No. 5;  
 44 Matches 4; Conservative 0; Mismatches 0; Indels 0;

1 QY 2 HKSR 5  
 1111  
 14 4 HKSR 7

## RESULT 15

US-08-723-425A-407

Sequence 407, Application US/08723425A

Patent No. 6165730

## GENERAL INFORMATION:

APPLICANT: DELEYS, ROBERT

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT

TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF

TITLE OF INVENTION: ANTIBODIES OR BICITINATED PEPTIDES CORRESPONDING TO

NUMBER OF SEQUENCES: 453

CORRESPONDENCE ADDRESSES:

ADDRESSEES: NIXON &amp; VANDERHYE, P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723,425A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 1487-13

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 407:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-723-425A-407

Query Match

Best Local Similarity 100.0%; Score 4; ID 3; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 2 RKSR 5

Db 1 RKSR 4

## RESULT 16

US-09-112-206-402

Sequence 402, Application US/09112206

Patent No. 6210903

## GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT PEPTIDES AND THEIR

TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BICITINATED

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

NUMBER OF SEQUENCES: 453

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

INFORMATION FOR SEQ ID NO: 402

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-112-206-402

Query Match

Best Local Similarity 100.0%; Score 4; ID 3; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 2 RKSR 5

Db 1 RKSR 4

## RESULT 17

US-09-112-206-402

Sequence 402, Application US/09112206

Patent No. 6210903

## GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT PEPTIDES AND THEIR

TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BICITINATED

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

NUMBER OF SEQUENCES: 453

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

INFORMATION FOR SEQ ID NO: 402

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-112-206-402

Query Match

Best Local Similarity 100.0%; Score 4; ID 3; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 2 RKSR 5

Db 1 RKSR 4

## RESULT 18

US-09-112-206-402

Sequence 402, Application US/09112206

Patent No. 6210903

## GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT PEPTIDES AND THEIR

TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BICITINATED

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

NUMBER OF SEQUENCES: 453

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/09/112,206
: APPLICATION NUMBER: US/09/112,206
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/146,028
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 404:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-112-206-404

```

```

Query Match 36.4% Score 4: DB 3: Length 9:
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 RKSR 5
   IIII
DB 4 RKSR 7

```

```

RESULT 19
US-09-112-206-405
: Sequence 405, Application US/09112206
: Patent No. 6210503
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
: TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
: TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOGENICATED
: TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
: TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
: NUMBER OF SEQUENCES: 453
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/09/112,206
: APPLICATION NUMBER: US/09/112,206
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/146,028
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 405:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-112-206-405

```

```

Query Match 36.4% Score 4: DB 3: Length 9:
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 RKSR 5
   IIII
DB 3 RKSR 6

```

```

RESULT 20
US-09-112-206-406
: Sequence 406, Application US/09112206

```

```

: Patent No. 6210503
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
: TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
: TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOGENICATED
: TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
: TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
: NUMBER OF SEQUENCES: 453
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/09/112,206
: APPLICATION NUMBER: US/09/112,206
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/146,028
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 406:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-112-206-406

```

```

Query Match 36.4% Score 4: DB 3: Length 9:
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 RKSR 5
   IIII
DB 4 RKSR 7

```

```

RESULT 21
US-09-112-206-407
: Sequence 407, Application US/09112206
: Patent No. 6210504
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
: TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
: TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOGENICATED
: TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
: TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
: NUMBER OF SEQUENCES: 453
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/09/112,206
: APPLICATION NUMBER: US/09/112,206
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/146,028
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 407:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-112-206-407

```

```

Query Match 36.4% Score 4: DB 3: Length 9:
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy	2	RKSR	5
		1111	
Db	1	RKSR	4

```

RESULT 22
US-09-258-689-1
; Sequence 1, Application US/09258689
; Patent No. 6451527
; GENERAL INFORMATION:
; APPLICANT: Larocca, David
; APPLICANT: Baird, Andrew
; APPLICANT: Kassner, Paul
; TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR
; TITLE OF INVENTION: SELECTING INTERNALIZING LIGANDS FOR GENE DELIVERY
; FILE REFERENCE: 760100.430C3
; CURRENT APPLICATION NUMBER: US/09/258,689
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: A screened
; OTHER INFORMATION: peptide, from a random peptide library, that binds
; OTHER INFORMATION: and internalizes in a rGF receptor overproducing
; OTHER INFORMATION: cell line
; US-09-258-689-1

```

```

Query Match      36.48; Score 4; DH 4; Length 10;
Best Local Similarity 100.00; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Idents 0; Gaps 0;

```

Qy	2	RKSR	5
Db	7	RKSR	10

```

RESULT 23
US-09-195-379-1
? Sequence 1, Application US/09195379
? Patent No. 6472146
? GENERAL INFORMATION:
? APPLICANT: Larocca, David
? APPLICANT: Baird, Andrew
? APPLICANT: Kassner, Paul
? TITLE OF INVENTION: METHODS FOR IDENTIFICATION OF TARGET CELLS
? TITLE OF INVENTION: FOR KNOWN AND PUTATIVE LIGANDS
? FILE REFERENCE: 760100.430C1
? CURRENT APPLICATION NUMBER: US/09/195,379
? CURRENT FILING DATE: 1998-11-17
? NUMBER OF SEQ ID NOS: 4
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Unknown
? FEATURE:
? OTHER INFORMATION: Description of Unknown organism: A secreted
? OTHER INFORMATION: peptide, from a random peptide library, that binds
? OTHER INFORMATION: and internalizes in a cell receptor over-producing
? OTHER INFORMATION: cell line
US-09-195-379-1

```

```
Query Match      36.4%; Score 4; DB 4; Length 10;
Best Global Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 RKSR 5

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SY	Z KSP 0
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RESULT 25	
US-06 747 137 65	
Sequence 48, Application 15/ 0347147	
Patent No. 594513	
GENERAL INFORMATION:	
APPLICANT:	VEN, Richard L K
TITLE OF INVENTION:	NON-CLASSIFIED PROTEIN PARTICLES FOR
TITLE OF INVENTION:	THERAPEUTIC AND DIAGNOSTIC USE
NUMBER OF SEQUENCES:	194



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,841
FILING DATE: 01-JUN-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: App.e, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-00284605
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
US-08-747-137-63

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```

Query Match      36.48; Score 4; DB 2; Length 11;
Best Local Similarity 100.08; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      2 RKSR 5
Db      5 RKSR 8

```

```

RESULT 26
US-08-696-8548-3
Sequence 3, Application US/08696854B
Patent No. 6017878
GENERAL INFORMATION:
APPLICANT: SARAGOVIT, Uri H.
APPLICANT: Lesauteur, Lynne
APPLICANT: CUELLO, Claudio A.
TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
TITLE OF INVENTION: AND THEIR USES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: Continental Plaza, 411 Hackensack Avenue
CITY: Hackensack
STATE: N.J.
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,841
FILING DATE: 01-JUN-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: App.e, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-00284605
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
US-08-747-137-63
Query Match      36.48; Score 4; DB 2; Length 11;
Best Local Similarity 100.08; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2 RKSR 5
Db      5 RKSR 8
RESULT 27
US-08-696-8548-3
Sequence 3, Application US/08696854B
Patent No. 6017878
GENERAL INFORMATION:
APPLICANT: SARAGOVIT, Uri H.
APPLICANT: Lesauteur, Lynne
APPLICANT: CUELLO, Claudio A.
TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
TITLE OF INVENTION: AND THEIR USES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: Continental Plaza, 411 Hackensack Avenue
CITY: Hackensack
STATE: N.J.
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,841
FILING DATE: 01-JUN-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: App.e, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-00284605
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
US-08-747-137-63

```



```

: CURRENT FILING DATE: 1999-11-29
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 1
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Feature(s)
: OTHER INFORMATION: SYNTHETIC ORIGIN
: OTHER INFORMATION: The first amino acid is
: OTHER INFORMATION: acetylated
US-09-451-034-3

```

Query Match 36.4%; Score 4; LB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 140.2;  
Matches 4; Conservative 0; Mismatches 0; Indels

Qy	1 ARKS 4
Dd	3 ARKS 11

```

RESULT 32
US-09-451-034-a
: Sequence 8, Application US/09451034
: Patent No. 6369030
: GENERAL INFORMATION:
: APPLICANT: Cole, Phillip et al
: TITLE OF INVENTION: INHIBITORS OF
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 600-1-265
: CURRENT APPLICATION NUMBER: US/09/
: CURRENT FILING DATE: 1999-11-29
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID No 8
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of
: OTHER INFORMATION: SYNTHETIC MOI-
: OTHER INFORMATION: The first a.a
: OTHER INFORMATION: acetylated.
: US-09-451-034-a

```

```

Query Match          36.4%; Score 4; BH 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Qy 1 ARKS 4  
Db 7 ARKS 10

```

RESULT 33
US - 09-115-204 28
: Sequence 28, Application US/09115204
: Patent No. 5998375
: GENERAL INFORMATION:
: APPLICANT: Thorgersen, Henning
: APPLICANT: Madsen, Kjeld
: APPLICANT: Olsen, Offe B.
: APPLICANT: Johansen, Nils L.
: APPLICANT: Scheidegger, Mark
: TITLE OF INVENTION: No. 5998375:accept
: FILE REFERENCE: 5285-200-US
: CURRENT APPLICATION NUMBER: US/09/115-204
: CURRENT FILING DATE: 1998-07-14
: EARLIER APPLICATION NUMBER: 0867/97
: EARLIER FILING DATE: 1997-07-15
: EARLIER APPLICATION NUMBER: 60/052-8

```

[illegible][illegible]

Query Match:  $\frac{1}{2} \times \text{score}(\text{seq}_1, \text{seq}_2, \text{length}_1)$   
 Best Local Similarity:  $\max_{i,j} \text{score}(\text{seq}_i, \text{seq}_j, \text{length}_i)$   
 Matches:  $\{i, j \mid \text{score}(\text{seq}_i, \text{seq}_j, \text{length}_i) \geq \text{threshold}\}$

cy  
10

```

RESULT 35
US-08-145-061-13
: Sequence 13, Application US/08145061
: Patent No. 5460955
: GENERAL INFORMATION:
: APPLICANT: Mosher, Deane F.
: APPLICANT: Sottile, Jane M.
: TITLE OF INVENTION: FIBRONECTIN PURIFICATION VECTOR
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carl R. Schwartz, Charles & Brady
: STREET: 411 East Wisconsin Avenue
: CITY: Milwaukee
: STATE: Wisconsin
: COUNTRY: USA
: ZIP: 53202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/145,061
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/637,250
: FILING DATE: 03-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Schwartz, Carl R.
: REGISTRATION NUMBER: 29,437
: REFERENCE/DOCKET NUMBER: 96-296-9170-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (414)277-5715
: TELEFAX: (414)277-5591
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide Fragment
US-08-145-061-13

Query Match 27.3%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAI 10
DB 5 TAI 7

RESULT 36
US-08-401-512-81
: Sequence 81, Application US/08401512
: Patent No. 5595673
: GENERAL INFORMATION:
: APPLICANT: Keating, Mark T.
: APPLICANT: Curran, Mark E.
: APPLICANT: Wang, Qing
: TITLE OF INVENTION: Long QT Syndrome Genes
: NUMBER OF SEQUENCES: 81
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Venable, Baetjer, Howard & Civiletti LLP
: STREET: 1201 New York Avenue, Suite 1000
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3917
: COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/401,512
: FILING DATE: 09 MAY 1999
: CLASSIFICATION: 435
: APPLICANT: Mosher, Deane F.
: APPLICANT: Sottile, Jane M.
: NAME: SARG, Stephen A.
: REGISTRATION NUMBER: 29,437
: REFERENCE/DOCKET NUMBER: 96-296-9170-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-331-2200
: TELEFAX: 202-331-2200
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide
: HYDROPHILIC: N
US-08-401-512-81

Query Match 27.3%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAI 8
DB 6 TAI 8

RESULT 37
US-08-440-874A-3
: Sequence 3, Application US/08440874A
: Patent No. 5744277
: GENERAL INFORMATION:
: APPLICANT: Stuber, Walter
: APPLICANT: Wozniak, Leszek
: APPLICANT: Zdrobnicka, Robert
: TITLE OF INVENTION: BMPV Specific Peptides, Agents Thereof
: TITLE OF INVENTION: BMPV Specific Peptides, Agents Thereof
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Biomed Research, Inc.
: ADDRESS: Biomed
: STREET: 3301 Y Street, N.W., Suite 700
: CITY: Washington,
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3416
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,874A
: FILING DATE: 20 JUN 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/936,279
: FILING DATE: 27 AUG 1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4412804.7
: FILING DATE: 29 AUG 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Forman, David S.
: REGISTRATION NUMBER: 33,694
: REFERENCE/DOCKET NUMBER: 05552-210-04060
: TELECOMMUNICATION INFORMATION:

```

```

: TELEPHONE: 202-408-4000
: TELEFAX: 202-408-4400
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1
: OTHER INFORMATION: /note= "xaa is Psp where ES is any
: OTHER INFORMATION: appropriate amino acid and p is an integer from 2
: OTHER INFORMATION: to 11."
: FEATURE:
: NAME/KEY: Region
: LOCATION: 8
: OTHER INFORMATION: /note= "xaa is Psp where ES is any
: OTHER INFORMATION: appropriate amino acid and q is an integer from 2
: OTHER INFORMATION: to 11."
: US-08-460-874A-3

```

```

Query Match 27.3%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 SRD 6
DB 3 SRD 5

```

```

RESULT 38
: Sequence 4, Application US/08616855
: Patent No. 5770357
: GENERAL INFORMATION:
: APPLICANT: Douvas, Angelina
: APPLICANT: Ehresmann, Glenn
: TITLE OF INVENTION: Method of Diagnosing Carcin
: TITLE OF INVENTION: Arthritis-Encephalitis Virus Infection
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell and Flores
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: United States
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.2/5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/616,855
: FILING DATE:
: CLASSIFICATION: 436
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-ST 1988
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-616-855-3

```

```

Query Match 27.3%; Score 3; DB 1; Length 8;

```

```

: Best Local Similarity 100.0%; Pred. No. 2.5e+05;
: Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
: QY 2 PKS 4
: DB 6 PKS 8
: RESULT 40
: Sequence 4, Application US/08616855
: Patent No. 5770357
: GENERAL INFORMATION:
: APPLICANT: Douvas, Angelina
: APPLICANT: Ehresmann, Glenn
: TITLE OF INVENTION: Method of Diagnosing Carcin
: TITLE OF INVENTION: Arthritis-Encephalitis Virus Infection
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell and Flores
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: United States
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.2/5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/616,855
: FILING DATE:
: CLASSIFICATION: 436
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-ST 1988
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-147-777-4
: Query Match 27.0%; Score 3; DB 2; Length 8;
: Best Local Similarity 100.0%; Pred. No. 2.5e+05;
: Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
: QY 2 PKS 4
: DB 3 PKS 5
: RESULT 40
: Sequence 20, Application US/08616855
: Patent No. 5770357

```

```

1  GENERAL INFORMATION:
2  APPLICANT: Inoue, Makoto
3  APPLICANT: Kikuchi, Kaoru
4  APPLICANT: Ishige, Yoko
5  APPLICANT: Ito, Akira
6  APPLICANT: Kimura, Toru
7  APPLICANT: Nakayama, Chikao
8  APPLICANT: No. 5939534uchi, Hiroshi
9  TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
10 NUMBER OF SEQUENCES: 35
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: SUCHRUE, MION, ZINN, MACPEAK & SEAS
13 STREET: 2100 Pennsylvania Avenue, N.W.
14 CITY: Washington
15 STATE: D.C.
16 COUNTRY: USA
17 ZIP: 20037
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patentin Release #1.0, Version #1.40
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/669,284B
26 FILING DATE: 28-JUN-1996
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: PCT/JP94/02265
29 FILING DATE: 27-DEC-1994
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: JP 06-268281
32 FILING DATE: 05-OCT-1994
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: JP 06-201504
35 FILING DATE: 02-AUG-1994
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: JP 05-350934
38 FILING DATE: 29-DEC-1993
39 ATTORNEY/AGENT INFORMATION:
40 NAME: Nakamura, Dean H.
41 REGISTRATION NUMBER: 33,981
42 REFERENCE/DOCKET NUMBER: Q-42041
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: (202)293-7060
45 TELEFAX: (202)293-7860
46 INFORMATION FOR SEQ ID NO: 20:
47 SEQUENCE CHARACTERISTICS:
48 LENGTH: 8 amino acids
49 TYPE: amino acid
50 STRANDEDNESS:
51 TOPOLOGY: linear
52 MOLECULE TYPE: peptide
53 US-08-669-284B-20
54
55 Query Match 27.38; Score 3; Db 2; Length 8;
56 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
57 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
58
59 QY 6 DMT 8
60 DB 5 DMT 7
61
62 RESULT 41
63 US-08-726-106A-181
64 Sequence 181, Application US/08726306A
65 Patent No. 5958684
66 GENERAL INFORMATION:
67 APPLICANT: van Leeuwen, Frederik Willem
68 APPLICANT: Burbach, Johannes Peter Henri
69 APPLICANT: Grosveld, Franklin G.
70 TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
71 NUMBER OF SEQUENCES: 189
72 CORRESPONDENCE ADDRESS:

```

```

1  ADDRESSEE: Kung'u, William H.
2  STREET: 1 Fairview Avenue
3  CITY: Boston
4  STATE: MA
5  COUNTRY: US
6  ZIP: 02111
7  COMPUTER READABLE FORM:
8  MEDIUM TYPE: Floppy disk
9  COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: WordPerfect 6.1
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/106,06A
14 FILING DATE: 02-JUN-1996
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US/08/669,284B
17 FILING DATE: 02-JUN-1996
18 PUBLICATION NUMBER: 5,939,534
19 NAME: William H. Kung'u
20 REFERENCE/DOCKET NUMBER: Q-42041
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (617) 445-9100
23 TELEFAX: (617) 445-9100
24 INFORMATION FOR SEQ ID NO: 181:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 8 amino acids
27 TYPE: amino acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 MOLECULE TYPE: peptide
31 US-08-726-106A-181
32
33 Query Match 27.38; Score 3; Db 2; Length 8;
34 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
35 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
36
37 QY 4 SKD 6
38 DB 5 SKD 5
39
40 RESULT 42
41 US-08-242-5400-21
42 Sequence 21, Application US/08242500
43 Patent No. 6665747
44 GENERAL INFORMATION:
45 APPLICANT: Picta, David J.
46 APPLICANT: Picta, David J.
47 TITLE OF INVENTION: THE AMINO ACIDS
48 NUMBER OF SEQUENCES: 6
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Picta, David J.
51 STREET: 1 DNA Way
52 CITY: South San Francisco
53 STATE: California
54 COUNTRY: USA
55 ZIP: 94080
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: Floppy disk
58 COMPUTER: IBM PC compatible
59 OPERATING SYSTEM: PC-DOS/MS-DOS
60 SOFTWARE: WordPerfect 6.03a
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/08/242,500
63 FILING DATE: 21-Apr-1994
64 CLASSIFICATION: 530
65 PRIOR APPLICATION DATA:
66 APPLICATION NUMBER: 08/174583
67 FILING DATE: 07-JAN-1994

```

1 PRIOR APPLICATION DATA:  
 2 APPLICATION NUMBER: 07/744768  
 3 FILING DATE: 14-AUG-1991  
 4 ATTORNEY/AGENT INFORMATION:  
 5 NAME: Svoboda, Craig G.  
 6 REGISTRATION NUMBER: 39,044  
 7 REFERENCE/DOCKET NUMBER: P3718P3  
 8 TELECOMMUNICATION INFORMATION:  
 9 TELEPHONE: 650/225-1489  
 10 TELEFAX: 650/952-9881  
 11 INFORMATION FOR SEQ ID NO: 21:  
 12 SEQUENCE CHARACTERISTICS:  
 13 LENGTH: 8 amino acids  
 14 TYPE: Amino Acid  
 15 TOPOLOGY: Linear  
 16 US-08-232-539D-21

Query Match 27.38; Score 8; DH 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 RKS 4  
 1:1  
 DB 6 RKS 8

## RESULT 43

1 US-08-978-404B-57  
 2 Sequence 57, Application US/08978404B  
 3 Patent No. 5968782  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Stevens, Richard L.  
 6 TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES  
 7 TITLE OF INVENTION: FIBRINOGEN  
 8 NUMBER OF SEQUENCES: 74  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
 11 STREET: 600 Atlantic Avenue  
 12 CITY: Boston  
 13 STATE: MA  
 14 COUNTRY: U.S.A.  
 15 ZIP: 02210-2211

1 COMPUTER READABLE FORM:  
 2 MEDIUM TYPE: Diskette  
 3 COMPUTER: IBM Compatible  
 4 OPERATING SYSTEM: DOS  
 5 SOFTWARE: FASTSEQ for Windows Version 2.0  
 6 CURRENT APPLICATION DATA:  
 7 APPLICATION NUMBER: US/08/978.404B  
 8 FILING DATE: 25-NOV-97  
 9 CLASSIFICATION: 435  
 10 PRIOR APPLICATION DATA:  
 11 APPLICATION NUMBER: 60/332.354  
 12 FILING DATE: 04-DEC-1996  
 13 ATTORNEY/AGENT INFORMATION:  
 14 NAME: Plumer, Elizabeth R.  
 15 REGISTRATION NUMBER: 36,637  
 16 REFERENCE/DOCKET NUMBER: B0901/7093  
 17 TELECOMMUNICATION INFORMATION:  
 18 TELEPHONE: 617-720-3500  
 19 TELEFAX: 617-720-2441  
 20 TELEX:  
 21 INFORMATION FOR SEQ ID NO: 57:  
 22 SEQUENCE CHARACTERISTICS:  
 23 LENGTH: 8 amino acids  
 24 TYPE: amino acid  
 25 STRANDEDNESS: single  
 26 TOPOLOGY: linear  
 27 MOLECULE TYPE: No. 5968782e

Query Match 27.38; Score 3; DH 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;

1 P3718P3  
 2 Sequence 57, Application US/08978404B  
 3 Patent No. 5968782  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Stevens, Richard L.  
 6 TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES  
 7 TITLE OF INVENTION: FIBRINOGEN  
 8 NUMBER OF SEQUENCES: 74  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
 11 STREET: 600 Atlantic Avenue  
 12 CITY: Boston  
 13 STATE: MA  
 14 COUNTRY: U.S.A.  
 15 ZIP: 02210-2211

Query Match 27.38; Score 8; DH 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 RKS 4  
 1:1  
 DB 6 RKS 8

## RESULT 45

1 US-08-978-404B-57  
 2 Sequence 57, Application US/08978404B  
 3 Patent No. 5968782  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Stevens, Richard L.  
 6 TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES  
 7 TITLE OF INVENTION: FIBRINOGEN  
 8 NUMBER OF SEQUENCES: 74  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
 11 STREET: 600 Atlantic Avenue  
 12 CITY: Boston  
 13 STATE: MA  
 14 COUNTRY: U.S.A.  
 15 ZIP: 02210-2211

1 COMPUTER READABLE FORM:  
 2 MEDIUM TYPE: Diskette  
 3 COMPUTER: IBM Compatible  
 4 OPERATING SYSTEM: DOS  
 5 SOFTWARE: FASTSEQ for Windows Version 2.0  
 6 CURRENT APPLICATION DATA:  
 7 APPLICATION NUMBER: US/08/978.404B  
 8 FILING DATE: 25-NOV-97  
 9 CLASSIFICATION: 435  
 10 PRIOR APPLICATION DATA:  
 11 APPLICATION NUMBER: 60/332.354  
 12 FILING DATE: 04-DEC-1996  
 13 ATTORNEY/AGENT INFORMATION:  
 14 NAME: Plumer, Elizabeth R.  
 15 REGISTRATION NUMBER: 36,637  
 16 REFERENCE/DOCKET NUMBER: B0901/7093  
 17 TELECOMMUNICATION INFORMATION:  
 18 TELEPHONE: 617-720-3500  
 19 TELEFAX: 617-720-2441  
 20 TELEX:  
 21 INFORMATION FOR SEQ ID NO: 57:  
 22 SEQUENCE CHARACTERISTICS:  
 23 LENGTH: 8 amino acids  
 24 TYPE: amino acid  
 25 STRANDEDNESS: single  
 26 TOPOLOGY: linear  
 27 MOLECULE TYPE: No. 5968782e

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 Best Local Similarity 100.0%; Pred. No. 2.5e+05;





APPLICATION NUMBER: 08/466163  
 FILING DATE: 06-Jun-1995  
 APPLICATION NUMBER: 08/405617  
 FILING DATE: 15-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/185899  
 FILING DATE: 26-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/879495  
 FILING DATE: 07-MAY-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/744768  
 FILING DATE: 14-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET NUMBER: P0718P20101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
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 SEQUENCE CHARACTERISTICS:  
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 TOPOLOGY: linear  
 US-08-466-161-27

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 Sequence 4; Application US/08452872  
 Patent No. 6057298  
 GENERAL INFORMATION:  
 APPLICANT: Roop, Dennis R.  
 APPLICANT: Rothnagel, Joseph A.  
 APPLICANT: Greenhalgh, David A.  
 APPLICANT: Yuspa, Stuart H.  
 TITLE OF INVENTION: KERATIN K1 EXPRESSION VECTORS  
 TITLE OF INVENTION: AND METHODS OF USE  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LYON & LYON  
 STREET: 611 West Sixth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90017  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB Storage  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/452,872  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/147,777  
 FILING DATE:  
 APPLICATION NUMBER: 07/876,289  
 FILING DATE: April 30, 1992  
 APPLICATION NUMBER: Unassigned (204/144)  
 FILING DATE: October 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.

REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER: P0718P20101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 1  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: linear  
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 Matches 3; Conservative 0; Mismatches 0; Indels 0;  
 QY 2 RKS 4  
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 Sequence 4; Application US/08452872  
 Patent No. 6057298  
 GENERAL INFORMATION:  
 APPLICANT: Roop, Dennis R.  
 APPLICANT: Rothnagel, Joseph A.  
 APPLICANT: Greenhalgh, David A.  
 APPLICANT: Yuspa, Stuart H.  
 TITLE OF INVENTION: KERATIN K1 EXPRESSION VECTORS  
 TITLE OF INVENTION: AND METHODS OF USE  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LYON & LYON  
 STREET: 611 West Sixth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90017  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB Storage  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/452,071-4  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/147,777  
 FILING DATE:  
 APPLICATION NUMBER: 07/876,289  
 FILING DATE: April 30, 1992  
 APPLICATION NUMBER: Unassigned (204/144)  
 FILING DATE: October 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.

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OM protein - protein search, using sw model

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Title: US-09-787-443-22

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	4	36.4	9	12	US-09-793-451-460
7	4	36.4	9	12	US-09-793-451-329
8	4	36.4	9	12	US-09-793-451-423
9	4	36.4	9	12	US-09-793-451-528
10	4	36.4	10	9	US-09-866-073-1
11	4	36.4	10	11	US-09-572-404B-1142
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291	3	27.3	10	11	US-09-799-250-668	Sequence 668, Appl	3	27.3	1	US-09-572-403A-3497	Sequence 3497, Appl
292	3	27.3	10	11	US-09-799-250-673	Sequence 673, Appl	3	27.3	1	US-09-572-403A-3643	Sequence 3643, Appl
293	3	27.3	10	11	US-09-799-250-713	Sequence 713, Appl	3	27.3	1	US-09-572-403A-3644	Sequence 3644, Appl
294	3	27.3	10	11	US-09-952-267-46	Sequence 46, Appl	3	27.3	1	US-09-572-403A-3845	Sequence 3845, Appl
295	3	27.3	10	11	US-09-809-638-46	Sequence 49, Appl	3	27.3	1	US-09-572-403A-3932	Sequence 3932, Appl
296	3	27.3	10	11	US-09-809-638-114	Sequence 113, Appl	3	27.3	1	US-09-572-403A-4114	Sequence 4114, Appl
297	3	27.3	10	11	US-09-809-638-176	Sequence 177, Appl	3	27.3	1	US-09-572-403A-4115	Sequence 4115, Appl
298	3	27.3	10	11	US-09-809-638-166	Sequence 306, Appl	3	27.3	1	US-09-572-403A-4116	Sequence 4116, Appl
299	3	27.3	10	11	US-09-809-638-381	Sequence 381, Appl	3	27.3	1	US-09-572-403A-4173	Sequence 4173, Appl
300	3	27.3	10	11	US-09-809-638-399	Sequence 399, Appl	3	27.3	1	US-09-572-403A-4177	Sequence 4177, Appl
301	3	27.3	10	11	US-09-809-638-565	Sequence 565, Appl	3	27.3	1	US-09-572-403A-4196	Sequence 4196, Appl
302	3	27.3	10	11	US-09-809-638-589	Sequence 589, Appl	3	27.3	1	US-09-572-403A-4197	Sequence 4197, Appl
303	3	27.3	10	11	US-09-809-638-667	Sequence 667, Appl	3	27.3	1	US-09-572-403A-4198	Sequence 4198, Appl
304	3	27.3	10	11	US-09-809-638-686	Sequence 686, Appl	3	27.3	1	US-09-572-403A-4199	Sequence 4199, Appl
305	3	27.3	10	11	US-09-809-638-691	Sequence 691, Appl	3	27.3	1	US-09-845-304-237	Sequence 37, Appl
306	3	27.3	10	11	US-09-809-638-714	Sequence 714, Appl	3	27.3	1	US-09-845-304-238	Sequence 38, Appl
307	3	27.3	10	11	US-09-876-904A-152	Sequence 152, Appl	3	27.3	1	US-09-932-165-769	Sequence 783, Appl
308	3	27.3	10	11	US-09-876-904A-274	Sequence 274, Appl	3	27.3	1	US-09-932-165-769	Sequence 783, Appl
309	3	27.3	10	11	US-09-876-904A-274	Sequence 274, Appl	3	27.3	1	US-09-932-165-769	Sequence 783, Appl

381	3	27.3	10	12	US-09-932-165-1072	Sequence 1072, App	454	1	1	US-09-932-165-1072	Sequence 1072, App
382	3	27.3	10	12	US-09-932-165-1271	Sequence 1271, App	455	1	1	US-09-932-165-1271	Sequence 1271, App
383	3	27.3	10	12	US-09-932-165-1305	Sequence 1305, App	456	1	1	US-09-932-165-1305	Sequence 1305, App
384	3	27.3	10	12	US-10-002-244-52	Sequence 52, Appl	457	1	1	US-10-002-244-52	Sequence 52, Appl
385	3	27.3	10	12	US-10-062-587-7	Sequence 7, Appl	458	1	1	US-10-062-587-7	Sequence 7, Appl
386	3	27.3	10	12	US-10-193-764-22	Sequence 22, Appl	459	1	1	US-10-193-764-22	Sequence 22, Appl
387	3	27.3	10	12	US-09-572-270A-94	Sequence 94, App	460	1	1	US-09-572-270A-94	Sequence 94, App
388	3	27.3	10	12	US-09-572-270A-240	Sequence 240, App	461	1	1	US-09-572-270A-240	Sequence 240, App
389	3	27.3	10	12	US-09-572-270A-242	Sequence 242, App	462	1	1	US-09-572-270A-242	Sequence 242, App
390	3	27.3	10	12	US-09-572-270A-243	Sequence 243, App	463	1	1	US-09-572-270A-243	Sequence 243, App
391	3	27.3	10	12	US-09-572-270A-656	Sequence 656, App	464	1	1	US-09-572-270A-656	Sequence 656, App
392	3	27.3	10	12	US-09-572-270A-739	Sequence 739, App	465	1	1	US-09-572-270A-739	Sequence 739, App
393	3	27.3	10	12	US-09-572-270A-743	Sequence 743, App	466	1	1	US-09-572-270A-743	Sequence 743, App
394	3	27.3	10	12	US-09-572-270A-788	Sequence 788, App	467	1	1	US-09-572-270A-788	Sequence 788, App
395	3	27.3	10	12	US-09-572-270A-787	Sequence 787, App	468	1	1	US-09-572-270A-787	Sequence 787, App
396	3	27.3	10	12	US-09-572-270A-818	Sequence 818, App	469	1	1	US-09-572-270A-818	Sequence 818, App
397	3	27.3	10	12	US-09-572-270A-853	Sequence 853, App	470	1	1	US-09-572-270A-853	Sequence 853, App
398	3	27.3	10	12	US-09-572-270A-872	Sequence 872, App	471	1	1	US-09-572-270A-872	Sequence 872, App
399	3	27.3	10	12	US-09-572-270A-882	Sequence 882, App	472	1	1	US-09-572-270A-882	Sequence 882, App
400	3	27.3	10	12	US-09-572-270A-895	Sequence 895, App	473	1	1	US-09-572-270A-895	Sequence 895, App
401	3	27.3	10	12	US-09-572-270A-897	Sequence 897, App	474	1	1	US-09-572-270A-897	Sequence 897, App
402	3	27.3	10	12	US-09-572-270A-1066	Sequence 1066, App	475	1	1	US-09-572-270A-1066	Sequence 1066, App
403	3	27.3	10	12	US-09-572-270A-1113	Sequence 1113, App	476	1	1	US-09-572-270A-1113	Sequence 1113, App
404	3	27.3	10	12	US-09-572-270A-1114	Sequence 1114, App	477	1	1	US-09-572-270A-1114	Sequence 1114, App
405	3	27.3	10	12	US-10-190-082-322	Sequence 322, App	478	1	1	US-10-190-082-322	Sequence 322, App
406	3	27.3	10	12	US-10-190-082-434	Sequence 434, App	479	1	1	US-10-190-082-434	Sequence 434, App
407	3	27.3	10	12	US-10-190-082-382	Sequence 382, App	480	1	1	US-10-190-082-382	Sequence 382, App
408	3	27.3	10	12	US-10-190-082-505	Sequence 505, App	481	1	1	US-10-190-082-505	Sequence 505, App
409	3	27.3	10	12	US-10-190-082-551	Sequence 551, App	482	1	1	US-10-190-082-551	Sequence 551, App
410	3	27.3	10	12	US-09-935-384-47	Sequence 47, Appl	483	1	1	US-09-935-384-47	Sequence 47, Appl
411	3	27.3	10	12	US-09-935-384-161	Sequence 161, App	484	1	1	US-09-935-384-161	Sequence 161, App</

OTHER INFORMATION: Description of Unknown Organism: C/ERP (CCAA7/enhancer  
US-09-876-904A-456

Query Match 45.5% Score 5; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSND 6  
IIII

DB 2 RKSND 6

#### RESULT 2

US-09-876-904A-504  
Sequence 504, Application US/09876904A  
Publication No. US20030072794A1

#### GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 504  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURE:

OTHER INFORMATION: Mouse AGP/ERP.

US-09-876-904A-504

Query Match 45.5% Score 5; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSND 6  
IIII

DB 2 RKSND 6

#### RESULT 3

US-09-876-904A-507  
Sequence 507, Application US/09876904A  
Publication No. US20030072794A1

#### GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 507  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Rattus sp.  
FEATURE:

OTHER INFORMATION: Rat LAP, a 32-kD liver-enriched transcriptional  
activator, also present in lung with 71% sequence  
similarity to C/ERP

US-09-876-904A-507

Query Match 45.5% Score 5; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5, 1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSND 6  
IIII

DB 2 RKSND 6

#### RESULT 4

US-09-876-904A-507  
Sequence 507, Application US/09876904A  
Publication No. US20030072794A1

#### GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 507  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Rattus sp.  
FEATURE:  
OTHER INFORMATION: Human AFP 11% (57-60).

Query Match 45.5% Score 5; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSND 6  
IIII

DB 2 RKSND 6

#### RESULT 5

US-09-876-904A-507  
Sequence 507, Application US/09876904A  
Publication No. US20030072794A1

#### GENERAL INFORMATION:

APPLICANT: KESSEF, SUSAN  
APPLICANT: GRAD, ROBERT  
APPLICANT: WU, YIN-CHI  
TITLE OF INVENTION: PEPTIDE ANTICOMPLEXONS FOR THE  
TITLE OF INVENTION: PEPTIDE ANTICOMPLEXONS FOR THE  
NUMBER OF SEQUENCES: 48  
CURRENT FILING DATE: 2001-06-08  
ADDRESS: 1000 HAWTHORNE BLVD  
STREET: 100 HAWTHORNE  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: DOS/MS DOS  
SOFTWARE: Patent In Ver. 2.1, Version 4.1.4  
CURRENT APPLICATION DATA  
APPLICATION NUMBER: US/09/876,904A  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: GREENHALGH, DUNCAN A  
REGISTRATION NUMBER: 48,628  
REFERENCE/DEPOSIT NUMBER: MTF 023 (R-95/27)  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000  
 TELEFAX: (617) 248-7100  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-315-355-4

Query Match 36.4% Score 4.18 12: Length 9:  
 Best Local Similarity 100.0% Pred. No. 5.1e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

QY 4 SRDM 7  
 Db 6 SRDM 9

## RESULT 6

US-09-793-451-250  
 : Sequence 260, Application US/09793451  
 : Publication No. US20030157597A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arthur B. Raitano  
 : APPLICANT: Daniel E.H. Afar  
 : APPLICANT: Gazelle S. Rastegar  
 : APPLICANT: Steve Chappell Mitchell  
 : APPLICANT: Rene S. Hubert  
 : APPLICANT: Pia M. Challita-Eid  
 : APPLICANT: Mary Faris  
 : APPLICANT: Aya Jakobovits  
 : TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY  
 : TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
 : FILE REFERENCE: 129,205U2  
 : CURRENT APPLICATION NUMBER: US/09/793,451  
 : CURRENT FILING DATE: 2001-02-26  
 : PRIOR APPLICATION NUMBER: 60/184,556  
 : PRIOR FILING DATE: 2000-02-24  
 : PRIOR APPLICATION NUMBER: 60/218,856  
 : PRIOR FILING DATE: 2000-07-13  
 : NUMBER OF SEQ ID NOS: 752  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 260  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: homo sapiens  
 US-09-793 451-250

Query Match 36.4% Score 4.18 12: Length 9:  
 Best Local Similarity 100.0% Pred. No. 5.1e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

QY 2 RKSR 5  
 Db 6 RKSR 9

## RESULT 7

US-09-793-451-329  
 : Sequence 129, Application US/09793451  
 : Publication No. US20030157597A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arthur B. Raitano  
 : APPLICANT: Daniel E.H. Afar  
 : APPLICANT: Gazelle S. Rastegar  
 : APPLICANT: Steve Chappell Mitchell  
 : APPLICANT: Rene S. Hubert  
 : APPLICANT: Pia M. Challita-Eid  
 : APPLICANT: Mary Faris  
 : APPLICANT: Aya Jakobovits  
 : TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY

TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY  
 FILE REFERENCE: 129,205U2  
 CURRENT APPLICATION NUMBER: US/09/793,451  
 PRIOR APPLICATION NUMBER: 60/184,556  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: 60/218,856  
 PRIOR FILING DATE: 2000-07-13  
 NUMBER OF SEQ ID NOS: 752  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 429  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-09-793 451-329

Query Match 36.4% Score 4.18 12: Length 9:  
 Best Local Similarity 100.0% Pred. No. 5.1e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

QY 4 RKSR 5  
 Db 6 RKSR 9

## RESULT 8

US-09-793-451-429  
 : Sequence 429, Application US/09793451  
 : Publication No. US20030157597A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arthur B. Raitano  
 : APPLICANT: Daniel E.H. Afar  
 : APPLICANT: Gazelle S. Rastegar  
 : APPLICANT: Steve Chappell Mitchell  
 : APPLICANT: Rene S. Hubert  
 : APPLICANT: Pia M. Challita-Eid  
 : APPLICANT: Mary Faris  
 : APPLICANT: Aya Jakobovits  
 : TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY  
 : TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
 : FILE REFERENCE: 129,205U2  
 : CURRENT APPLICATION NUMBER: US/09/793,451  
 : CURRENT FILING DATE: 2001-02-26  
 : PRIOR APPLICATION NUMBER: 60/184,556  
 : PRIOR FILING DATE: 2000-02-24  
 : PRIOR APPLICATION NUMBER: 60/218,856  
 : PRIOR FILING DATE: 2000-07-13  
 : NUMBER OF SEQ ID NOS: 752  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 429  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: homo sapiens  
 US-09 793-451-429

Query Match 36.4% Score 4.18 12: Length 9:  
 Best Local Similarity 100.0% Pred. No. 5.1e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

QY 2 RKSR 5  
 Db 6 RKSR 9

## RESULT 9

US-09-793-451-529  
 : Sequence 529, Application US/09793451  
 : Publication No. US20030157597A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arthur B. Raitano  
 : APPLICANT: Daniel E.H. Afar  
 : APPLICANT: Gazelle S. Rastegar  
 : APPLICANT: Steve Chappell Mitchell



```

1 APPLICANT: Rene S. Hubert
2 APPLICANT: Pia M. Challita-Eid
3 APPLICANT: Mary Faris
4 APPLICANT: Aya Jakobovits
5 TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
6 FILE REFERENCE: EXPRESSION IN VARIOUS CANCERS
7 CURRENT FILING DATE: 2001-02-24
8 CURRENT APPLICATION NUMBER: US/09/793,451
9 PRIOR FILING DATE: 2001-02-26
10 PRIOR APPLICATION NUMBER: 60/184,558
11 PRIOR FILING DATE: 2000-02-24
12 PRIOR APPLICATION NUMBER: 60/218,856
13 NUMBER OF SEQ ID NOS: 752
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO 528
16 LENGTH: 9
17 TYPE: PRT
18 ORGANISM: homo sapiens
19 US-09-793-451-528

```

```

Query Match 36.4% Score 4: 16 12: 16 4: 16
Best Local Similarity 100.0% Pred. No. 5, 16-05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

```

```

QY 2 RKSR 5
DB 3 RKSR 6

```

## RESULT 10

US-09-866-073-1

```

1 Sequence i: Application US/09866073
2 Patent No. US20020068272A1

```

## GENERAL INFORMATION:

```

1 APPLICANT: Larocca, David
2 APPLICANT: Baird, Andrew
3 APPLICANT: Kassner, Paul
4 TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR
5 DETECTING AND IDENTIFYING PROTEIN PROTEIN
6 TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERNALIZATION
7 TITLE OF INVENTION: AND TRANSGENE EXPRESSION AND CELLS OR TISSUE
8 TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING
9 TITLE OF INVENTION: GENE DELIVERY VECTORS
10 FILE REFERENCE: 760100.430C4
11 CURRENT APPLICATION NUMBER: US/09/866.073
12 CURRENT FILING DATE: 2001-05-24
13 NUMBER OF SEQ ID NOS: 17
14 SOFTWARE: PatentIn Ver. 2.0
15 SEQ ID NO 1
16 LENGTH: 10
17 TYPE: PRT
18 ORGANISM: Unknown
19 FEATURE:
20 OTHER INFORMATION: Description of Unknown Organism: A software
21 OTHER INFORMATION: peptide, from a random peptide library that binds
22 OTHER INFORMATION: and internalizes in a cell receptor receptor
23 OTHER INFORMATION: cell line
24 US-09-866-073-1

```

```

Query Match 36.4% Score 4: 16 4: 16 4: 16
Best Local Similarity 100.0% Pred. No. 2, 40-02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

```

```

QY 2 RKSR 5
DB 7 RKSR 10

```

## RESULT 11

US-09-572-404B-1142

```

1 Sequence 1142: Application US/09572404B
2 Publication No. US20030078374A1

```

```

1 GENERAL INFORMATION
2 APPLICANT: Patent 1142
3 TITLE OF INVENTION: Computer-implemented methods for the rapid detection
4 FILE REFERENCE: Biotech Patent
5 CURRENT FILING DATE: 2001-02-24
6 NUMBER OF SEQ ID NOS: 400
7 SOFTWARE: PatentIn Ver. 2.0
8 SEQ ID NO 1142
9 LENGTH: 10
10 TYPE: PRT
11 ORGANISM: Homo Sapiens
12 FEATURE:
13 OTHER INFORMATION: This is a computer-implemented method for the rapid
14 OTHER INFORMATION: detection of a disease state in a patient
15 US-09-572-404B-1142

```

```

Query Match 36.4% Score 4: 16 12: 16 4: 16
Best Local Similarity 100.0% Pred. No. 5, 16-05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

```

```

QY 1 APPS 3
DB 3 APPS 6

```

## RESULT 12

US-09-572-404B-1144

```

1 Sequence 1144: Application US/09572404B
2 Publication No. US20030078374A1

```

## GENERAL INFORMATION:

```

1 APPLICANT: Patent 1144
2 TITLE OF INVENTION: Computer-implemented methods for the rapid detection
3 FILE REFERENCE: Biotech Patent
4 CURRENT FILING DATE: 2001-02-24
5 NUMBER OF SEQ ID NOS: 400
6 SOFTWARE: PatentIn Ver. 2.0
7 SEQ ID NO 1144
8 LENGTH: 10
9 TYPE: PRT
10 ORGANISM: Homo Sapiens
11 FEATURE:
12 OTHER INFORMATION: This is a computer-implemented method for the rapid
13 OTHER INFORMATION: detection of a disease state in a patient
14 US-09-572-404B-1144

```

```

Query Match 36.4% Score 4: 16 12: 16 4: 16
Best Local Similarity 100.0% Pred. No. 2, 40-02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

```

```

QY 1 APPS 4
DB 4 APPS 7

```

## RESULT 13

US-09-572-404B-1146

```

1 Sequence 1146: Application US/09572404B
2 Publication No. US20030078374A1

```

## GENERAL INFORMATION:

```

1 APPLICANT: Patent 1146
2 TITLE OF INVENTION: Computer-implemented methods for the rapid detection
3 FILE REFERENCE: Biotech Patent
4 CURRENT FILING DATE: 2001-02-24
5 NUMBER OF SEQ ID NOS: 400
6 SOFTWARE: PatentIn Ver. 2.0
7 SEQ ID NO 1146
8 LENGTH: 10
9 TYPE: PRT
10 ORGANISM: Homo Sapiens
11 FEATURE:

```

OTHER INFORMATION: sequence located in SEQ ID NO: 3890 or SEQ ID NO: 3891 at 240-245 and may differ from the human genome.  
 OTHER INFORMATION: with Sequence 2993 in this patent.  
 US-09-572-404B-2994

Query Match 36.4%, Score 4, DB 11, Length 10  
 Best Local Similarity 100.0%, Pred. No. 2.4e+02  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0  
 QY 2 RKSR 5  
 Db 2 RKSR 5  
 1111

## RESULT 14

US-09-572-404B-3890  
 Sequence 3890, Application US/09572404B  
 Publication No. US20030078374A1  
 GENERAL INFORMATION:  
 APPLICANT: Proteom Ltd  
 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 FILE REFERENCE: Human Patent  
 CURRENT APPLICATION NUMBER: US/09/572.404B  
 CURRENT FILING DATE: 2000-05-17  
 NUMBER OF SEQ ID NOS: 4203  
 SOFTWARE: ProtPatent version 1.0  
 SEQ ID NO 3890  
 LENGTH: 10  
 TYPE: PPT  
 ORGANISM: Homo Sapiens  
 FEATURE:  
 OTHER INFORMATION: sequence located in SEQ ID NO: 3891 at 240-245 and may differ from the human genome.  
 OTHER INFORMATION: Sequence 3891 in this patent.  
 US-09-572-404B-3890

Query Match 36.4%, Score 4, DB 11, Length 10  
 Best Local Similarity 100.0%, Pred. No. 2.4e+02  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 ARKS 4  
 Db 1 ARKS 4  
 1111

## RESULT 15

US-09-572-404B-3891  
 Sequence 3891, Application US/09572404B  
 Publication No. US20030078374A1  
 GENERAL INFORMATION:  
 APPLICANT: Proteom Ltd  
 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 FILE REFERENCE: Human Patent  
 CURRENT APPLICATION NUMBER: US/09/572.404B  
 CURRENT FILING DATE: 2000-05-17  
 NUMBER OF SEQ ID NOS: 4203  
 SOFTWARE: ProtPatent version 1.0  
 SEQ ID NO 3891  
 LENGTH: 10  
 TYPE: PPT  
 ORGANISM: Homo Sapiens  
 FEATURE:  
 OTHER INFORMATION: sequence located in SEQ ID NO: 3890 at 240-245 and may differ from the human genome.  
 OTHER INFORMATION: Sequence 3890 in this patent.  
 US-09-572-404B-3891

Query Match 36.4%, Score 4, DB 11, Length 10  
 Best Local Similarity 100.0%, Pred. No. 2.4e+02  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0  
 QY 1 ARKS 4  
 Db 1 ARKS 4  
 1111

RESULT 16  
 US-09-572-404B-3892  
 Sequence 3892, Application US/09572404B  
 Publication No. US20030078374A1  
 GENERAL INFORMATION:  
 APPLICANT: Proteom Ltd  
 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 FILE REFERENCE: Human Patent  
 CURRENT APPLICATION NUMBER: US/09/572.404B  
 CURRENT FILING DATE: 2000-05-17  
 NUMBER OF SEQ ID NOS: 4203  
 SOFTWARE: ProtPatent version 1.0  
 SEQ ID NO 3892  
 LENGTH: 10  
 TYPE: PPT  
 ORGANISM: Homo Sapiens  
 FEATURE:  
 OTHER INFORMATION: sequence located in SEQ ID NO: 3890 at 240-245 and may differ from the human genome.  
 OTHER INFORMATION: Sequence 3890 in this patent.  
 US-09-572-404B-3892

Query Match 36.4%, Score 4, DB 11, Length 10  
 Best Local Similarity 100.0%, Pred. No. 2.4e+02  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 ARKS 4  
 Db 1 ARKS 4  
 1111

## RESULT 17

US-09-572-404B-3893  
 Sequence 3893, Application US/09572404B  
 Publication No. US20030078374A1  
 GENERAL INFORMATION:  
 APPLICANT: Proteom Ltd  
 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 FILE REFERENCE: Human Patent  
 CURRENT APPLICATION NUMBER: US/09/572.404B  
 CURRENT FILING DATE: 2000-05-17  
 NUMBER OF SEQ ID NOS: 4203  
 SOFTWARE: ProtPatent version 1.0  
 SEQ ID NO 3893  
 LENGTH: 10  
 TYPE: PPT  
 ORGANISM: Homo Sapiens  
 FEATURE:  
 OTHER INFORMATION: sequence located in SEQ ID NO: 3890 at 240-245 and may differ from the human genome.  
 OTHER INFORMATION: Sequence 3890 in this patent.  
 US-09-572-404B-3893

Query Match 36.4%, Score 4, DB 11, Length 10  
 Best Local Similarity 100.0%, Pred. No. 2.4e+02  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 ARKS 4  
 Db 1 ARKS 4  
 1111

## RESULT 18

US-09-572-404B-4130  
 Sequence 4130, Application US/09572404B  
 Publication No. US20030078374A1  
 GENERAL INFORMATION:  
 APPLICANT: Proteom Ltd  
 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 FILE REFERENCE: Human Patent  
 CURRENT APPLICATION NUMBER: US/09/572.404B  
 CURRENT FILING DATE: 2000-05-17  
 NUMBER OF SEQ ID NOS: 4203  
 SOFTWARE: ProtPatent version 1.0  
 SEQ ID NO 4130

; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence located in PNCV OR SEQ at 131 140 and may interact with  
 ; OTHER INFORMATION: Sequence 4131 in this patent.  
 US-09-572-404B-4130

Query Match 36.4%; Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ARKS 4  
 DB 6 ARKS 9

#### RESULT 19

; Sequence 4131, Application US/09572404B  
 ; Publication No. US20030078374A1  
 ; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 ; FILE REFERENCE: Human Patent  
 ; CURRENT APPLICATION NUMBER: US/09/572,404B  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 4203  
 ; SOFTWARE: ProPatent version 1.0  
 ; SEQ ID NO 4131  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:

; OTHER INFORMATION: sequence located in PNCV OR SEQ at 131 140 and may interact with  
 ; OTHER INFORMATION: Sequence 4130 in this patent.  
 US-09-572-404B-4131

Query Match 36.4%; Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ARKS 4  
 DB 6 ARKS 9

#### RESULT 20

; Sequence 741, Application US/09572270A  
 ; Publication No. US20030148368A1  
 ; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Inter- complementary peptide listing  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/09/572,270A  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 1144  
 ; SOFTWARE: ProPatent version 1.0  
 ; SEQ ID NO 741  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis Thaliana  
 ; OTHER INFORMATION: Sequence located in Unknown at 7 16 and may interact with  
 US-09-572-270A-741

Query Match 36.4%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ARKS 4  
 DB 1 ARKS 4

#### RESULT 21

; Sequence 741, Application US/09572270A  
 ; Publication No. US20030148368A1  
 ; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Inter- complementary peptide listing  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/09/572,270A  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 1144  
 ; SOFTWARE: ProPatent version 1.0  
 ; SEQ ID NO 745  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis Thaliana  
 ; OTHER INFORMATION: Sequence located in Unknown at 7 16 and may interact with  
 US-09-572-270A-745

Query Match 36.4%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ARKS 4  
 DB 1 ARKS 4

#### RESULT 22

; Sequence 741, Application US/09572270A  
 ; Publication No. US20030148368A1  
 ; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Inter- complementary peptide listing  
 ; FILE REFERENCE: 760106.43005  
 ; CURRENT APPLICATION NUMBER: US/09/572,270A  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: ProPatent version 1.0  
 ; SEQ ID NO 1  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:

; OTHER INFORMATION: Description of Unknown sequence: A sequence of  
 ; OTHER INFORMATION: peptides from a random peptide library, that binds  
 ; OTHER INFORMATION: and internalizes in a PCR receptor constructed  
 ; OTHER INFORMATION: from 1134  
 US-09-572-270A-1

Query Match 36.4%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 ARKS 5  
 DB 7 ARKS 10

#### RESULT 23

; Sequence 288, Application US/090062  
 ; Publication No. US2003014264A1  
 ; GENERAL INFORMATION:

; APPLICANT: Lasky, Lawrence A.  
 ; APPLICANT: Sidhu, Sardeep S.

; APPLICANT: Held, Heike A.  
 ; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
 ; FILE REFERENCE: P1905R1  
 ; CURRENT APPLICATION NUMBER: US/10/190.082  
 ; CURRENT FILING DATE: 2002-07-03  
 ; PRIOR APPLICATION NUMBER: US 60/303.634  
 ; PRIOR FILING DATE: 2001-07-06  
 ; NUMBER OF SEQ ID NOS: 683  
 ; SEQ ID NO 288  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-10-190-082-288

Query Match 36.4% Score 4; 18 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKSR 5  
 Db 1 RKSR 4

RESULT 24  
 US-09-793-451-376  
 ; Sequence 376, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103PD6; TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129,20SU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version: 4.0  
 ; SEQ ID NO 376  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-376

Query Match 36.4% Score 4; 18 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKSR 5  
 Db 6 RKSR 9

RESULT 25  
 US-09-793-451-401  
 ; Sequence 401, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell

; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Elm M. Chaitana-Eid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129,20SU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version: 4.0  
 ; SEQ ID NO 401  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-401

Query Match 36.4% Score 4; 18 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKSR 5  
 Db 7 RKSR 10

RESULT 26  
 US-09-793-451-478  
 ; Sequence 478, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Elm M. Chaitana-Eid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129,20SU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version: 4.0  
 ; SEQ ID NO 478  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-478

Query Match 36.4% Score 4; 18 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKSR 5  
 Db 4 RKSR 7

RESULT 27  
 US-09-793-451-548  
 ; Sequence 548, Application US/09793451  
 ; Publication No. US20030157597A1

GENERAL INFORMATION:  
 APPLICANT: Arthur B. Raitano  
 APPLICANT: Daniel E.H. Afar  
 APPLICANT: Gazelle S. Rastegar  
 APPLICANT: Steve Chappell Mitchell  
 APPLICANT: Rene S. Hubert  
 APPLICANT: Pia M. Challita-Eid  
 APPLICANT: Mary Faris  
 APPLICANT: Aya Jakobovits  
 TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 FILE REFERENCE: 129.20SU2 EXPRESSED IN VARIOUS CANCERS  
 CURRENT APPLICATION NUMBER: US/09/793.451  
 PRIOR FILING DATE: 2001-02-26  
 PRIOR APPLICATION NUMBER: 60/184,558  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: 60/218,856  
 PRIOR FILING DATE: 2000-07-13  
 NUMBER OF SEQ ID NOS: 752  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 568  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-09-793-451-568

Query Match 36.4% Score 4: Db 12: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 2.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 Db 4 RKSR 7

RESULT 28  
 US-09-793-451-704  
 Sequence 704, Application US/09793451  
 Publication No. US20030157597A1  
 GENERAL INFORMATION:  
 APPLICANT: Arthur B. Raitano  
 APPLICANT: Daniel E.H. Afar  
 APPLICANT: Gazelle S. Rastegar  
 APPLICANT: Steve Chappell Mitchell  
 APPLICANT: Rene S. Hubert  
 APPLICANT: Pia M. Challita-Eid  
 APPLICANT: Mary Faris  
 APPLICANT: Aya Jakobovits  
 TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 FILE REFERENCE: 129.20SU2 EXPRESSED IN VARIOUS CANCERS  
 CURRENT APPLICATION NUMBER: US/09/793.451  
 PRIOR FILING DATE: 2001-02-26  
 PRIOR APPLICATION NUMBER: 60/184,558  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: 60/218,856  
 PRIOR FILING DATE: 2000-07-13  
 NUMBER OF SEQ ID NOS: 752  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 704  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-09-793-451-704

Query Match 36.4% Score 4: Db 12: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 2.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 Db 4 RKSR 7

RESULT 29  
 US-10-050-200-40  
 Sequence 40, Application US/05020040  
 Publication No. US20050000000A1  
 GENERAL INFORMATION:  
 APPLICANT: Raitano, Arthur  
 APPLICANT: Gazelle, Eve  
 APPLICANT: Rastegar, Daniel  
 APPLICANT: Mitchell, Steve  
 APPLICANT: Hubert, Rene  
 APPLICANT: Challita-Eid, Pia  
 APPLICANT: Faris, Mary  
 APPLICANT: Jakobovits, Aya  
 TITLE OF INVENTION: ANTICANCER AGENTS AND Peptide Substrates and Methods  
 FILE REFERENCE: 08/1117  
 CURRENT APPLICATION NUMBER: US/05/000,200  
 CURRENT FILING DATE: 2005-11-01  
 NUMBER OF SEQ ID NOS: 60  
 SOFTWARE: Patent Office  
 SEQ ID NO 40  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURES:  
 OTHER INFORMATION: PRT OF Anticancer  
 US-10-050-200-40

Query Match 36.4% Score 4: Db 12: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 2.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 RKSR 7  
 Db 5 RKSR 7

RESULT 30  
 US-10-040-805-12  
 Sequence 12, Application US/1004080512  
 Publication No. US20050000000A1  
 GENERAL INFORMATION:  
 APPLICANT: Raitano, Arthur  
 APPLICANT: Gazelle, Eve  
 APPLICANT: Rastegar, Daniel  
 APPLICANT: Mitchell, Steve  
 APPLICANT: Hubert, Rene  
 APPLICANT: Challita-Eid, Pia  
 APPLICANT: Faris, Mary  
 APPLICANT: Jakobovits, Aya  
 TITLE OF INVENTION: ANTICANCER AGENTS AND Peptide Substrates and Methods  
 FILE REFERENCE: 08/1117  
 CURRENT APPLICATION NUMBER: US/10/040,805-12  
 CURRENT FILING DATE: 2004-11-01  
 PRIOR APPLICATION NUMBER: US/05/000,200  
 PRIOR FILING DATE: 2005-11-01  
 PRIOR APPLICATION NUMBER: US/05/000,200  
 PRIOR FILING DATE: 2005-11-01  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Patent Office  
 SEQ ID NO 12  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 US-10-040-805-12

Query Match 36.4% Score 4: Db 12: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 2.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 RKSR 4  
 Db 5 RKSR 4

RESULT 41  
 US-09-429-549A-27  
 Sequence 27, Application US/09429549A  
 Patent No. US20020000000A1  
 GENERAL INFORMATION:  
 APPLICANT: THE UNIVERSITY OF MISSOURI  
 TITLE OF INVENTION: PHASE DISPLAY SELECTION OF ANTI-FUNGAL PROPERTIES  
 FILE REFERENCE: DMG 1521.1  
 CURRENT APPLICATION NUMBER: US/09/429,549A

2 CURRENT FILING DATE: 2001-04-10  
 2 PRIOR APPLICATION NUMBER: US 60/195,785  
 2 PRIOR FILING DATE: 2000-04-10  
 2 NUMBER OF SEQ ID NOS: 48  
 2 SOFTWARE: PatentIn version 3.0  
 2 SEQ ID NO 27  
 2 LENGTH: 15  
 2 TYPE: PRT  
 2 ORGANISM: Artificial Sequence  
 2 FEATURE:  
 2 NAME/KEY: DOMAIN  
 2 LOCATION: (1)..(15)  
 2 OTHER INFORMATION: Random peptide insert  
 US-09-829-549A-27

Query Match 36.4%; Score 4; ID 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3,400,927  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 7 MTAT 10  
 1111  
 Db 10 MTAT 13

RESULT 32  
 US-09-876-904A-186  
 2 Sequence 186; Application US/09876904A  
 2 Publication No. US20030072794A1  
 2 GENERAL INFORMATION:  
 2 APPLICANT: BOULIKAS, TENI  
 2 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (DETERMINES IN) AND THERAPEUTIC  
 2 AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/POSITIVE PEPTIDE  
 2 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 2 FILE REFERENCE: TB-2002-06  
 2 CURRENT APPLICATION NUMBER: US/09/876,904A  
 2 CURRENT FILING DATE: 2001-06-08  
 2 PRIOR APPLICATION NUMBER: US 60/210,925  
 2 PRIOR FILING DATE: 2000-06-09  
 2 NUMBER OF SEQ ID NOS: 629  
 2 SOFTWARE: PatentIn Ver. 2.1  
 2 SEQ ID NO 186  
 2 LENGTH: 15  
 2 TYPE: PRT  
 2 ORGANISM: Homo sapiens  
 2 FEATURE:  
 2 OTHER INFORMATION: Karyophilic peptide  
 US-09-876-904A-186

Query Match 36.4%; Score 4; ID 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3,400,927  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 2 RKSR 5  
 1111  
 Db 9 RKSR 12

RESULT 33  
 US-10-041-030-16  
 2 Sequence 16; Application US/10041030  
 2 Publication No. US20020150934A1  
 2 GENERAL INFORMATION:  
 2 APPLICANT: Powers, Scott  
 2 APPLICANT: MU, David  
 2 APPLICANT: Xiang, Phil  
 2 APPLICANT: Peng, Yue  
 2 APPLICANT: Tularik Inc.  
 2 TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Marmalium  
 2 FILE REFERENCE: 018781-006610US  
 2 CURRENT APPLICATION NUMBER: US/10/041,030  
 2 CURRENT FILING DATE: 2001-12-28  
 2 PRIOR APPLICATION NUMBER: US 60/259,502

2 PRIOR FILING DATE: 2001-04-10  
 2 NUMBER OF SEQ ID NOS: 48  
 2 SOFTWARE: PatentIn version 3.0  
 2 SEQ ID NO 16  
 2 LENGTH: 15  
 2 TYPE: PRT  
 2 ORGANISM: Artificial Sequence  
 2 FEATURE:  
 2 NAME/KEY: DOMAIN  
 2 LOCATION: (1)..(15)  
 2 OTHER INFORMATION: Random peptide insert  
 US-09-829-549A-27

Query Match 36.4%; Score 4; ID 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3,400,927  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 7 MTAT 10  
 1111  
 Db 10 MTAT 13

RESULT 34  
 US-09-829-549A-27  
 2 Sequence 27; Application US/09829549A  
 2 Publication No. US20030072794A1  
 2 GENERAL INFORMATION:  
 2 APPLICANT: BOULIKAS, TENI  
 2 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (DETERMINES IN) AND THERAPEUTIC  
 2 AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/POSITIVE PEPTIDE  
 2 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 2 FILE REFERENCE: TB-2002-06  
 2 CURRENT APPLICATION NUMBER: US/09/829,549A  
 2 CURRENT FILING DATE: 2001-06-08  
 2 PRIOR APPLICATION NUMBER: US 60/210,925  
 2 PRIOR FILING DATE: 2000-06-09  
 2 NUMBER OF SEQ ID NOS: 629  
 2 SOFTWARE: PatentIn Ver. 2.1  
 2 SEQ ID NO 16  
 2 LENGTH: 15  
 2 TYPE: PRT  
 2 ORGANISM: Homo sapiens  
 2 FEATURE:  
 2 OTHER INFORMATION: Karyophilic peptide  
 US-09-829-549A-27

Query Match 36.4%; Score 4; ID 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3,400,927  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 2 RKSR 5  
 1111  
 Db 9 RKSR 12

RESULT 35  
 US-10-041-030-16  
 2 Sequence 16; Application US/10041030  
 2 Publication No. US20020150934A1  
 2 GENERAL INFORMATION:  
 2 APPLICANT: Powers, Scott  
 2 APPLICANT: MU, David  
 2 APPLICANT: Xiang, Phil  
 2 APPLICANT: Peng, Yue  
 2 APPLICANT: Tularik Inc.  
 2 TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Marmalium  
 2 FILE REFERENCE: 018781-006610US  
 2 CURRENT APPLICATION NUMBER: US/10/041,030  
 2 CURRENT FILING DATE: 2001-12-28  
 2 PRIOR APPLICATION NUMBER: US 60/259,502

; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR APPLICATION NUMBER: US 07/744,768  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 27  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-802-077-27

Query Match: 27.3%; Score 3; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5, 10-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 RKS 4  
 III  
 DB 6 RKS 8

## RESULT 36

US-09-735-995-116  
 ; Sequence 116, Application US/09735995  
 ; Patent No. US200103402441

; GENERAL INFORMATION:  
 ; APPLICANT: Keating, Mark T.  
 ; APPLICANT: Splawski, Igor  
 ; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF *hERG* - A LONG QT  
 ; TITLE OF INVENTION: SYNDROME GENE  
 ; FILE REFERENCE: 2323-136  
 ; CURRENT APPLICATION NUMBER: US/09/735,995  
 ; CURRENT FILING DATE: 2000-12-14  
 ; PRIOR APPLICATION NUMBER: 09/226,012  
 ; PRIOR FILING DATE: 1999-01-06  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 116

; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-735-995-116

Query Match: 27.3%; Score 3; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5, 10-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 DMT 8  
 III  
 DB 6 DMT 8

## RESULT 37

US-09-802-096-10  
 ; Sequence 10, Application US/09802096  
 ; Patent No. US2001003839A1

; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Method of Preventing the onset of Allergic Disorders (as amended)  
 ; FILE REFERENCE: P0718P2C30S  
 ; CURRENT APPLICATION NUMBER: US/09/802,096  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 08/405,617  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07

; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR APPLICATION NUMBER: US 07/744,768  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 27  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-802-077-27

Query Match: 27.3%; Score 3; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5, 10-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 RKS 4  
 III  
 DB 6 RKS 8

; GENERAL INFORMATION:  
 ; APPLICANT: Keating, Mark T.  
 ; APPLICANT: Splawski, Igor  
 ; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF *hERG* - A LONG QT  
 ; TITLE OF INVENTION: SYNDROME GENE  
 ; FILE REFERENCE: 2323-136  
 ; CURRENT APPLICATION NUMBER: US/09/735,995  
 ; CURRENT FILING DATE: 2000-12-14  
 ; PRIOR APPLICATION NUMBER: 09/226,012  
 ; PRIOR FILING DATE: 1999-01-06  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 116

; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-735-995-116

Query Match: 27.3%; Score 3; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5, 10-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 RKS 4  
 III  
 DB 6 RKS 8

## RESULT 38

US-09-802-096-10  
 ; Sequence 10, Application US/09802096  
 ; Patent No. US2001003839A1

; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Method of Preventing the onset of Allergic Disorders (as amended)  
 ; FILE REFERENCE: P0718P2C30S  
 ; CURRENT APPLICATION NUMBER: US/09/802,096  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 08/405,617  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07

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? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
?   APPLICATION NUMBER: US/09/854,799
?   FILING DATE: 14-May-2001
?   CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
?   APPLICATION NUMBER: 08/392,459
?   FILING DATE: <Unknown>
?   APPLICATION NUMBER: US 07/618,066
?   FILING DATE: 14-NOV-1990
? ATTORNEY/AGENT INFORMATION:
?   NAME: King, William T.
?   REGISTRATION NUMBER: 30,954
?   REFERENCE/DOCKET NUMBER: SEQ 14542B
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: (215) 270-5015
?   TELEFAX: (215) 270-5090
? INFORMATION FOR SEQ ID NO: 52:
?   SEQUENCE CHARACTERISTICS:
?     LENGTH: 8 amino acids
?     TYPE: amino acid
?     TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-854-799-52

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Query Match      27.3% Score 3; LB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 TAI 10
DB      6 TAI 8

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RESULT 40
US-09-949-559-111
? Sequence 111: Application US/09949559
? Patent No. US20020151682A1
? GENERAL INFORMATION:
?   APPLICANT: Athwal, Diljeet Singh
?   APPLICANT: Brown, Derek Thomas
?   APPLICANT: Weir, Andrew Neil Charles
?   APPLICANT: Popplewell, Andrew George
?   APPLICANT: Chapman, Andrew Paul
?   APPLICANT: King, David John
? TITLE OF INVENTION: Biological Products
? FILE REFERENCE: Carp-0095
? CURRENT APPLICATION NUMBER: US/09/949,559
? PRIOR FILING DATE: 2001-12-20
? PRIOR APPLICATION NUMBER: 0013810.78R
? PRIOR FILING DATE: 2000-06-06
? PRIOR APPLICATION NUMBER: 09/875,221
? PRIOR FILING DATE: 2001-06-06
? NUMBER OF SEQ ID NOS: 130
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 111
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: IGS cassette-1
US-09-949-559-111

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Query Match      27.3% Score 3; LB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 TAI 10
DB      4 TAI 6

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RESULT 41
US-09-949-559-114
? Sequence 114: Application US/09949559
? Patent No. US20020151682A1
? GENERAL INFORMATION:
?   APPLICANT: Athwal, Diljeet Singh
?   APPLICANT: Brown, Derek Thomas
?   APPLICANT: Weir, Andrew Neil Charles
?   APPLICANT: Popplewell, Andrew George
?   APPLICANT: Chapman, Andrew Paul
?   APPLICANT: King, David John
? TITLE OF INVENTION: Biological Products
? FILE REFERENCE: Carp-0095
? CURRENT APPLICATION NUMBER: US/09/949,559
? PRIOR FILING DATE: 2001-12-20
? PRIOR APPLICATION NUMBER: 0013810.78R
? PRIOR FILING DATE: 2000-06-06
? PRIOR APPLICATION NUMBER: 09/875,221
? PRIOR FILING DATE: 2001-06-06
? NUMBER OF SEQ ID NOS: 130
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 114
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: IGS cassette-1
US-09-949-559-114

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Query Match      27.3% Score 3; LB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 TAI 10
DB      4 TAI 6

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RESULT 42
US-09-949-559-117
? Sequence 117: Application US/09949559
? Patent No. US20020151682A1
? GENERAL INFORMATION:
?   APPLICANT: Athwal, Diljeet Singh
?   APPLICANT: Brown, Derek Thomas
?   APPLICANT: Weir, Andrew Neil Charles
?   APPLICANT: Popplewell, Andrew George
?   APPLICANT: Chapman, Andrew Paul
?   APPLICANT: King, David John
? TITLE OF INVENTION: Biological Products
? FILE REFERENCE: Carp-0095
? CURRENT APPLICATION NUMBER: US/09/949,559
? PRIOR FILING DATE: 2001-12-20
? PRIOR APPLICATION NUMBER: 0013810.78R
? PRIOR FILING DATE: 2000-06-06
? PRIOR APPLICATION NUMBER: 09/875,221
? PRIOR FILING DATE: 2001-06-06
? NUMBER OF SEQ ID NOS: 130
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 117
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: IGS cassette-1
US-09-949-559-117

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Query Match      27.3% Score 3; LB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CPAL amino terminal
; OTHER INFORMATION: sequence motif
US-09-362-286-9

Query Match      27.3%   Score 3: DB 10: Length 8:
Best Local Similarity 100.0%   Pred. No. 5.1e-05:
Matches      3: Conservative      0: Mismatches      0: Gaps      0:

QY      1 ARK 3
Db      2 ARK 4

RESULT 47
US-09-983-802-330
; Sequence 130, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/227,457
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/14684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,792
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,940
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,922
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,796
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,955
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,944
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,980
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,963
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,956
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,951
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 130
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-330

Query Match      27.3%   Score 3: DB 10: Length 8:
Best Local Similarity 100.0%   Pred. No. 5.1e-05:
Matches      3: Conservative      0: Mismatches      0: Gaps      0:

QY      6 DB1 4
Db      1
      1 DB1 4

RESULT 48
US-09-983-802-330
; Sequence 47, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/227,457
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/14684
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70 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
71 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
72 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
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100 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

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SEQUENCE: Patent In Ver. 2.0

SEQ ID NO 420

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

US-09-981 802-420

Query Match 27.3% Score 42 GR 111 Length 8

Best local Similarity 100.0% Prod No 511091

Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 9 A1K 11

111

Db 2 A1K 4

RESULT 49

US-09-875-221A-111

Sequence 111, Application US/0987522:A

Publication No. US2003026805A1

GENERAL INFORMATION:

APPLICANT: Athwal, Diljeet Singh

APPLICANT: Brown, Derek Thomas

APPLICANT: Weir, Andrew Neil Charles

APPLICANT: Popplewell, Andrew George

APPLICANT: Chapman, Andrew Paul

```

1 APPLICATION NUMBER: 1997-07-08
2 TITLE OF INVENTION: EARLIER APPLICATION NUMBER: 60/051,916
3 CURRENT APPLICATION NUMBER: 60/051,916
4 CURRENT FILING DATE: 1997-07-08
5 PRIOR APPLICATION NUMBER: 60/051,916
6 PRIOR FILING DATE: 1997-07-08
7 NUMBER OF SEQ ID NOS: 8
8 SOFTWARE: Patent In Ver. 2.0
9 SEQ ID NO 111
10 LENGTH: 8
11 TYPE: PRT
12 ORGANISM: Homo sapiens
13 OTHER INFORMATION: US-09-981 802-420
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SEQUENCE: Patent In Ver. 2.0

SEQ ID NO 114

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

US-09-875-221A-111

Query Match 27.3% Score 42 GR 111 Length 8

Best local Similarity 100.0% Prod No 511091

Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 9 A1K 11

111

Db 2 A1K 4

RESULT 49

US-09-875-221A-111

Sequence 111, Application US/0987522:A

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